76496

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From: Mertz, Prema
Sent: Wednesday, September 25, 2002 2:48 PM
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Please search SEQ ID NO:1, 3, wit DNA databases.

Please searc SEQ ID NO:2, 4 with protein databases.

Thanks

Prema Mertz, Ph.D.
Primary Examiner
Art Unit 1646
Crystal Mall 1, Room 10E-01
United States Patent & Trademark Office
(703) 308-4229

CRFC

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher:
Phone:
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Date Picked Up: 9/26/02
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Searcher Prep/Review:
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TYPE OF SEARCH:
NA Sequences: 2
AA Sequences: 2
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.: ΦG
WWW/Internet:
Other (specify):

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                    GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:          September 27, 2002, 20:16:49 ; Search time 2277.04 Seconds
                                                (without alignments)
                                                9530.275 Million cell updates/sec

Title:           US-09-904-954-1
Perfect score:   1037
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters:      3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                31:  em_htg_inv:*
                32:  em_htg_other:*
                33:  em_htgo_inv:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

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     2    1037   100.0   1037  6  AR080871              AR080871 Sequence
     3    1037   100.0   1037  6  AR164469              AR164469 Sequence
     4    1037   100.0   1037  6  I20809                I20809 Sequence 1
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     8     736    71.0    758  9  HUMEFL2               L37360 Homo sapien
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1037)
  AUTHORS   Beckmann,M.Patricia. and Cerretti,D.P.
  TITLE     Cytokines that bind the cell surface receptor hek
  JOURNAL   Patent: US 5738844-A 1 14-APR-1998;
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ORIGIN

  Query Match            100.0%;  Score 1037;  DB 6;  Length 1037;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-151;
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DEFINITION  Sequence 1 from patent US 5969110.
ACCESSION   AR080871
VERSION     AR080871.1  GI:10007600
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1037)
  AUTHORS   Beckmann,M.Patricia and Cerretti,D.P.
  TITLE     Antibodies that bind hek ligands
  JOURNAL   Patent: US 5969110-A 1 19-OCT-1999;
FEATURES             Location/Qualifiers
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BASE COUNT      187 a    343 c    337 g    170 t
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1037)
  AUTHORS   Beckmann,M.Patricia and Cerretti,D.P.
  TITLE     Cytokines that bind the cell surface receptor Hek
  JOURNAL   Patent: US 6274117-A 1 14-AUG-2001;
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Db      781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCT 840

Qy      841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900
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Db      841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900

Qy      901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960
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Db      901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960

Qy      961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020
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Db      961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020

Qy     1021 GTCTCGTTCCAAGATCC 1037
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Db     1021 GTCTCGTTCCAAGATCC 1037


RESULT   4
I20809
LOCUS       I20809                 1037 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 1 from patent US 5516658.
ACCESSION   I20809
VERSION     I20809.1  GI:1601164
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1037)
  AUTHORS   Beckmann,M.Patricia. and Cerretti,D.P.
  TITLE     DNA encoding cytokines that bind the cell surface receptor hek
  JOURNAL   Patent: US 5516658-A 1 14-MAY-1996;
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     source          1..1037
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ORIGIN
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  Matches 1037;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGC 60
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Qy       61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120
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Db       61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120

Qy      121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180

Qy      181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240
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Db      181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240

Qy      241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300
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Db      241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300

Qy      301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360
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Db      301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360

Qy      361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420
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Db      361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420

Qy      421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480
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Db      421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480

Qy      481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540
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Db      481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540

Qy      541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600
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Qy      601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660
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Db      601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660

Qy      661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720
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Db      661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720

Qy      721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780
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Db      721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780

Qy      781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCT 840
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Db      781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCT 840

Qy      841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900
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Db      841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900

Qy      901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960
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Qy      961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020
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Db      961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020

Qy     1021 GTCTCGTTCCAAGATCC 1037
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Db     1021 GTCTCGTTCCAAGATCC 1037


RESULT 5
BC017722
LOCUS       BC017722                1769 bp    mRNA    linear   PRI 06-DEC-2001
DEFINITION  Homo sapiens, ephrin-A3, clone MGC:21335 IMAGE:4397263, mRNA,
            complete cds.
ACCESSION   BC017722
VERSION     BC017722.1  GI:17389356
KEYWORDS    MGC.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1769)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 27 Row: d Column: 19.
FEATURES             Location/Qualifiers
     source          1. .1769
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BASE COUNT      343 a    577 c    514 g    335 t
ORIGIN


  Query Match             95.4%;  Score 988.8;  DB 9;  Length 1769;
  Best Local Similarity   99.8%;  Pred. No. 4.7e-144;
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Qy       26 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATG 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       14 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATG 73

Qy       86 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 145
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Db       74 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 133

Qy      146 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 205
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Db      134 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 193

Qy      206 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 265
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Db      194 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 253

Qy      266 TACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGACCGGGGCCCGGAGGC 325
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Db      254 TACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGACCGGGGCCCGGAGGC 313

Qy      326 GGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCC 385
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Db      314 GGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCC 373

Qy      386 AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAG 445
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Qy      506 CACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATG 565
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Qy      566 AAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTC 625
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Db      554 AAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTC 613

Qy      626 CCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAG 685
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Qy      686 AACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACAC 745
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Qy      746 CTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGC 805
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Qy      806 CCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCC 865
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Db      794 CCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCC 853

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Qy      986 CAAGCACGGGGACAGCCATGGTCCCGAGCAG 1017
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Db      974 CAAGCACGGGGACAGCCATGGTCCCGGGCGG 1005


RESULT   6
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LOCUS       HSU14187                 987 bp    mRNA    linear   PRI 04-FEB-1995
DEFINITION  Human receptor tyrosine kinase ligand LERK-3 (EPLG3) mRNA, complete
            cds.
ACCESSION   U14187
VERSION     U14187.1  GI:642832
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   Kozlosky,C.J., Maraskovsky,E., McGrew,J.T., VandenBos,T., Teepe,M.,
            Lyman,S.D., Srinivasan,S., Fletcher,F.A., Gayle,R.B. III,
            Cerretti,D.P. and Beckmann,M.P.
  TITLE     Ligands for the receptor tyrosine kinases hek and elk: isolation of
            cDNAs encoding a family of proteins
  JOURNAL   Oncogene 10 (2), 299-306 (1995)
  MEDLINE   95140419
REFERENCE   2  (bases 1 to 987)
  AUTHORS   Cerretti,D.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1994) Immunex Corp., 51 University St., Seattle,
            WA 98101, USA
FEATURES             Location/Qualifiers
     source          1. .987
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                     /db_xref="taxon:9606"
     gene            1. .987
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     CDS             58. .774
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                     /note="membrane-bound protein;
                     glycosyl-phosphatidylinositol (GPI) anchored"
                     /codon_start=1
                     /product="LERK-3"
                     /protein_id="AAC50078.1"
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BASE COUNT      176 a    329 c    323 g    159 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 9.9e-144;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       26 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCTCCGGGGATG 85
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Db        1 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCTCCGGGGATG 60

Qy       86 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 145
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Db       61 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 120

Qy      146 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 205
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Qy      206 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 265
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Db      181 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 240

Qy      266 TACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGACCGGGGCCCGGAGGC 325
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Qy    386 AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAG 445
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Qy    446 TTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGC 505
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Db    421 TTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGC 480

Qy    506 CACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATG 565
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Db    481 CACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATG 540

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Qy    626 CCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAG 685
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Qy    686 AACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACAC 745
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Db    721 CTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGC 780

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Qy    986 CAAGCACGGGGACAGCCATGGGTCCCG 1012
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RESULT    7
AR004292
LOCUS       AR004292                1070 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 8 from patent US 5747033.
ACCESSION   AR004292
VERSION     AR004292.1  GI:3965171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1070)
  AUTHORS   Davis,S., Gale,N.W., Aldrich,T.H., Maisonpierre,P.C., Goldfarb,M.
            and Yancopoulos,G.D.
  TITLE     Method of enhancing the biological activity of Eph family ligands
  JOURNAL   Patent: US 5747033-A 8 05-MAY-1998;
FEATURES             Location/Qualifiers
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Qy     44 GGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTG 103
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Qy    104 CTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGG 163
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Qy    284 AGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTG 343
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Qy    344 CTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGC 403
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Qy    404 TGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAG 463
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Qy    704 CTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGC 763
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Db    775 AGAGATGGGGCGGGGNTTGGAAGGAGNAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAG 834

Qy    884 TGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCG 943
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Db    835 TGGGCCTAGACCCCTCCTCCCATGGTTAGAAGTGGGGCCTGNACCATACATCTGTGTCCG 894

Qy    944 CCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCA 1003
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Db    895 CCCCCTCTACCCCTTCCCCCCANGTAGGGNACTGTAGTGGACCAAGCACGGNGACAGACA 954

Qy   1004 TGGGTCCCGAGCAGG 1018
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Db    955 TGGNTCCCGGGNGGG 969

RESULT    8
HUMEFL2
LOCUS       HUMEFL2                  758 bp    mRNA    linear   PRI 09-NOV-1994
DEFINITION  Homo sapiens (clone hEHK1-L) EHK1 receptor tyrosine kinase ligand
            (EFL-2) mRNA, complete cds.
ACCESSION   L37360
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VERSION     L37360.1  GI:567003
KEYWORDS    ligand.
SOURCE      Homo sapiens cDNA to mRNA.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 758)
  AUTHORS   Davis,S., Gale,N.W., Aldrich,T.H., Maisonpierre,P.C., Lhotak,V.,
            Pawson,T., Goldfarb,M. and Yancopoulos,G.D.
  TITLE     Ligands for EPH-related receptor tyrosine kinases that require
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  JOURNAL   Science (1994) In press
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                     RWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVF
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BASE COUNT      139 a    255 c    239 g    125 t
ORIGIN


  Query Match             71.0%;  Score 736;  DB 9;  Length 758;
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Qy        425 GCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTG 484
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Qy        485 GGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTG 544
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Qy        545 CACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGG 604
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Db        469 CACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGG 528

Qy        605 GAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTG 664
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Qy        665 CTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGG 724
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Qy        725 ACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACG 784
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RESULT   9
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LOCUS       AC021890               175826 bp    DNA     linear   HTG 10-NOV-2000
DEFINITION  Homo sapiens chromosome 3 clone RP11-498A2, WORKING DRAFT SEQUENCE,
            22 unordered pieces.
ACCESSION   AC021890
VERSION     AC021890.12  GI:11128300
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 175826)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
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            and Gibbs,R.
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  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 175826)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JAN-2000) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 9, 2000 this sequence version replaced gi:9719697.
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                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: HMZE
                Center clone name: RP11-498A2
            -------------- Summary Statistics
                Sequencing vector: M13; L08821
                Chemistry: Dye-terminator Big Dye: 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 144734 bases at least Q40
                Consensus quality: 162873 bases at least Q30
                Consensus quality: 169424 bases at least Q20
                Estimated insert size: 170770; sum-of-contigs estimation
                Quality coverage: 0x in Q20 bases; agarose-fp estimation
                Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation
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            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 22 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
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            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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ORIGIN


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RESULT  10
AB051678
LOCUS       AB051678                1838 bp    mRNA    linear   VRT 20-SEP-2001
DEFINITION  Danio rerio mRNA for ephrin-A3, complete cds.
ACCESSION   AB051678
VERSION     AB051678.1  GI:14196230
KEYWORDS    .
SOURCE      Danio rerio cDNA to mRNA.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 1838)
  AUTHORS   Hirate,Y., Mieda,M., Harada,T., Yamasu,K. and Okamoto,H.
  TITLE     Identification of ephrin-A3 and novel genes specific to the
            midbrain-MHB in embryonic zebrafish by ordered differential display
  JOURNAL   Mechanisms of development. 107 (1-2), 83-96 (2001)
  MEDLINE   21412237
REFERENCE   2  (bases 1 to 1838)
  AUTHORS   Hirate,Y., Mieda,M., Harada,T., Yamasu,K. and Okamoto,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-NOV-2000) Yoshikazu Hirate, Brain Science Institute,
            RIKEN, Lab. of Developmental Gene Regulation; 2-1, Hirosawa,
            Wako-shi, Saitama 351-0198, Japan (E-mail:hirate@brain.riken.go.jp,
            Tel:81-48-467-9713, Fax:81-48-467-9714)
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                     PIKFSEKFQRYSAFSLGYEFHVGQEYYYISTPTHHHGRSCLRLRVYVCCSTASDSDDE
                     PQPTEPDYTLRPNIKIDDLDDYDNPEVPKLEKSISGSSPSRDRLLLTVASLLLIALSV
                     S"
BASE COUNT      474 a    458 c    437 g    469 t
ORIGIN


  Query Match             24.4%;  Score 253;  DB 5;  Length 1838;
  Best Local Similarity   68.0%;  Pred. No. 4.2e-30;
  Matches  399;  Conservative    0;  Mismatches  155;  Indels   33;  Gaps    2;

Qy    175 CCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGT 234
          | |||| |||||  |||||||||| || |||   |  || ||    |||||||||||  |
Db    621 CAGGCACGCGGTACACTGGAACAGTTCAAACATACTACTTCGTAAGGAGGGCTACACGTT 680

Qy    235 GCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGT 294
          ||||||||| || |||||||||||||| || ||||| || ||||||||||||
Db    681 GCAGGTGAATGTCAACGACTATCTGGACATCTACTGTCCTCACTACAACAGC-------- 732

Qy    295 GGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGT 354
                              | |   | |||   || || ||||| ||||| ||||||||
Db    733 -------------------AGTCAGAGGGGCATCGCGGAACAGTATGTGCTCTACATGGT 773

Qy    355 GAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAA 414
           ||      ||| ||||| |||||  || |    | ||||||||||||||||||||| ||
Db    774 CAGTTATCGCGGTTACCGGACCTGTGACCCACAGCTGGGCTTCAAGCGCTGGGAGTGTAA 833

Qy    415 CCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGC 474
          ||| || |||||||| ||    |||||||| ||||| |||||||||||||||||||||||
Db    834 CCGTCCTCACGCCCCTCATGCTCCCATCAAATTCTCAGAGAAGTTCCAGCGCTACAGCGC 893

Qy    475 CTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCAC 534
          |||||| || ||||||||||| ||||  ||||| ||||| || || |||||||| |||||
Db    894 CTTCTCGCTCGGCTACGAGTTTCACGTTGGCCAGGAGTATTATTATATCTCCACACCCAC 953

Qy    535 TCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATC 594
          |||  |||    | |||  || |||||  | |  |||| |||||||||| |  |  ||||
Db    954 TCATCACCACGGCCGGAGCTGCCTGAGATTAAGAGTGTACGTCTGCTGCTCAACAGCATC 1013

Qy    595 GCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAA 654
            | || |  ||  ||||    || ||    ||  | | |||  || | || ||  | ||
Db   1014 TGATTCAGATGATGAGCCACAGCCTACAGAGCCAGACTACACTCTGAGACCTAACATCAA 1073

Qy    655 GATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAG 714
           ||| |||  || || |||| |      || || ||  |||| ||||| || ||||||||
Db   1074 AATCGACGACCTCGATGACTAT------GATAATCCCGAGGTTCCCAAACTGGAGAAGAG 1127

Qy    715 CATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGG 761
          ||||||||| | ||| ||     | || |  || | |||  | ||||
Db   1128 CATCAGCGGCAGCAGTCCATCCAGAGACCGGCTTCTCCTAACAGTGG 1174


RESULT  11
AY045577
LOCUS       AY045577                 355 bp    mRNA    linear   ROD 25-AUG-2001
DEFINITION  Rattus norvegicus ephrin A3 mRNA, partial cds.
ACCESSION   AY045577
VERSION     AY045577.1  GI:15290522
KEYWORDS    .
SOURCE      Norway rat.
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  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 355)
  AUTHORS   Munoz,J.J., Alonso-C,L.M., Sacedon,R., Crompton,T., Vicente,A.,
            Jimenez,E., Varas,A. and Zapata,A.G.
  TITLE     Expression and function of the Eph A receptors and their ligands
            ephrins A in the rat thymus
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 355)
  AUTHORS   Munoz,J.J., Alonso-C,L.M., Sacedon,R., Crompton,T., Vicente,A.,
            Jimenez,E., Varas,A. and Zapata,A.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUL-2001) Cell Biology, Complutense University of
            Madrid, Av. Complutense, Madrid 28040, Spain
FEATURES             Location/Qualifiers
     source          1..355
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     CDS             <1..>355
                     /note="Eph-related receptor tyrosine kinases ligand"
                     /codon_start=1
                     /product="ephrin A3"
                     /protein_id="AAK92219.1"
                     /db_xref="GI:15290523"
                     /translation="CPHYNSSGPGGGAEQYVLYMVNLSGYRTCNASQGSKRWECNRQH
                     ASHSPIKFSEKFQRYSAFSLGYEFHAGQEYYYISTPTHNLHWKCLRMKVFVCCASKDF
                     EGENPQVPKLEKSISG"
BASE COUNT       86 a    109 c     96 g     64 t
ORIGIN


  Query Match             23.3%;  Score 241.8;  DB 10;  Length 355;
  Best Local Similarity   87.7%;  Pred. No. 3e-28;
  Matches  264;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy    312 CGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACC 371
          | ||||| || |||||||| || |||||||| || |||||||||| ||  | ||||||||
Db     20 CAGGGCCTGGCGGCGGGGCGGAACAGTACGTACTATACATGGTGAACCTGAGCGGCTACC 79

Qy    372 GCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGC 431
          ||||||||||||||||||| |||| |||||||||||| |||||||||| ||||||| |||
Db     80 GCACCTGCAACGCCAGCCAAGGCTCCAAGCGCTGGGAATGCAACCGGCAGCACGCCTCGC 139

Qy    432 ACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACG 491
          ||||||||||||||||||| ||||||||||||||||||||||||||||| |||||||| |
Db    140 ACAGCCCCATCAAGTTCTCCGAGAAGTTCCAGCGCTACAGCGCCTTCTCGCTGGGCTATG 199

Qy    492 AGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGA 551
          | ||||| |||||||| || |||||||| |||||||||||||||||||||||||| ||||
Db    200 AATTCCATGCCGGCCAAGAATACTACTATATCTCCACGCCCACTCACAACCTGCATTGGA 259

Qy    552 AGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGC 611
          ||||||||||||||||||||||||||||||||||||||| |         || ||||| |
Db    260 AGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAAAGACTTTGAGGGAGAGAATC 319

Qy    612 C 612
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Db    320 C 320


RESULT  12
U92885
LOCUS       U92885                  2535 bp    DNA     linear   ROD 07-FEB-1998
DEFINITION  Mus musculus LERK-3 (Epl3) gene, partial cds.
ACCESSION   U92885
VERSION     U92885.1  GI:2843098
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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REFERENCE   1  (bases 1 to 2535)
  AUTHORS   Cerretti,D.P. and Nelson,N.
  TITLE     Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
            mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
            conservation of intron/exon structure
  JOURNAL   Genomics 47 (1), 131-135 (1998)
  MEDLINE   98126446
REFERENCE   2  (bases 1 to 2535)
  AUTHORS   Cerretti,D.P. and Nelson,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-MAR-1997) Molecular Biology, Immunex Corp., 51
            University Street, Seattle, WA 98101, USA
FEATURES             Location/Qualifiers
     source          1. .2535
                     /organism="Mus musculus"
                     /strain="129"
                     /db_xref="taxon:10090"
                     /chromosome="3"
     gene            1. .2535
                     /gene="Epl3"
     CDS             join(<926. .1215,1543. .1608,1793. .1870,2111. .2241)
                     /gene="Epl3"
                     /note="GPI-anchored ligand"
                     /codon_start=2
                     /product="LERK-3"
                     /protein_id="AAC39961.1"
                     /db_xref="GI:2843099"
                     /translation="LRREGYTVQVNVNDYLDIYCPHYNSSGPGGGAEQYVLYMVNLSG
                     YRTCNASQGSKRWECNRQHASHSPIKFSEKFQRYSAFSLGYEFHAGQEYYYISTPTHN
                     LHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKS
                     ISGTSPKREHLPLAVGIAFFLMTLLAS"
     exon            926. .1215
                     /gene="Epl3"
                     /number=2
     mRNA            join(<926. .1215,1543. .1608,1793. .1870,2111. .2535)
                     /gene="Epl3"
                     /product="LERK-3"
     exon            1543. .1608
                     /gene="Epl3"
                     /number=3
     exon            1793. .1870
                     /gene="Epl3"
                     /number=4
     exon            2111. .2535
                     /gene="Epl3"
                     /number=5
BASE COUNT      532 a    700 c    758 g    545 t
ORIGIN


  Query Match             21.4%;  Score 222;  DB 10;  Length 2535;
  Best Local Similarity   84.7%;  Pred. No. 2.6e-25;
  Matches  271;  Conservative    0;  Mismatches   25;  Indels   24;  Gaps    1;

Qy        205 CCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 264
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 CCACAGCCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 979

Qy        265 TTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGG 324
              |||||| ||||||||||||||||                        | ||||| || ||
Db        980 TTACTGTCCGCACTACAACAGCT------------------------CAGGGCCTGGCGG 1015

Qy        325 CGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGC 384
              |||||| ||||||||||||||||||||||||| ||  | |||||||||||||||||||||
Db       1016 CGGGGCGGAGCAGTACGTGCTGTACATGGTGAACCTGAGCGGCTACCGCACCTGCAACGC 1075

Qy        385 CAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAA 444
              |||||| |||| |||||||||||| ||||||||||| ||||||| ||||||||||||||||
Db       1076 CAGCCAAGGCTCCAAGCGCTGGGAATGCAACCGGCAGCACGCCTCGCACAGCCCCATCAA 1135

Qy        445 GTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGG 504
              |||||| |||||||||||||| |||||||||||||| |||||||| || ||||| |||||
Db       1136 GTTCTCCGAGAAGTTCCAGCGTTACAGCGCCTTCTCGCTGGGCTATGAATTCCATGCCGG 1195
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```
Qy        505 CCACGAGTACTACTACATCT 524
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Db       1196 CCAAGAATACTACTACATCT 1215


RESULT 13
AC104632/c
LOCUS       AC104632              289579 bp    DNA     linear   HTG 29-DEC-2001
DEFINITION  Mus musculus clone rp23-368d24 strain C57BL/6J, WORKING DRAFT
            SEQUENCE, 72 unordered pieces.
ACCESSION   AC104632
VERSION     AC104632.2  GI:17998594
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 289579)
  AUTHORS   Hua,A. and Roe,B.A.
  TITLE     Mus musculus BAC Clone rp23-368d24
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 289579)
  AUTHORS   Hua,A. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-DEC-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT     On Dec 29, 2001 this sequence version replaced gi:17861055.
            -------------- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            ----------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 72 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *          1     2055: contig of 2055 bp in length
            *       2056     2155: gap of unknown length
            *       2156     4235: contig of 2080 bp in length
            *       4236     4335: gap of unknown length
            *       4336     6526: contig of 2191 bp in length
            *       6527     6626: gap of unknown length
            *       6627     9454: contig of 2828 bp in length
            *       9455     9554: gap of unknown length
            *       9555    12042: contig of 2488 bp in length
            *      12043    12142: gap of unknown length
            *      12143    14176: contig of 2034 bp in length
            *      14177    14276: gap of unknown length
            *      14277    16599: contig of 2323 bp in length
            *      16600    16699: gap of unknown length
            *      16700    18844: contig of 2145 bp in length
            *      18845    18944: gap of unknown length
            *      18945    21106: contig of 2162 bp in length
            *      21107    21206: gap of unknown length
            *      21207    23193: contig of 1987 bp in length
            *      23194    23293: gap of unknown length
            *      23294    25652: contig of 2359 bp in length
            *      25653    25752: gap of unknown length
            *      25753    27729: contig of 1977 bp in length
            *      27730    27829: gap of unknown length
            *      27830    30718: contig of 2889 bp in length
            *      30719    30818: gap of unknown length
            *      30819    33823: contig of 3005 bp in length
            *      33824    33923: gap of unknown length
            *      33924    35961: contig of 2038 bp in length
            *      35962    36061: gap of unknown length
            *      36062    38732: contig of 2671 bp in length
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*    38733    38832: gap of unknown length
*    38833    40937: contig of 2105 bp in length
*    40938    41037: gap of unknown length
*    41038    43594: contig of 2557 bp in length
*    43595    43694: gap of unknown length
*    43695    45995: contig of 2301 bp in length
*    45996    46095: gap of unknown length
*    46096    48083: contig of 1988 bp in length
*    48084    48183: gap of unknown length
*    48184    50630: contig of 2447 bp in length
*    50631    50730: gap of unknown length
*    50731    53982: contig of 3252 bp in length
*    53983    54082: gap of unknown length
*    54083    56167: contig of 2085 bp in length
*    56168    56267: gap of unknown length
*    56268    59028: contig of 2761 bp in length
*    59029    59128: gap of unknown length
*    59129    61945: contig of 2817 bp in length
*    61946    62045: gap of unknown length
*    62046    65116: contig of 3071 bp in length
*    65117    65216: gap of unknown length
*    65217    67626: contig of 2410 bp in length
*    67627    67726: gap of unknown length
*    67727    70795: contig of 3069 bp in length
*    70796    70895: gap of unknown length
*    70896    73334: contig of 2439 bp in length
*    73335    73434: gap of unknown length
*    73435    75894: contig of 2460 bp in length
*    75895    75994: gap of unknown length
*    75995    78387: contig of 2393 bp in length
*    78388    78487: gap of unknown length
*    78488    80841: contig of 2354 bp in length
*    80842    80941: gap of unknown length
*    80942    84112: contig of 3171 bp in length
*    84113    84212: gap of unknown length
*    84213    87107: contig of 2895 bp in length
*    87108    87207: gap of unknown length
*    87208    90387: contig of 3180 bp in length
*    90388    90487: gap of unknown length
*    90488    92854: contig of 2367 bp in length
*    92855    92954: gap of unknown length
*    92955    96442: contig of 3488 bp in length
*    96443    96542: gap of unknown length
*    96543    98997: contig of 2455 bp in length
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*    99098   102593: contig of 3496 bp in length
*   102594   102693: gap of unknown length
*   102694   105584: contig of 2891 bp in length
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*   108443   108542: gap of unknown length
*   108543   111917: contig of 3375 bp in length
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*   112018   116076: contig of 4059 bp in length
*   116077   116176: gap of unknown length
*   116177   119383: contig of 3207 bp in length
*   119384   119483: gap of unknown length
*   119484   123902: contig of 4419 bp in length
*   123903   124002: gap of unknown length
*   124003   127609: contig of 3607 bp in length
*   127610   127709: gap of unknown length
*   127710   131621: contig of 3912 bp in length
*   131622   131721: gap of unknown length
*   131722   135933: contig of 4212 bp in length
*   135934   136033: gap of unknown length
*   136034   140801: contig of 4768 bp in length
*   140802   140901: gap of unknown length
*   140902   144622: contig of 3721 bp in length
*   144623   144722: gap of unknown length
*   144723   148869: contig of 4147 bp in length
*   148870   148969: gap of unknown length
*   148970   153203: contig of 4234 bp in length
*   153204   153303: gap of unknown length
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          *    157195    157294: gap of unknown length
          *    157295    162013: contig of 4719 bp in length
          *    162014    162113: gap of unknown length
          *    162114    167799: contig of 5686 bp in length
          *    167800    167899: gap of unknown length
          *    167900    173081: contig of 5182 bp in length
          *    173082    173181: gap of unknown length
          *    173182    180558: contig of 7377 bp in length
          *    180559    180658: gap of unknown length
          *    180659    186794: contig of 6136 bp in length
          *    186795    186894: gap of unknown length
          *    186895    192068: contig of 5174 bp in length
          *    192069    192168: gap of unknown length
          *    192169    198394: contig of 6226 bp in length
          *    198395    198494: gap of unknown length
          *    198495    203084: contig of 4590 bp in length
          *    203085    203184: gap of unknown length
          *    203185    208688: contig of 5504 bp in length
          *    208689    208788: gap of unknown length
          *    208789    214457: contig of 5669 bp in length
          *    214458    214557: gap of unknown length
          *    214558    219456: contig of 4899 bp in length
          *    219457    219556: gap of unknown length
          *    219557    226019: contig of 6463 bp in length
          *    226020    226119: gap of unknown length
          *    226120    234001: contig of 7882 bp in length
          *    234002    234101: gap of unknown length
          *    234102    241499: contig of 7398 bp in length
          *    241500    241599: gap of unknown length
          *    241600    249134: contig of 7535 bp in length
          *    249135    249234: gap of unknown length
          *    249235    259781: contig of 10547 bp in length
          *    259782    259881: gap of unknown length
          *    259882    267444: contig of 7563 bp in length
          *    267445    267544: gap of unknown length
          *    267545    279432: contig of 11888 bp in length
          *    279433    279532: gap of unknown length
          *    279533    289579: contig of 10047 bp in length.
FEATURES             Location/Qualifiers
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="rp23-368d24"
                     /clone_lib="RPCI mouse BAC library 23"
BASE COUNT    70974 a  71815 c  70765 g  68626 t   7399 others
ORIGIN


  Query Match             21.4%;  Score 222;  DB 2;  Length 289579;
  Best Local Similarity   84.7%;  Pred. No. 1.2e-25;
  Matches  271;  Conservative    0;  Mismatches   25;  Indels   24;  Gaps    1;

Qy        205 CCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 264
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185995 CCACAGCCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 185936

Qy        265 TTACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGG 324
              |||||| ||||||||||||||||                        | ||||| || ||
Db     185935 TTACTGTCCGCACTACAACAGCT------------------------CAGGGCCTGGCGG 185900

Qy        325 CGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGC 384
              |||||| ||||||||||||||||||||||||| ||  | |||||||||||||||||||||
Db     185899 CGGGGCGGAGCAGTACGTGCTGTACATGGTGAACCTGAGCGGCTACCGCACCTGCAACGC 185840

Qy        385 CAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAA 444
              |||||| |||| |||||||||||| |||||||||| ||||||| ||||||||||||||||
Db     185839 CAGCCAAGGCTCCAAGCGCTGGGAATGCAACCGGCAGCACGCCTCGCACAGCCCCATCAA 185780

Qy        445 GTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGG 504
              |||||| |||||||||||||| |||||||||||||| |||||||| || ||||| |||||
Db     185779 GTTCTCCGAGAAGTTCCAGCGTTACAGCGCCTTCTCGCTGGGCTATGAATTCCATGCCGG 185720
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Qy     505 CCACGAGTACTACTACATCT 524
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Db 185719 CCAAGAATACTACTACATCT 185700


RESULT  14
AC104327
LOCUS       AC104327               326750 bp    DNA     linear   HTG 24-DEC-2001
DEFINITION  Mus musculus clone rp23-295a4 strain C57BL/6J, WORKING DRAFT
            SEQUENCE, 66 unordered pieces.
ACCESSION   AC104327
VERSION     AC104327.2  GI:17978117
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 326750)
  AUTHORS   Hua,A. and Roe,B.A.
  TITLE     Mus musculus BAC Clone rp23-295a4
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 326750)
  AUTHORS   Hua,A. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT     On Dec 24, 2001 this sequence version replaced gi:17439220.
            ------------- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            ----------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 66 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *       7448      10057: contig of 2610 bp in length
            *      10058      10157: gap of unknown length
            *      10158      12254: contig of 2097 bp in length
            *      12255      12354: gap of unknown length
            *      12355      14417: contig of 2063 bp in length
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            *      14518      18079: contig of 3562 bp in length
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            *      24603      26620: contig of 2018 bp in length
            *      26621      26720: gap of unknown length
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            *      30777      30876: gap of unknown length
            *      30877      33188: contig of 2312 bp in length
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            *      33289      36016: contig of 2728 bp in length
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            *      79465      82599: contig of 3135 bp in length
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            *     173173     173272: gap of unknown length
            *     173273     178980: contig of 5708 bp in length
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             *     192849     192948: gap of unknown length
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             *     206132     210282: contig of 4151 bp in length
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             *     210383     218415: contig of 8033 bp in length
             *     218416     218515: gap of unknown length
             *     218516     226120: contig of 7605 bp in length
             *     226121     226220: gap of unknown length
             *     226221     236580: contig of 10360 bp in length
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             *     236681     245273: contig of 8593 bp in length
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  Best Local Similarity   84.7%;  Pred. No. 1.2e-25;
  Matches  271;  Conservative    0;  Mismatches   25;  Indels   24;  Gaps    1;

Qy    205 CCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 264
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 194171 CCACAGCCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 194230

Qy    265 TTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGG 324
          |||||| ||||||||||||||||                        | ||||| || ||
Db 194231 TTACTGTCCGCACTACAACAGCT------------------------CAGGGCCTGGCGG 194266

Qy    325 CGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGC 384
          |||||| ||||||||||||||||||||||||| ||  | |||||||||||||||||||||
Db 194267 CGGGGCGGAGCAGTACGTGCTGTACATGGTGAACCTGAGCGGCTACCGCACCTGCAACGC 194326

Qy    385 CAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAA 444
          |||||| |||| |||||||||||| |||||||||| ||||||| ||||||||||||||||
Db 194327 CAGCCAAGGCTCCAAGCGCTGGGAATGCAACCGGCAGCACGCCTCGCACAGCCCCATCAA 194386

Qy    445 GTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGG 504
          |||||| |||||||||||||| |||||||||||||| |||||||| || ||||| |||||
Db 194387 GTTCTCCGAGAAGTTCCAGCGTTACAGCGCCTTCTCGCTGGGCTATGAATTCCATGCCGG 194446

Qy    505 CCACGAGTACTACTACATCT 524
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Db 194447 CCAAGAATACTACTACATCT 194466


RESULT 15
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DEFINITION  Mus musculus clone rp23-368d24 strain C57BL/6J, WORKING DRAFT
            SEQUENCE, 72 unordered pieces.
ACCESSION   AC104632
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VERSION     AC104632.2  GI:17998594
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SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 289579)
  AUTHORS   Hua,A. and Roe,B.A.
  TITLE     Mus musculus BAC Clone rp23-368d24
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 289579)
  AUTHORS   Hua,A. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-DEC-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT     On Dec 29, 2001 this sequence version replaced gi:17861055.
            ------------- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            ----------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 72 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *      38833     40937: contig of 2105 bp in length
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ORIGIN

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Qy         27 GAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCTCCGGGGATGG 86
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Qy         87 CGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGG 146
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Qy        147 CCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACC 206
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Qy        207 AGCA 210
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Db      49254 AGCA 49257


Search completed: September 27, 2002, 22:47:01
Job time: 9012 sec
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                    GenCore version 4.5
          Copyright (c) 1993 - 2000  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          September 27, 2002, 21:19:25 ; Search time 239.05 Seconds
                                                (without alignments)
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Title:           US-09-904-954-1
Perfect score:   1037
Sequence:        1 GGATCTTGGAACGAGACGAC..........GTCGTCTCGTTCCAAGATCC 1037

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters:      3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
                    %
Result            Query
  No.     Score   Match Length DB  ID                          Description
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    1      1037   100.0   1037  16  AAQ85887                    Human hek-L protei
    2     907.4    87.5   1070  16  AAT03883                    Eph transmembrane
    3     205.8    19.8    358  21  AAC03424                    Human secreted pro
    4     151.8    14.6    642  20  AAX32767                    Human LERK-6 polyp
    5     149.2    14.4    783  17  AAT15009                    Chicken elf-1 cDNA
    6     149.2    14.4    783  19  AAV42927                    cDNA encoding an a
    7     149.2    14.4   1809  17  AAT15008                    Mouse Elf-1 cDNA.
    8     149.2    14.4   1809  19  AAV42926                    cDNA encoding a ma
    9     135.4    13.1    314  17  AAT14010                    LERK-6 exon.  Homo
   10     135.4    13.1    314  20  AAX32766                    Exon sequence of h
   11     128.8    12.4    555  17  AAT32700                    Lerk-6 coding sequ
   12     128.8    12.4    555  17  AAT14009                    LERK-6 coding sequ
   13     128.8    12.4    555  20  AAX32761                    Murine LERK-6 poly
   14     116.4    11.2   1438  13  AAQ24595                    B61 cDNA sequence.
   15     116.4    11.2   1480  15  AAQ63770                    B61 gene.  Homo sa
   16     116.4    11.2   1496  22  AAS21387                    Human cDNA sequenc
   17     116.4    11.2   1496  22  AAC90574                    Human PRO202 cDNA.
   18     116.4    11.2   1496  22  AAC91576                    Human PRO202 cDNA.
   19     116.4    11.2   1527  21  AAC98823                    Human pancreatic c
   20     114.8    11.1    439  22  AAH81578                    Human differential
   21     108.6    10.5   1176  23  AAS92024                    DNA encoding novel
   22       104    10.0   1574  23  AAS92779                    DNA encoding novel
   23       104    10.0   1728  17  AAT34292                    HEK4 binding prote
   24       104    10.0   1839  17  AAT18897                    Human AL-1 cDNA.
   25     103.4    10.0    636  16  AAQ85888                    Human hek-L protei
   26       102     9.8    687  17  AAT32699                    Lerk-7 coding sequ
c  27      73.2     7.1   3066  23  AAS75651                    DNA encoding novel
c  28      58.8     5.7   1002  22  AAK51628                    Human polynucleoti
c  29      55.2     5.3    515  20  AAX18930                    Human huntingtin g
c  30      55.2     5.3  10348  20  AAZ23426                    Human huntingtin p
c  31      55.2     5.3  10348  22  ABA08651                    Human Huntington's
   32      55.2     5.3  10348  23  AAS91971                    DNA encoding novel
c  33      55.2     5.3  10366  15  AAQ67401                    Huntingtin DNA\IT1
c  34      55.2     5.3  10366  18  AAT97924                    Composite sequence
c  35      55.2     5.3  10366  19  AAV05828                    Human huntingtin c
   36      54.8     5.3    645  17  AAT42476                    HuntL4 coding sequ
c  37      53.6     5.2  10348  22  ABA08714                    Human Huntington's
c  38      52.6     5.1   3389  23  AAS86290                    DNA encoding novel
   39        52     5.0   1059  20  AAV72336                    Actinomycete sp. 3
c  40        52     5.0   9732  23  AAS79690                    DNA encoding novel
c  41      51.2     4.9    270  20  AAX37239                    Seq ID No: 8 of WO
c  42      51.2     4.9   1924  22  AAF59598                    Human cell cycle a
   43      50.6     4.9    255  22  AAH82125                    Rat differential t
   44      50.2     4.8   1833  23  ABL22159                    Drosophila melanog
   45      50.2     4.8 4403765  22  AAI99683                    Mycobacterium tube


                                   ALIGNMENTS


RESULT   1
AAQ85887
ID   AAQ85887 standard; cDNA to mRNA; 1037 BP.
XX
AC   AAQ85887;
XX
DT   03-OCT-1995  (first entry)
XX
DE   Human hek-L protein cDNA clone A2.
XX
KW   Ligand; cell surface; tyrosine kinase receptor; tumorigenesis;
KW   immunogen; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             83..799
FT                   /*tag=  a
FT   sig_peptide     83..139
FT                   /*tag=  b
FT   mat_peptide     140..796
FT                   /*tag=  c
XX
PN   WO9506065-A.
XX
PD   02-MAR-1995.
XX
PF   17-AUG-1994;   94WO-US09282.
XX
PR   20-AUG-1993;   93US-0109745.
PR   30-AUG-1993;   93US-0114426.
PR   03-DEC-1993;   93US-0161132.
```

```
PR   09-MAY-1994;   94US-0240124.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Beckmann MP,  Cerretti DP;
XX
DR   WPI; 1995-106811/14.
DR   P-PSDB; AAR71481.
XX
PT   New isolated DNA encoding hek-L protein or its fusion products  -
PT   useful as assay reagent or for carrying therapeutic and
PT   diagnostic compounds to leukaemia cells.
XX
PS   Claim 1; Page 34; 45pp; English.
XX
CC   The sequence is that of a clone encoding hek-L protein, a protein
CC   that can bind hek (a cell surface receptor tyrosine kinase).  Hek-L
CC   is the first known ligand for hek and can be used to study cellular
CC   processes regulated by hek (which may be involved in tumorigenesis).
CC   It is also an immunogen for antibody production, as a reagent for
CC   detecting hek or hek-L in in vitro assays, to determine binding of
CC   hek proteins, to purify hek proteins, and to carry diagnostic or
CC   cytotoxic agents to particular leukaemia cells that express the hek
CC   antigen.  Hek-L also binds the elk tyrosine kinase receptors.
CC   See also AAQ85888.
XX
SQ   Sequence 1037 BP; 187 A; 343 C; 337 G; 170 T; 0 other;


  Query Match             100.0%;  Score 1037;  DB 16;  Length 1037;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-186;
  Matches 1037;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ggatcttggaacgagacgacctgctggagaagccgggagcgcggggctcagtcggggggc 60

Qy       61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ggcggcggcggcggctccggggatggcggcggctccgctgctgctgctgctgctgctcgt 120

Qy      121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 gcccgtgccgctgctgccgctgctggcccaagggcccggaggggcgctgggaaaccggca 180

Qy      181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 tgcggtgtactggaacagctccaaccagcacctgcggcgagagggctacaccgtgcaggt 240

Qy      241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 gaacgtgaacgactatctggatatttactgcccgcactacaacagctcgggggtgggccc 300

Qy      301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 cggggcgggaccggggcccggaggcggggcagagcagtacgtgctgtacatggtgagccg 360

Qy      361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 caacggctaccgcacctgcaacgccagccagggcttcaagcgctgggagtgcaaccggcc 420

Qy      421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 gcacgccccgcacagccccatcaagttctcggagaagttccagcgctacagcgccttctc 480

Qy      481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 tctgggctacgagttccacgccggccacgagtactactacatctccacgcccactcacaa 540

Qy      541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 cctgcactggaagtgtctgaggatgaaggtgttcgtctgctgcgcctccacatcgcactc 600
```

```
Qy      601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 cggggagaagccggtccccactctcccccagttcaccatgggccccaatgtgaagatcaa 660

Qy      661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 cgtgctggaagactttgagggagagaaccctcaggtgcccaagcttgagaagagcatcag 720

Qy      721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 cgggaccagccccaaacgggaacacctgcccctggccgtgggcatcgccttcttcctcat 780

Qy      781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGGGCGGGGCT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 gacgttcttggcctcctagctctgccccctcccctgggggggagagatggggcggggct 840

Qy      841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 tggaaggagcagggagcctttggcctctccaagggaagcctagtgggcctagacccctcc 900

Qy      901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 tcccatggctagaagtggggcctgcaccatacatctgtgtccgccccctctaccccttcc 960

Qy      961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 ccccacgtagggcactgtagtggaccaagcacggggacagccatgggtcccgagcaggtc 1020

Qy     1021 GTCTCGTTCCAAGATCC 1037
              |||||||||||||||||
Db     1021 gtctcgttccaagatcc 1037


RESULT   2
AAT03883
ID   AAT03883 standard; DNA; 1070 BP.
XX
AC   AAT03883;
XX
DT   16-MAY-1996  (first entry)
XX
DE   Eph transmembrane tyrosine kinase family ligand, Efl-2 encoding DNA.
XX
KW   Efl-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand;
KW   neurological disorder; identification; diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             46..750
FT                   /*tag=  a
FT                   /product= Efl-2
XX
PN   WO9527060-A2.
XX
PD   12-OCT-1995.
XX
PF   04-APR-1995;   95WO-US04208.
XX
PR   21-OCT-1994;   94US-0327423.
PR   04-APR-1994;   94US-0222075.
PR   12-APR-1994;   94US-0229402.
PR   01-SEP-1994;   94US-0299567.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Aldrich TH,  Davis S,  Gale N,  Goldfarb M,  Maisonpierre PC;
PI   Yancopoulos GD;
XX
DR   WPI; 1995-358635/46.
DR   P-PSDB; AAR82605.
XX
PT   Ligands which bind Eph family receptors - used in the diagnosis of
```

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PT   neurological disorders
XX
PS   Disclosure; Fig 3; 58pp; English.
XX
CC   The DNA encodes an Eph transmembrane tyrosine kinase family ligand
CC   designated Efl-2. Efl-2 is useful for identifying other ligands for
CC   Ehk-1, -2, -3, Eck and Elk receptors.  The ligands are useful in
CC   promoting a differential function and/or influencing the phenotye,
CC   such as growth and/or proliferation, of receptor bearing cells. They
CC   may be used in the diagnosis, and treatment of neurological disorders.
XX
SQ   Sequence 1070 BP; 196 A; 341 C; 334 G; 189 T; 10 other;

  Query Match             87.5%;  Score 907.4;  DB 16;  Length 1070;
  Best Local Similarity   96.3%;  Pred. No. 3.2e-162;
  Matches  939;  Conservative    0;  Mismatches   24;  Indels   12;  Gaps    1;

Qy         44 GGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTG 103
              | | ||  | | | |  |    ||||||||||||||||||||||||||||||||||||||||
Db          7 gagatccattgtgctggaaaggcggcggcggctccggggatggcggcggctccgctgctg 66

Qy        104 CTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGG 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ctgctgctgctgctcgtgcccgtgccgctgctgccgctgctggcccaagggcccggaggg 126

Qy        164 GCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAG 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 gcgctgggaaaccggcatgcggtgtactggaacagctccaaccagcacctgcggcgagag 186

Qy        224 GGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAAC 283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ggctacaccgtgcaggtgaacgtgaacgactatctggatatttactgcccgcactacaac 246

Qy        284 AGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTG 343
              ||||||            ||||||||||||||||||||||||||||||||||||||||||
Db        247 agctcg------------ggggcggaccggggcccggaggcggggcagagcagtacgtg 294

Qy        344 CTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGC 403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 ctgtacatggtgagccgcaacggctaccgcacctgcaacgccagccagggcttcaagcgc 354

Qy        404 TGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAG 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 tgggagtgcaaccggccgcacgccccgcacagccccatcaagttctcggagaagttccag 414

Qy        464 CGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATC 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 cgctacagcgccttctctctgggctacgagttccacgccggccacgagtactactacatc 474

Qy        524 TCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGC 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 tccacgcccactcacaacctgcactggaagtgtctgaggatgaaggtgttcgtctgctgc 534

Qy        584 GCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGC 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 gcctccacatcgcactccggggagaagccggtccccactctcccccagttcaccatgggc 594

Qy        644 CCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAG 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 cccaatgtgaagatcaacgtgctggaagactttgagggagagaaccctcaggtgcccaag 654

Qy        704 CTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGC 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 cttgagaagagcatcagcgggaccagccccaaacgggaacacctgcccctggccgtgggc 714

Qy        764 ATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGG 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 atcgccttcttcctcatgacgttcttggcctcctagctctgcccccTcccctgggggggg 774

Qy        824 AGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAG 883
              ||||||||||||||| |||||||||| |||||||||||||||||||||||||||||||||
Db        775 agagatggggcggggnttggaaggagnagggagcctttggcctctccaagggaagcctag 834

Qy        884 TGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCG 943
              ||||||||||||||||||||||||| ||||||||||||||| ||||||||||||||||||
Db        835 tgggcctagacccctcctcccatggttagaagtggggcctgnaccatacatctgtgtccg 894

Qy        944 CCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCA 1003
              |||||||||||||||||||||| |||||| ||||||||||||||||||||| ||||| ||
Db        895 ccccctctaccccttccccccangtagggnactgtagtggaccaagcacggngacagaca 954

Qy       1004 TGGGTCCCGAGCAGG 1018
              ||| ||||| |  ||
Db        955 tggntcccgggnggg 969


RESULT   3
AAC03424
ID   AAC03424 standard; cDNA; 358 BP.
XX
AC   AAC03424;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 3422.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
DR   P-PSDB; AAG03418.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 3422; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. An ORF has been identified within the
CC   sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC   derived from 30 different tissues. EST sequences usually correspond
CC   mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC   often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC   well suited for isolating cDNA sequences derived from the 5' ends of
CC   mRNAs and even in those cases where longer cDNA sequences have been
CC   obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC   mRNAs with intact 5' ends and can therefore be used to obtain full length
CC   cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC   gene therapy and chromosome mapping procedures. They are used to obtain
CC   upstream regulatory sequences and to design expression and secretion
CC   vectors.
XX
SQ   Sequence 358 BP; 74 A; 102 C; 122 G; 60 T; 0 other;


  Query Match             19.8%;  Score 205.8;  DB 21;  Length 358;
  Best Local Similarity   94.7%;  Pred. No. 4.1e-30;
  Matches  213;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy        509 GAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAG 568
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          ||| |   ||   |||||||||||||||||||||||||||||||||||||||||||||||
Db    131 gagaatcgctgtttctccacgcccactcacaacctgcactggaagtgtctgaggatgaag 190

Qy    569 GTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCC 628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 gtgttcgtctgctgcgcctccacatcgcactccggggagaagccggtccccactctcccc 250

Qy    629 CAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAAC 688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 cagttcaccatgggccccaatgtgaagatcaacgtgctggaagactttgagggagagaac 310

Qy    689 CCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCC 733
          ||||||||||||||||||||||||||||||||||||  |   |||
Db    311 cctcaggtgcccaagcttgagaagagcatcagcggggaccagccc 355


RESULT   4
AAX32767
ID   AAX32767 standard; cDNA to mRNA; 642 BP.
XX
AC   AAX32767;
XX
DT   24-JUN-1999  (first entry)
XX
DE   Human LERK-6 polypeptide encoding cDNA.
XX
KW   LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury;
KW   cell proliferation; neural growth; neural tissue; neurological disease;
KW   neurodegenerative; excitotoxicity; ss.
XX
OS   Homo sapiens.
XX
PN   WO9910495-A1.
XX
PD   04-MAR-1999.
XX
PF   27-AUG-1998;   98WO-US17772.
XX
PR   29-AUG-1997;   97US-0920440.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1999-243567/20.
DR   P-PSDB; AAY06822.
XX
PT   New cytokine designated LERK-6
XX
PS   Claim 3; Page 42; 46pp; English.
XX
CC   The invention relates murine and human LERK-6 polypeptides that bind to
CC   hek/elk receptors. Host cells transfected or transformed with vectors
CC   comprising the LERK-6 nucleic acid sequences are used for the recombinant
CC   production of the proteins. LERK-6 polypeptides may be useful in the
CC   enhancement, stimulation, proliferation or growth of cells expressing the
CC   hek or elk receptor. The ligand and receptor complex may be involved in
CC   neural growth, development and/or maintenance. LERK-6 can be used for
CC   treating disorders of neural tissue such as injury or neurological
CC   diseases, either chronic or acute. LERK-6 may be employed in treating
CC   neurodegenerative conditions where there is neural death, excitotoxicity.
CC   In addition, they may be administered to a mammal to exert a trophic
CC   effect on neural tissue. They can also be used as reagents for those
CC   conducting quality assurance studies e.g. to monitor shelf life and
CC   stability of elk protein under different conditions. The polypeptides can
CC   also be used as carriers for delivering agents attached to cells bearing
CC   the elk or hek cell surface receptor. The present sequence represents a
CC   cDNA encoding a human LERK-6 polypeptide.
XX
SQ   Sequence 642 BP; 97 A; 247 C; 193 G; 105 T; 0 other;

  Query Match             14.6%;  Score 151.8;  DB 20;  Length 642;
  Best Local Similarity   61.0%;  Pred. No. 6.2e-20;
  Matches  340;  Conservative    0;  Mismatches  172;  Indels   45;  Gaps    4;

Qy     73 GGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCT 132
          ||| || | |  |    ||   |  | ||||||||| |||||| |   ||    |||||
Db      3 ggcgcccgcgcagcgcccgctgctcccgctgctgctcctgctgttaccgctgccgccgcc 62

Qy    133 GCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTG 192
          ||       ||  ||| | |   |||   | ||        ||||  | || || |||||
Db     63 gcccttcgcgcgcgccgaggacgccgcccgcgccaactcggaccgctacgccgtctactg 122

Qy    193 GAACAGCTCCAACCAGCACCTGCGGCGAGA------------------GGGCTACACCGT 234
          |||| ||  |||||      | |    ||                   ||||||||| ||
Db    123 gaaccgcagcaaccccaggttccacgcaggcgcgggggacgacggcgggggctacacggt 182

Qy    235 GCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGT 294
          | |||||| | | || ||||| ||||| || ||||||||||||||
Db    183 ggaggtgagcatcaatgactacctggacatctactgcccgcactat-------------- 228

Qy    295 GGGCCCCGGGGCGGACCGGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGT 354
                 ||||||   | |  ||| |  |   |    ||||| |||||||||||||||||
Db    229 -------ggggcgccgctgccgccggccgagcgcatggagcactacgtgctgtacatggt 281

Qy    355 GAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCTTCAAGCGCTGGGAGTG 411
           | | || | ||| ||  | ||||| ||  | |||||   ||||||||||||||||||||
Db    282 caacggcgagggccacgcctcctgcgaccaccgccagcgcggcttcaagcgctgggagtg 341

Qy    412 CAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAG 471
          |||||||||    || ||      | ||  |||||||||||||||||||||||| || ||
Db    342 caaccggcccgcggcgcccggggggccgctcaagttctcggagaagttccagctcttcac 401

Qy    472 CGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCT---CCAC 528
            ||||||| ||||||| ||||||||   ||||||||||||| ||||||||||   ||||
Db    402 gcccttctccctgggcttcgagttccggcccggccacgagtattactacatctctgccac 461

Qy    529 GCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTC 588
          |||  |  |     || || ||   || ||| |  ||||||||| |||  |     ||
Db    462 gcctcccaatgctgtggaccggccctgcctgcgactgaaggtgtacgtgcggccgaccaa 521

Qy    589 CACATCGCACTCCGGGG 605
          |    | |  | || ||
Db    522 cgagaccctgtacgagg 538


RESULT   5
AAT15009
ID   AAT15009 standard; cDNA; 783 BP.
XX
AC   AAT15009;
XX
DT   02-JUL-1996  (first entry)
XX
DE   Chicken elf-1 cDNA.
XX
KW   Elf-1; EPH receptor ligand; dementia; tachycardia; gene therapy;
KW   diagnosis; transgenic animal; ss; ds.
XX
OS   Gallus sp.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..85
FT                   /*tag=  a
FT   CDS             86..688
FT                   /*tag=  b
FT   sig_peptide     86..148
FT                   /*tag=  c
FT   mat_peptide     149..685
FT                   /*tag=  d
FT   3'UTR           686..783
FT                   /*tag=  e
FT   polyA_signal    1471..1476
FT                   /*tag=  f
XX
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PN   WO9609384-A1.
XX
PD   28-MAR-1996.
XX
PF   19-SEP-1995;   95WO-US11869.
XX
PR   27-FEB-1995;   95US-0393462.
PR   19-SEP-1994;   94US-0308814.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1996-188446/19.
DR   P-PSDB; AAR94767.
XX
PT   Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis
PT   and treatment of disorders associated with the Elf-1 gene, e.g.
PT   dementia, tachycardia , etc.
XX
PS   Claim 36; Page 87-88; 107pp; English.
XX
CC   A chicken cDNA clone (AAT15009) codes for a novel EPH receptor ligand,
CC   Elf-1 (AAR94766), involved in the formation and maintenance of
CC   ordered spatial arrangements of differentiated tissue.  It was
CC   obtd. from a day-3 chick embryo cDNA library using mouse Elf-1
CC   cDNA (see AAT15008) as probe.  The cDNA can be used for the prodn.
CC   of recombinant Elf-1, in the breeding of transgenic animals,
CC   for the design of diagnostic probes, and for gene (or antisense)
CC   therapy of cellular and tissue disorders.
XX
SQ   Sequence 783 BP; 140 A; 270 C; 232 G; 141 T; 0 other;


  Query Match            14.4%;  Score 149.2;  DB 17;  Length 783;
  Best Local Similarity  63.3%;  Pred. No. 2e-19;
  Matches  276;  Conservative    0;  Mismatches  133;  Indels   27;  Gaps    2;

Qy     112 GCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGG 171
           ||||||||   |  |        |     ||  |  | | |  |||||    | | |
Db     109 gctgctcgccgcgatcgtcggcgtctgcgtgtggagcgacgaccccggcaaagtgatctc 168

Qy     172 AAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACAC 231
             ||||  | || || || |||||| ||  |||||      | |  || | ||  |||||
Db     169 ggaccgctacgccgtctattggaaccgcagcaaccccaggttccaccgcggggattacac 228

Qy     232 CGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGG 291
           |||| |||||| | | || ||||| ||||| || |||||||| |||||| |
Db     229 cgtggaggtgagcatcaatgactacctggacatctactgccctcactacga--------- 279

Qy     292 GGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACAT 351
                          ||  |||  |||||  |   |    ||||  ||||| || |||||
Db     280 ---------------ggagccgctgcccgccgagcgcatggagcgctacgtcctctacat 324

Qy     352 GGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCC---AGGGCTTCAAGCGCTGGGA 408
           ||| | |  | | ||| ||    ||||| ||  | | |   |||||||||| || |||||
Db     325 ggtcaactacgagggccacgcgtcctgcgaccaccggcagaagggcttcaaacgttggga 384

Qy     409 GTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTA 468
           ||||||||||||  || ||||   | | ||| |||||||||| ||||||||||||| ||
Db     385 gtgcaaccggcccgactcccccagcggacccctcaagttctcagagaagttccagctctt 444

Qy     469 CAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCAC 528
           || | |||||||| |||||| ||||||||   ||||||||||||| |||||||||||  |
Db     445 cacccccttctctttgggcttcgagttccgtcccggccacgagtattactacatctctgc 504

Qy     529 GCCCACTCACAACCTG 544
           | |  | |  ||| ||
Db     505 gtctcccccgaacgtg 520


RESULT   6
AAV42927
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```
ID   AAV42927 standard; cDNA; 783 BP.
XX
AC   AAV42927;
XX
DT   20-OCT-1998  (first entry)
XX
DE   cDNA encoding an avian Elf-1 protein.
XX
KW   Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP;
KW   tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation;
KW   intracellular signalling; increased; survival; neuronal cell;
KW   neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour;
KW   artificial liver; cartilage; bone formation; ss.
XX
OS   Gallus sp.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..85
FT                   /*tag=  a
FT   CDS             86..688
FT                   /*tag=  b
FT                   /product= Elf-1
FT   sig_peptide     86..148
FT                   /*tag=  c
FT   3'UTR           686..783
FT                   /*tag=  d
XX
PN   US5795734-A.
XX
PD   18-AUG-1998.
XX
PF   31-MAY-1995;   95US-0455001.
XX
PR   31-MAY-1995;   95US-0455001.
PR   19-SEP-1994;   94US-0308814.
PR   27-FEB-1995;   95US-0393462.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1998-466665/40.
DR   P-PSDB; AAW71007.
XX
PT   Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor
PT   - for production of Elf-1 protein, useful for regulating
PT   proliferation, differentiation, and survival of cells
XX
PS   Claim 12; Columns 73-76; 53pp; English.
XX
CC   The present sequence encodes an avian EPH receptor ligand designated
CC   Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a
CC   tyrosine kinase ligand, which is linked to the membrane through a
CC   phosphatidylinositol linkage. It shares some homology to 2 other EPH
CC   receptor ligands, B61 and LERK-2. The Elf-1 protein modulates
CC   proliferation, differentiation and survival of EPH receptor-expressing
CC   cells by stimulating or antagonising intracellular signalling mediated
CC   by the EPH receptor. Typical of many potential applications are
CC   increasing survival of neuronal cells in culture (e.g. where intended for
CC   transplantation), also therapeutically in increase neuron survival
CC   (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent
CC   nervous system and lymphatic tumours, to induce differentiation of
CC   hepatocytes to form an artificial liver, to induce cartilage and bone
CC   formation.
XX
SQ   Sequence 783 BP; 140 A; 270 C; 232 G; 141 T; 0 other;


  Query Match            14.4%;  Score 149.2;  DB 19;  Length 783;
  Best Local Similarity  63.3%;  Pred. No. 2e-19;
  Matches  276;  Conservative    0;  Mismatches  133;  Indels   27;  Gaps    2;

Qy     112 GCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGG 171
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          ||||||||   |  |        |     ||  |  | | |  |||||    | | |
Db    109 gctgctcgccgcgatcgtcggcgtctgcgtgtggagcgacgaccccggcaaagtgatctc 168

Qy    172 AAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACAC 231
            ||||  | || || || |||||| ||  |||||      | |  || | ||  |||||
Db    169 ggaccgctacgccgtctattggaaccgcagcaaccccaggttccaccgcggggattacac 228

Qy    232 CGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGG 291
          |||| |||||| | | || ||||| ||||| || |||||||| |||||| |
Db    229 cgtggaggtgagcatcaatgactacctggacatctactgccctcactacga--------- 279

Qy    292 GGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACAT 351
                         ||  |||  |||||  |   |    ||||  ||||| || |||||
Db    280 ---------------ggagccgctgcccgccgagcgcatggagcgctacgtcctctacat 324

Qy    352 GGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCC---AGGGCTTCAAGCGCTGGGA 408
          ||| | |  | | ||| ||    ||||| ||  | | |   |||||||||| || |||||
Db    325 ggtcaactacgagggccacgcgtcctgcgaccaccggcagaagggcttcaaacgttggga 384

Qy    409 GTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTA 468
          ||||||||||||  || ||||   | | ||| |||||||||| ||||||||||||| ||
Db    385 gtgcaaccggcccgactcccccagcggacccctcaagttctcagagaagttccagctctt 444

Qy    469 CAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCAC 528
          || | |||||||| |||||| ||||||||   ||||||||||||| |||||||||||  |
Db    445 cacccccttctctttgggcttcgagttccgtcccggccacgagtattactacatctctgc 504

Qy    529 GCCCACTCACAACCTG 544
          | |  | |  ||| ||
Db    505 gtctcccccgaacgtg 520


RESULT    7
AAT15008
ID   AAT15008 standard; cDNA; 1809 BP.
XX
AC   AAT15008;
XX
DT   02-JUL-1996  (first entry)
XX
DE   Mouse Elf-1 cDNA.
XX
KW   Elf-1; EPH receptor ligand; dementia; tachycardia; gene therapy;
KW   diagnosis; transgenic animal; ss; ds.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..264
FT                   /*tag= a
FT   CDS             265..893
FT                   /*tag= b
FT   sig_peptide     265..324
FT                   /*tag= c
FT   mat_peptide     325..891
FT                   /*tag= d
FT   3'UTR           892..1809
FT                   /*tag= e
FT   polyA_signal    1471..1476
FT                   /*tag= f
XX
PN   WO9609384-A1.
XX
PD   28-MAR-1996.
XX
PF   19-SEP-1995;   95WO-US11869.
XX
PR   27-FEB-1995;   95US-0393462.
PR   19-SEP-1994;   94US-0308814.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1996-188446/19.
DR   P-PSDB; AAR94777.
XX
PT   Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis
PT   and treatment of disorders associated with the Elf-1 gene, e.g.
PT   dementia, tachycardia , etc.
XX
PS   Claim 36; Page 84-85; 107pp; English.
XX
CC   A mouse cDNA clone (AAT15008) codes for a novel EPH receptor ligand,
CC   Elf-1 (AAR94766), involved in the formation and maintenance of
CC   ordered spatial arrangements of differentiated tissue.  It was
CC   obtd. from an embryo mid- and hind-brain cDNA expression library
CC   using a receptor affinity probe technique with mek4-AP and sek-AP
CC   (AP = alkaline phosphatase) reagents.  The cDNA is used for the
CC   prodn. of recombinant Elf-1, in the breeding of transgenic animals,
CC   for the design of diagnostic probes, and for gene (or antisense)
CC   therapy of cellular and tissue disorders.
XX
SQ   Sequence 1809 BP; 342 A; 590 C; 504 G; 373 T; 0 other;

  Query Match             14.4%;  Score 149.2;  DB 17;  Length 1809;
  Best Local Similarity   62.6%;  Pred. No. 2.1e-19;
  Matches  322;  Conservative    0;  Mismatches  148;  Indels   44;  Gaps    4;

Qy     53 CGGGGGGCGGCGGCGGCGGCGGCTCCGGGG--ATGGCGGCGGCTCCGCTGCTGCTGCTGC 110
          || |||   | |   ||||| || ||||||  |||||| | || | ||  | ||||||||
Db    233 cgagggagcgagcgcgcggcagcaccggggccatggcgcccgcgcagcgcccgctgctgc 292

Qy    111 TGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGG 170
           ||||||  |||   ||| || |||||    ||    | | |  || |   ||||    |
Db    293 cgctgctgctgctgctgctgccgctgcgtgcgcgcaacgaggacccggcccgggccaacg 352

Qy    171 GAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGC------------ 218
             ||||  | || || ||||||||| |   |||||      | | |
Db    353 ctgaccgatacgcagtctactggaaccgtagcaaccccaggtttcaggtgagcgctgtgg 412

Qy    219 ------GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCC 272
                | |  ||||| |||||| |||||| | | |||||||| |||||||| |||||||
Db    413 gtgatggcggcggctataccgtggaggtgagcatcaacgactacctggatatctactgcc 472

Qy    273 CGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAG 332
          | |||||                     |||||||   | |   || |  |   |    |
Db    473 cacacta---------------------cggggcgccgctgcccccggctgagcgcatgg 511

Qy    333 AGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG- 391
          ||| |||| | |||||||||||||   |  | ||| ||  | ||||  ||  | | |||
Db    512 agcggtacatcctgtacatggtgaatggtgagggccacgcctcctgtgaccaccggcagc 571

Qy    392 --GGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCT 449
            ||||||||||||||||| |||||||||||    || ||     | ||| |||||||||
Db    572 gaggcttcaagcgctgggaatgcaaccggcccgcagcgcccgggggacccctcaagttct 631

Qy    450 CGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACG 509
          | ||||||||||| | || || | |||| || |||||||  |||||||   | |||||||
Db    632 cagagaagttccaactcttcacccccttttccctgggctttgagttccggcctggccacg 691

Qy    510 AGTACTACTACATCTCCACGCCCACTCACAACCT 543
          | ||||||||||||||  |  |  ||| ||||||
Db    692 aatactactacatctctgccacacctcccaacct 725


RESULT    8
AAV42926
ID   AAV42926 standard; cDNA; 1809 BP.
XX
AC   AAV42926;
XX
DT   20-OCT-1998  (first entry)
XX
DE   cDNA encoding a mammalian Elf-1 protein.
```

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XX
KW   Mouse; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand;
KW   B61; LERK-2; proliferation; differentiation; intracellular signalling;
KW   increased; survival; neuronal cell; neuron survival; treatment;
KW   Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage;
KW   bone formation; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..264
FT                   /*tag=  a
FT   CDS             265..894
FT                   /*tag=  b
FT                   /product= Elf-1
FT   3'UTR           892..1809
FT                   /*tag=  c
FT   sig_peptide     255..324
FT                   /*tag=  d
FT   polyA_signal    1724..1729
FT                   /*tag=  e
XX
PN   US5795734-A.
XX
PD   18-AUG-1998.
XX
PF   31-MAY-1995;   95US-0455001.
XX
PR   31-MAY-1995;   95US-0455001.
PR   19-SEP-1994;   94US-0308814.
PR   27-FEB-1995;   95US-0393462.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1998-466665/40.
DR   P-PSDB; AAW71006.
XX
PT   Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor
PT   - for production of Elf-1 protein, useful for regulating
PT   proliferation, differentiation, and survival of cells
XX
PS   Claim 12; Fig 2A; 53pp; English.
XX
CC   The present sequence encodes a mammalian EPH receptor ligand designated
CC   Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a
CC   tyrosine kinase ligand, which is linked to the membrane through a
CC   phosphatidylinositol linkage. It shares some homology to 2 other EPH
CC   receptor ligands, B61 and LERK-2. The Elf-1 protein modulates
CC   proliferation, differentiation and survival of EPH receptor-expressing
CC   cells by stimulating or antagonising intracellular signalling mediated
CC   by the EPH receptor. Typical of many potential applications are
CC   increasing survival of neuronal cells in culture (e.g. where intended for
CC   transplantation), also therapeutically in increase neuron survival
CC   (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent
CC   nervous system and lymphatic tumours, to induce differentiation of
CC   hepatocytes to form an artificial liver, to induce cartilage and bone
CC   formation.
XX
SQ   Sequence 1809 BP; 342 A; 590 C; 504 G; 373 T; 0 other;


  Query Match             14.4%;  Score 149.2;  DB 19;  Length 1809;
  Best Local Similarity   62.6%;  Pred. No. 2.1e-19;
  Matches  322;  Conservative    0;  Mismatches  148;  Indels   44;  Gaps    4;

Qy     53 CGGGGGGCGGCGGCGGCGGCGGCTCCGGGG--ATGGCGGCGGCTCCGCTGCTGCTGCTGC 110
          || |||   | |   ||||| || ||||||  |||||| | || | ||  | ||||||||
Db    233 cgagggagcgagcgcgcggcagcaccggggccatggcgcccgcgcagcgcccgctgctgc 292

Qy    111 TGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGG 170
           ||||||  |||   ||| ||| |||||    ||    | | |  || |   ||||    |
Db    293 cgctgctgctgctgctgctgccgctgcgtgcgcgcaacgaggacccggcccgggccaacg 352

Qy    171 GAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGC------------ 218
             ||||  | || || |||||||||| |   |||||      | | |
Db    353 ctgaccgatacgcagtctactggaaccgtagcaaccccaggtttcaggtgagcgctgtgg 412

Qy    219 ------GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCC 272
                | |  ||||| |||||| |||||| | | |||||||| |||||||| |||||||
Db    413 gtgatggcggcggctataccgtggaggtgagcatcaacgactacctggatatctactgcc 472

Qy    273 CGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGACCGGGGGCCCGGAGGCGGGGCAG 332
          | |||||                     |||||||   | |   || |  |   |    |
Db    473 cacacta---------------------cggggcgccgctgcccccggctgagcgcatgg 511

Qy    333 AGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG- 391
          ||| |||| | |||||||||||||   |  | ||| ||  | ||||  ||  | | |||
Db    512 agcggtacatcctgtacatggtgaatggtgagggccacgcctcctgtgaccaccggcagc 571

Qy    392 --GGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCT 449
            ||||||||||||||||| |||||||||||    || ||     | ||| |||||||||
Db    572 gaggcttcaagcgctgggaatgcaaccggcccgcagcgcccgggggacccctcaagttct 631

Qy    450 CGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACG 509
          | ||||||||||| | || || | |||| || |||||||  |||||||   | |||||||
Db    632 cagagaagttccaactcttcacccccttttccctgggctttgagttccggcctggccacg 691

Qy    510 AGTACTACTACATCTCCACGCCCACTCACAACCT 543
          | ||||||||||||||  |  |  ||| ||||||
Db    692 aatactactacatctctgccacacctcccaacct 725


RESULT   9
AAT14010
ID   AAT14010 standard; cDNA to mRNA; 314 BP.
XX
AC   AAT14010;
XX
DT   11-OCT-1996  (first entry)
XX
DE   LERK-6 exon.
XX
KW   LERK-6; hek; elk; cell surface receptors; culture; reagent;
KW   neurons; disorder; injury; delivery agent; diagnostic; therapeutic;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon             2..313
FT                   /*tag=  a
FT                   /product= LERK-6 protein fragment.
XX
PN   WO9610911-A1.
XX
PD   18-APR-1996.
XX
PF   04-OCT-1995;   95WO-US12779.
XX
PR   03-OCT-1995;   95US-0538709.
PR   05-OCT-1994;   94US-0318393.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1996-209575/21.
DR   P-PSDB; AAR91284.
XX
PT   Isolated DNA encoding cytokine designated LERK-6 which binds to hek
PT   and elk cell surface receptors - useful for drug delivery and
PT   screening procedures.
XX
PS   Claim 3; Page 36; 44pp; English.
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XX
CC   The LERK-6 polypeptide encoded by this sequence can be used to
CC   isolate cells expressing hek/elk cell surface receptors, or to
CC   measure the biological activity of such receptors.  The protein may
CC   also be used as a delivery agent, taking diagnostic and therapeutic
CC   agents to cells expressing such receptors. LERK-6 can also be used
CC   as a tissue culture reagent to enhance the viability or prolong the
CC   lifespan of the neurons.  Neural tissue disorders and injuries may
CC   be treated by contact with the polypeptide.
XX
SQ   Sequence 314 BP; 51 A; 108 C; 104 G; 51 T; 0 other;


  Query Match             13.1%;  Score 135.4;  DB 17;  Length 314;
  Best Local Similarity   70.9%;  Pred. No. 7.3e-17;
  Matches  219;  Conservative    0;  Mismatches   66;  Indels   24;  Gaps    2;

Qy     219 GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACT 278
           | | ||||||||| ||| |||||| | | || ||||| ||||| || |||||||||||||
Db      27 gcgggggctacacggtggaggtgagcatcaatgactacctggacatctactgcccgcact 86

Qy     279 ACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGGCGGGGCAGAGCAGT 338
           |                      ||||||   | |  ||| |  |   |    ||||| |
Db      87 at---------------------ggggcgccgctgccgccggccgagcgcatggagcact 125

Qy     339 ACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCT 395
           |||||||||||||||| | | || | ||| ||  | ||||| ||  | |||||   ||||
Db     126 acgtgctgtacatggtcaacggcgagggccacgcctcctgcgaccaccgccagcgcggct 185

Qy     396 TCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGA 455
           |||||||||||||||||||||||||    || ||     |  ||  |||||||||||||||
Db     186 tcaagcgctgggagtgcaaccggcccgcggcgcccgggggggccgctcaagttctcggaga 245

Qy     456 AGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACT 515
           ||||||||| || ||   ||||||| ||||||| ||||||||   ||||||||||||| |
Db     246 agttccagctcttcacgcccttctccctgggcttcgagttccggcccggccacgagtatt 305

Qy     516 ACTACATCT 524
           |||||||||
Db     306 actacatct 314


RESULT  10
AAX32766
ID   AAX32766 standard; cDNA to mRNA; 314 BP.
XX
AC   AAX32766;
XX
DT   24-JUN-1999  (first entry)
XX
DE   Exon sequence of human LERK-6.
XX
KW   LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury;
KW   cell proliferation; neural growth; neural tissue; neurological disease;
KW   neurodegenerative; excitotoxicity; ss.
XX
OS   Homo sapiens.
XX
PN   WO9910495-A1.
XX
PD   04-MAR-1999.
XX
PF   27-AUG-1998;   98WO-US17772.
XX
PR   29-AUG-1997;   97US-0920440.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1999-243567/20.
DR   P-PSDB; AAY06821.
XX
```

```
PT   New cytokine designated LERK-6
XX
PS   Claim 3; Page 24; 46pp; English.
XX
CC   The invention relates murine and human LERK-6 polypeptides that bind to
CC   hek/elk receptors. Host cells transfected or transformed with vectors
CC   comprising the LERK-6 nucleic acid sequences are used for the recombinant
CC   production of the proteins. LERK-6 polypeptides may be useful in the
CC   enhancement, stimulation, proliferation or growth of cells expressing the
CC   hek or elk receptor. The ligand and receptor complex may be involved in
CC   neural growth, development and/or maintenance. LERK-6 can be used for
CC   treating disorders of neural tissue such as injury or neurological
CC   diseases, either chronic or acute. LERK-6 may be employed in treating
CC   neurodegenerative conditions where there is neural death, excitotoxicity.
CC   In addition, they may be administered to a mammal to exert a trophic
CC   effect on neural tissue. They can also be used as reagents for those
CC   conducting quality assurance studies e.g. to monitor shelf life and
CC   stability of elk protein under different conditions. The polypeptides can
CC   also be used as carriers for delivering agents attached to cells bearing
CC   the elk or hek cell surface receptor. The present sequence represents a
CC   exon sequence from human LERK-6 cDNA.
XX
SQ   Sequence 314 BP; 51 A; 108 C; 104 G; 51 T; 0 other;


  Query Match             13.1%;  Score 135.4;  DB 20;  Length 314;
  Best Local Similarity   70.9%;  Pred. No. 7.3e-17;
  Matches  219;  Conservative    0;  Mismatches   66;  Indels   24;  Gaps    2;

Qy     219 GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACT 278
           | | ||||||||| ||| |||||| | | || ||||| ||||| || |||||||||||||
Db      27 gcgggggctacacggtggaggtgagcatcaatgactacctggacatctactgcccgcact 86

Qy     279 ACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGGCGGGGCAGAGCAGT 338
           |                      ||||||   | |  ||| |  |   |    ||||| |
Db      87 at---------------------ggggcgccgctgccgccggccgagcgcatggagcact 125

Qy     339 ACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCT 395
           |||||||||||||||| | | || | ||| ||  | ||||| ||  | |||||   ||||
Db     126 acgtgctgtacatggtcaacggcgagggccacgcctcctgcgaccaccgccagcgcggct 185

Qy     396 TCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGA 455
           |||||||||||||||||||||||||    || ||     |  ||  |||||||||||||||
Db     186 tcaagcgctgggagtgcaaccggcccgcggcgcccgggggggccgctcaagttctcggaga 245

Qy     456 AGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACT 515
           ||||||||| || ||   ||||||| ||||||| ||||||||   ||||||||||||| |
Db     246 agttccagctcttcacgcccttctccctgggcttcgagttccggcccggccacgagtatt 305

Qy     516 ACTACATCT 524
           |||||||||
Db     306 actacatct 314


RESULT  11
AAT32700
ID   AAT32700 standard; cDNA; 555 BP.
XX
AC   AAT32700;
XX
DT   28-NOV-1996  (first entry)
XX
DE   Lerk-6 coding sequence.
XX
KW   Lerk-6; hek; elk; cell surface receptor; culture; reagent;
KW   neuron; disorder; injury; delivery agent; diagnostic; therapeutic;
KW   Lerk-7; probe; cytokine; ss.
XX
OS   Mus musculus.
XX
PN   WO9617925-A1.
XX
PD   13-JUN-1996.
```

```
XX
PF   05-DEC-1995;   95WO-US15781.
XX
PR   01-MAR-1995;   95US-0396946.
PR   06-DEC-1994;   94US-0351025.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1996-287171/29.
DR   P-PSDB; AAW02587.
XX
PT   New isolated human Lerk-7 cytokine - which binds to cell surface
PT   receptors elk, hek and eck, useful for delivering agents to cells or
PT   for treating neural disorders
XX
PS   Example 1; Page 34; 49pp; English.
XX
CC   A fragment of murine Lerk-6 DNA was isolated by PCR for use as a probe
CC   for a human Lerk-6 homologue. The probe however led to the
CC   identification of a human Lerk-7 gene (see AAT32699). The Lerk-7 gene and
CC   protein can be used for studying the role of Lerk-7 in conjunction with
CC   elk, hek and eck receptors. They can also be used for delivering
CC   diagnostic or therapeutic agents to cells, e.g. cancer cells.  The Lerk-7
CC   proteins can also exhibit neuroprotective or neurotrophic properties and
CC   can be used to treat neural tissue disorders.
XX
SQ   Sequence 555 BP; 102 A; 191 C; 151 G; 111 T; 0 other;


  Query Match             12.4%;  Score 128.8;  DB 17;  Length 555;
  Best Local Similarity   67.7%;  Pred. No. 1.3e-15;
  Matches  222;  Conservative    0;  Mismatches   82;  Indels   24;  Gaps    2;

Qy     219 GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACT 278
           | |  ||||| |||||| |||||| | | |||||||| |||||||| |||||||| ||||
Db      80 gcggcggctataccgtggaggtgagcatcaacgactacctggatatctactgcccacact 139

Qy     279 ACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGT 338
           |                     |||||||   | |   || |  |   |    |||| ||
Db     140 a---------------------cggggcgccgctgcccccggctgagcgcatggagcggt 178

Qy     339 ACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCT 395
           || | |||||||||||||   |  | ||| ||  | ||||  ||  | | |||   ||||
Db     179 acatcctgtacatggtgaatggtgagggccacgcctcctgtgaccaccggcagcgaggct 238

Qy     396 TCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGA 455
           ||||||||||||| |||||||||||    || ||     | ||| |||||||||| ||||
Db     239 tcaagcgctgggaatgcaaccggcccgcagcgcccgggggacccctcaagttctcagaga 298

Qy     456 AGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACT 515
           ||||||| | || || | |||| || |||||||  |||||||   | |||||||| ||||
Db     299 agttccaactcttcacccccttttccctgggctttgagttccggcctggccacgaatact 358

Qy     516 ACTACATCTCCACGCCCACTCACAACCT 543
           ||||||||||  |  |  ||| ||||||
Db     359 actacatctctgccacacctcccaacct 386


RESULT  12
AAT14009
ID   AAT14009 standard; cDNA; 555 BP.
XX
AC   AAT14009;
XX
DT   10-OCT-1996  (first entry)
XX
DE   LERK-6 coding sequence.
XX
KW   LERK-6; hek; elk; cell surface receptors; culture; reagent;
KW   neurons; disorder; injury; delivery agent; diagnostic; therapeutic;
KW   ss.
```

```
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..555
FT                   /*tag=  a
FT                   /product= LERK-6
XX
PN   WO9610911-A1.
XX
PD   18-APR-1996.
XX
PF   04-OCT-1995;   95WO-US12779.
XX
PR   03-OCT-1995;   95US-0538709.
PR   05-OCT-1994;   94US-0318393.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1996-209575/21.
XX
PT   Isolated DNA encoding cytokine designated LERK-6 which binds to hek
PT   and elk cell surface receptors - useful for drug delivery and
PT   screening procedures.
XX
PS   Claim 3; Page 33; 44pp; English.
XX
CC   The LERK-6 polypeptide encoded by this sequence can be used to
CC   isolate cells expressing hek/elk cell surface receptors, or to
CC   measure the biological activity of such receptors.  The protein may
CC   also be used as a delivery agent, taking diagnostic and therapeutic
CC   agents to cells expressing such receptors. LERK-6 can also be used
CC   as a tissue culture reagent to enhance the viability or prolong the
CC   lifespan of the neurons.  Neural tissue disorders and injuries may
CC   be treated by contact with the polypeptide.
XX
SQ   Sequence 555 BP; 102 A; 191 C; 151 G; 111 T; 0 other;


  Query Match             12.4%;  Score 128.8;  DB 17;  Length 555;
  Best Local Similarity   67.7%;  Pred. No. 1.3e-15;
  Matches  222;  Conservative    0;  Mismatches   82;  Indels   24;  Gaps    2;

Qy     219 GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACT 278
           | |  ||||| |||||| |||||| | | |||||||| |||||||| |||||||| ||||
Db      80 gcggcggctataccgtggaggtgagcatcaacgactacctggatatctactgcccacact 139

Qy     279 ACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGT 338
           |                     |||||||   | |   || |  |   |    |||| ||
Db     140 a---------------------cggggcgccgctgcccccggctgagcgcatggagcggt 178

Qy     339 ACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCT 395
           || | |||||||||||||   |  | ||| ||  | ||||  ||  | | |||   ||||
Db     179 acatcctgtacatggtgaatggtgagggccacgcctcctgtgaccaccggcagcgaggct 238

Qy     396 TCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGA 455
           ||||||||||||| |||||||||||    || ||     | ||| |||||||||| ||||
Db     239 tcaagcgctgggaatgcaaccggcccgcagcgcccgggggacccctcaagttctcagaga 298

Qy     456 AGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACT 515
           ||||||| | || || | |||| || |||||||  |||||||   | |||||||| ||||
Db     299 agttccaactcttcacccccttttccctgggctttgagttccggcctggccacgaatact 358

Qy     516 ACTACATCTCCACGCCCACTCACAACCT 543
           ||||||||||  |  |  ||| ||||||
Db     359 actacatctctgccacacctcccaacct 386


RESULT  13
AAX32761
ID   AAX32761 standard; cDNA; 555 BP.
```

```
XX
AC   AAX32761;
XX
DT   24-JUN-1999  (first entry)
XX
DE   Murine LERK-6 polypeptide encoding cDNA.
XX
KW   LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury;
KW   cell proliferation; neural growth; neural tissue; neurological disease;
KW   neurodegenerative; excitotoxicity; ss.
XX
OS   Mus sp.
XX
PN   WO9910495-A1.
XX
PD   04-MAR-1999.
XX
PF   27-AUG-1998;   98WO-US17772.
XX
PR   29-AUG-1997;   97US-0920440.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1999-243567/20.
DR   P-PSDB; AAY06820.
XX
PT   New cytokine designated LERK-6
XX
PS   Claim 3; Page 37-38; 46pp; English.
XX
CC   The invention relates murine and human LERK-6 polypeptides that bind to
CC   hek/elk receptors. Host cells transfected or transformed with vectors
CC   comprising the LERK-6 nucleic acid sequences are used for the recombinant
CC   production of the proteins. LERK-6 polypeptides may be useful in the
CC   enhancement, stimulation, proliferation or growth of cells expressing the
CC   hek or elk receptor. The ligand and receptor complex may be involved in
CC   neural growth, development and/or maintenance. LERK-6 can be used for
CC   treating disorders of neural tissue such as injury or neurological
CC   diseases, either chronic or acute. LERK-6 may be employed in treating
CC   neurodegenerative conditions where there is neural death, excitotoxicity.
CC   In addition, they may be administered to a mammal to exert a trophic
CC   effect on neural tissue. They can also be used as reagents for those
CC   conducting quality assurance studies e.g. to monitor shelf life and
CC   stability of elk protein under different conditions. The polypeptides can
CC   also be used as carriers for delivering agents attached to cells bearing
CC   the elk or hek cell surface receptor. The present sequence represents a
CC   cDNA encoding a murine LERK-6 polypeptide.
XX
SQ   Sequence 555 BP; 102 A; 191 C; 151 G; 111 T; 0 other;


  Query Match             12.4%;  Score 128.8;  DB 20;  Length 555;
  Best Local Similarity   67.7%;  Pred. No. 1.3e-15;
  Matches  222;  Conservative    0;  Mismatches   82;  Indels   24;  Gaps    2;

Qy    219 GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACT 278
          | |  ||||| ||||||  ||||| | | ||||||||| ||||||||| |||||||| ||||
Db     80 gcggcggctataccgtggaggtgagcatcaacgactacctggatatctactgcccacact 139

Qy    279 ACAACAGCTCGGGGGTGGCCCCCGGGGCGGACCGGGGGCCCGGAGGCGGGGCAGAGCAGT 338
          |                     |||||||   | |   || |  |   |    |||| ||
Db    140 a---------------------cggggcgccgctgcccccggctgagcgcatggagcggt 178

Qy    339 ACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCT 395
          || | |||||||||||||   |  | ||| ||  | ||||  ||  | | |||   ||||
Db    179 acatcctgtacatggtgaatggtgagggccacgcctcctgtgaccaccggcagcgaggct 238

Qy    396 TCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGA 455
          ||||||||||||| |||||||||||    || ||     | ||| |||||||||| ||||
Db    239 tcaagcgctgggaatgcaaccggcccgcagcgcccgggggacccctcaagttctcagaga 298
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```
Qy    456 AGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACT 515
          ||||||| | || || | |||| || |||||||  |||||||   | |||||||| ||||
Db    299 agttccaactcttcacccccttttccctgggctttgagttccggcctggccacgaatact 358

Qy    516 ACTACATCTCCACGCCCACTCACAACCT 543
          ||||||||||  |  |  ||| ||||||
Db    359 actacatctctgccacacctcccaacct 386


RESULT  14
AAQ24595
ID   AAQ24595 standard; cDNA to mRNA; 1438 BP.
XX
AC   AAQ24595;
XX
DT   06-NOV-1992  (first entry)
XX
DE   B61 cDNA sequence.
XX
KW   Early inflammatory response; marker; antibody; therapy; induction;
KW   lipopolysaccharides; cytokines; Interleukin-2; IL-2; TNF; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..691
FT                   /*tag=  a
FT   sig_peptide     74..128
FT                   /*tag=  b
FT   polyA_signal    1458..1463
FT                   /*tag=  c
XX
PN   WO9207094-A.
XX
PD   30-APR-1992.
XX
PF   15-OCT-1991;   91WO-US07704.
XX
PR   16-OCT-1990;   90US-0607741.
XX
PA   (UNMI ) UNIV MICHIGAN.
XX
PI   Dixit VM;
XX
DR   WPI; 1992-167172/20.
DR   P-PSDB; AAR23895.
XX
PT   Gene prod. used as marker to detect inflammatory response - by
PT   detecting the B61 gene in biological fluids or by using
PT   hybridisation probes
XX
PS   Claim 1; Fig 3; 39pp; English.
XX
CC   Poly(A)+ mRNA isolated from human umbilical vein endothelial cells
CC   (HUVE) was treated with TNF cyclohexamide and used to construct a
CC   lambda gt11 cDNA library.  The library was screened using
CC   radiolabelled cDNA fragments derived from the 5' end of B61 DNA.
CC   Hybridising cDNA inserts were isolated and subcloned into pGEM 7zf
CC   (+) for sequencing.  Clone B61.1 contained the entire OFR encoding a
CC   protein of 205 residues (24 kD).  The B61 gene is involved in early
CC   inflammatory response and serves as a marker.  It may be detected by
CC   probes or by antibody-based immunoassay of biological fluids such as
CC   plasma, CSF or urine.  These assays make it possible to predict a
CC   worsening in a disease process and allow the quantitative
CC   assessment of the magnitude of the inflammatory response.  This
CC   information will allow the earlier admin. of appropriate therapy,
CC   thereby shortening the disease process and limiting the patient's
CC   exposure to anti-inflammatory/immunosuppressive therapy.  B61
CC   induction is rapid and profound, hence it is easily detectable.
CC   The B61 response is highly specific to proinflammatory stimuli,
CC   being only made by cells exposed to lipopolysaccharides or cytokines
CC   such as IL-2 and TNF and not growth factors or interferon.
XX
```

```
SQ   Sequence 1438 BP; 358 A; 412 C; 373 G; 295 T; 0 other;

  Query Match             11.2%;  Score 116.4;  DB 13;  Length 1438;
  Best Local Similarity   57.4%;  Pred. No. 3.1e-13;
  Matches  263;  Conservative    0;  Mismatches  171;  Indels   24;  Gaps    2;

Qy    137 CCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAAC 196
          || ||  |||  |   |   | |   |||    |   | || ||  | || | |||||||
Db     92 cctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccgtcttctggaac 151

Qy    197 AGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTAT 256
          || || || |   |  | |||   |||| ||||||| | || ||| |  |||| |||||
Db    152 agttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactac 211

Qy    257 CTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGG 316
           |||| ||   ||| ||||||||  |          ||||    ||  ||
Db    212 gtggacatcatctgtccgcactatgaagatcactctgtggcagacgctgccatg------ 265

Qy    317 CCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACC 376
                         ||||||||| | |||||| |||||   |   | |  ||||
Db    266 ---------------gagcagtacatactgtacctggtggagcatgaggagtaccagctg 310

Qy    377 TGCAACGCCAG---CCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCAC 433
          ||| |  ||     | ||| |      |||||| |||||||||||||    |||  |||
Db    311 tgccagccccagtccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcat 370

Qy    434 AGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAG 493
           ||||    ||| | || |||||||||||||||| ||   | ||| | |||||| | |||
Db    371 ggcccggagaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggag 430

Qy    494 TTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAG 553
          ||| | |  || |||   ||||||||||||||||  ||||  ||| | |   |
Db    431 ttcaaagaaggacacagctactactacatctccaaacccatccaccagcatgaagaccgc 490

Qy    554 TGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
          ||  ||||| ||||||||   ||| |  ||     |||
Db    491 tgcttgaggttgaaggtgactgtcagtggcaaaatcac 528


RESULT 15
AAQ63770
ID   AAQ63770 standard; DNA; 1480 BP.
XX
AC   AAQ63770;
XX
DT   10-JAN-1995  (first entry)
XX
DE   B61 gene.
XX
KW   eck receptor; eck receptor binding protein; EBP; B61;
KW   cancer; inflammation; wound; cytokine; protein tyrosine kinase;
KW   PTK; phosphorylation; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..691
FT                   /*tag=  a
XX
PN   EP597503-A.
XX
PD   18-MAY-1994.
XX
PF   15-NOV-1993;   93EP-0118469.
XX
PR   13-NOV-1992;   92US-0977708.
PR   09-NOV-1993;   93US-0145616.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Bartley TD,  Boyle WJ,  Fox GM,  Parker VP,  Welcher AA;
XX
```

```
DR   WPI; 1994-160538/20.
DR   P-PSDB; AAR53634.
XX
PT   New eck receptor binding proteins - useful for treating cancer,
PT   inflammation, wounds, etc.
XX
PS   Disclosure; Page 27-28; 41pp; English.
XX
CC   The N-terminal sequence of EBP isolated from the conditioned medium
CC   of the SK-BR-3 cell line was identical to the N-terminal amino acid
CC   sequence predicted from the expression of the B61 gene (Holzman et al.,
CC   Mol. Cell Biol. 10, 5830 (1990); WO9207094).
CC   cDNA encoding EBP having the N-terminal
CC   NH2-DRHTVFW(N)SSNPKFRNEDYTIHVQ was cloned
CC   and sequenced and, as expected, found to be identical to the B61 gene.
CC   The EBP gene expressed in CHO cells resulted in at least two
CC   polypeptides having different mol. wts. C-terminal sequencing
CC   revealed only the sequence KRLAA-COOH which indicated a polypeptide
CC   of 150 amino acids (EBP1-150).
XX
SQ   Sequence 1480 BP; 359 A; 421 C; 393 G; 307 T; 0 other;

  Query Match             11.2%;  Score 116.4;  DB 15;  Length 1480;
  Best Local Similarity   57.4%;  Pred. No. 3.1e-13;
  Matches  263;  Conservative    0;  Mismatches  171;  Indels   24;  Gaps    2;

Qy    137 CCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAAC 196
          || ||  |||  |   |   | |   |||    |   | || ||  | || | |||||||
Db     92 cctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccgtcttctggaac 151

Qy    197 AGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTAT 256
          || || || |   |  | |||   |||| ||||||| | || ||| |  |||| |||||
Db    152 agttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactac 211

Qy    257 CTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGG 316
           |||| ||   ||| ||||||||  |          ||||    ||  ||
Db    212 gtggacatcatctgtccgcactatgaagatcactctgtggcagacgctgccatg------ 265

Qy    317 CCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACC 376
                         ||||||||| | |||||| |||||   |   | |  ||||
Db    266 ---------------gagcagtacatactgtacctggtggagcatgaggagtaccagctg 310

Qy    377 TGCAACGCCAG---CCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCAC 433
          ||| |  ||     | ||| |      |||||| |||||||||||||    |||  |||
Db    311 tgccagccccagtccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcat 370

Qy    434 AGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAG 493
           ||||    ||| | || |||||||||||||||| ||   | ||| | |||||| | |||
Db    371 ggcccggagaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggag 430

Qy    494 TTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAG 553
          ||| | |  || |||   ||||||||||||||||  ||||  ||| | |   |
Db    431 ttcaaagaaggacacagctactactacatctccaaacccatccaccagcatgaagaccgc 490

Qy    554 TGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
          ||  ||||| ||||||||   ||| |  ||     |||
Db    491 tgcttgaggttgaaggtgactgtcagtggcaaaatcac 528


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                          GenCore version 4.5
                 Copyright (c) 1993 - 2000  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          September 27, 2002, 20:18:44 ; Search time 65.52 Seconds
                                                (without alignments)
                                                3887.698 Million cell updates/sec

Title:           US-09-904-954-1
Perfect score:   1037
Sequence:        1 GGATCTTGGAACGAGACGAC..........GTCGTCTCGTTCCAAGATCC 1037

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters:      767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
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                6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                      SUMMARIES
                  %
Result          Query
  No.   Score   Match Length DB  ID                          Description
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    2    1037   100.0   1037  1  US-08-453-943-1              Sequence 1, Appli
    3    1037   100.0   1037  2  US-09-057-121-1              Sequence 1, Appli
    4    1037   100.0   1037  4  US-09-358-734-1              Sequence 1, Appli
    5   907.4    87.5   1070  1  US-08-299-567-8              Sequence 8, Appli
    6   151.8    14.6    642  1  US-09-609-324A-9             Sequence 9, Appli
    7   151.8    14.6    642  2  US-08-920-440B-9             Sequence 9, Appli
    8   151.8    14.6    642  4  US-09-173-492-9              Sequence 9, Appli
    9   151.8    14.6    642  4  US-09-173-133-9              Sequence 9, Appli
   10   149.2    14.4    783  1  US-08-455-001-3              Sequence 3, Appli
   11   149.2    14.4    783  5  PCT-US95-11869-3             Sequence 3, Appli
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   15   135.4    13.1    314  1  US-09-609-324A-7             Sequence 7, Appli
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   42   103.4    10.0    636  4  US-09-358-734-3              Sequence 3, Appli
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                                  ALIGNMENTS


RESULT   1
US-08-240-124-1
; Sequence 1, Application US/08240124
; Patent No. 5516658
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/240,124
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1037 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
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;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  hek-L A2
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  83..799
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;      NAME/KEY:  sig_peptide
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  Query Match            100.0%;  Score 1037;  DB 1;  Length 1037;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-194;
  Matches 1037;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 1, Application US/08453943
; Patent No. 5738844
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,943
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/240,124
;      FILING DATE:  09-MAY-1994
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1037 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
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;    ANTI-SENSE:  NO
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;      CLONE:  hek-L A2
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;      NAME/KEY:  CDS
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US-08-453-943-1


  Query Match             100.0%;  Score 1037;  DB 1;  Length 1037;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-194;
  Matches 1037;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT   3
US-09-057-121-1
; Sequence 1, Application US/09057121
; Patent No. 5969110
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,121
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,124
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1037 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
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;      LOCATION:  140..796
US-09-057-121-1

  Query Match            100.0%;  Score 1037;  DB 2;  Length 1037;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-194;
  Matches 1037;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGC 60
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Db        1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGC 60

Qy       61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120
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Db       61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120

Qy      121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180

Qy      181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240

Qy      241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300

Qy      301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360

Qy      361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420

Qy      421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480
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Qy      481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540

Qy      541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600

Qy      601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660

Qy      661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720

Qy      721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780

Qy      781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGGGCGGGGCT 840
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Db      781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGGGCGGGGCT 840

Qy      841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900

Qy      901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960

Qy      961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020

Qy     1021 GTCTCGTTCCAAGATCC 1037
            |||||||||||||||||
Db     1021 GTCTCGTTCCAAGATCC 1037


RESULT   4
US-09-358-734-1
; Sequence 1, Application US/09358734
; Patent No. 6274117
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/358,734
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,124
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1037 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  hek-L A2
;    FEATURE:
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;       NAME/KEY:  CDS
;       LOCATION:  83..799
;     FEATURE:
;       NAME/KEY:  sig_peptide
;       LOCATION:  83..139
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  140..796
US-09-358-734-1


  Query Match             100.0%;  Score 1037;  DB 4;  Length 1037;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-194;
  Matches 1037;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGC 60

Qy       61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120

Qy      121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180

Qy      181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240

Qy      241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300
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Db      241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300

Qy      301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360

Qy      361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420
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Db      361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420

Qy      421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480
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Db      421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480

Qy      481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540
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Db      481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540

Qy      541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600
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Db      541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600

Qy      601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660
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Db      601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660

Qy      661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720
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Db      661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720

Qy      721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780
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Db      721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780

Qy      781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGGGCGGGGCT 840
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Db      781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGGGCGGGGCT 840

Qy      841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900
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Db      841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900

Qy      901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960
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Db      901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960

Qy      961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020
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Db      961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020

Qy     1021 GTCTCGTTCCAAGATCC 1037
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Db     1021 GTCTCGTTCCAAGATCC 1037


RESULT   5
US-08-299-567-8
; Sequence 8, Application US/08299567
; Patent No. 5747033
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, et al.
;    TITLE OF INVENTION:  METHOD OF ENHANCING THE BIOLOGICAL
;    TITLE OF INVENTION:  ACTIVITY OF EPH FAMILY LIGANDS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Regeneron Pharmaceuticals, Inc.
;      STREET:  777 Old Saw Mill River Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10591-6707
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/299,567
;      FILING DATE:  01-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kempler, Gail M.
;      REGISTRATION NUMBER:  32,143
;      REFERENCE/DOCKET NUMBER:  REG 290
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  914-345-7400
;      TELEFAX:  914-345-7721
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1070 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-299-567-8


  Query Match             87.5%;  Score 907.4;  DB 1;  Length 1070;
  Best Local Similarity   96.3%;  Pred. No. 3.6e-169;
  Matches  939;  Conservative    0;  Mismatches   24;  Indels   12;  Gaps    1;

Qy       44 GGGCTCAGTCGGGGGGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTG 103
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Db        7 GAGATCCATTGTGCTGGAAAGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTG 66

Qy      104 CTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGG 163
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       67 CTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGG 126

Qy      164 GCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAG 223
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Db      127 GCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAG 186
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Qy    224 GGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAAC 283
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Db    187 GGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAAC 246

Qy    284 AGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTG 343
          ||||||            ||||||||||||||||||||||||||||||||||||||||||
Db    247 AGCTCG------------GGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTG 294

Qy    344 CTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGC 403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 CTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGC 354

Qy    404 TGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAG 463
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Db    355 TGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAG 414

Qy    464 CGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATC 523
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Db    415 CGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATC 474

Qy    524 TCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGC 583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    475 TCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGC 534

Qy    584 GCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGC 643
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Db    535 GCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGC 594

Qy    644 CCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAG 703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    595 CCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAG 654

Qy    704 CTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGC 763
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Db    655 CTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGC 714

Qy    764 ATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGG 823
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    715 ATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGG 774

Qy    824 AGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAG 883
          ||||||||||||||| |||||||||| |||||||||||||||||||||||||||||||||
Db    775 AGAGATGGGGCGGGGNTTGGAAGGAGNAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAG 834

Qy    884 TGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCG 943
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Db    835 TGGGCCTAGACCCCTCCTCCCATGGTTAGAAGTGGGGCCTGNACCATACATCTGTGTCCG 894

Qy    944 CCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCA 1003
          |||||||||||||||||||||| |||||| ||||||||||||||||||||| ||||| ||
Db    895 CCCCCTCTACCCCTTCCCCCCANGTAGGGNACTGTAGTGGACCAAGCACGGNGACAGACA 954

Qy   1004 TGGGTCCCGAGCAGG 1018
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Db    955 TGGNTCCCGGGNGGG 969
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RESULT    6
US-09-609-324A-9
; Sequence 9, Application US/09609324A
; Patent No. RE37582
; GENERAL INFORMATION:
;  APPLICANT: CERRETTI, Douglas P.
;  TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
;  FILE REFERENCE: A7772
;  CURRENT APPLICATION NUMBER: US/09/609,324A
;  CURRENT FILING DATE:  2000-06-30
;  PRIOR APPLICATION NUMBER: 08/920,440
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/538,709
;  PRIOR FILING DATE: 1995-10-03
;  PRIOR APPLICATION NUMBER: 08/318,393
;  PRIOR FILING DATE: 1994-10-05
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 642
;   TYPE: DNA
;   ORGANISM: LERK-6
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(639)
;   NAME/KEY: mat_peptide
;   LOCATION: (88)..(639)
US-09-609-324A-9

  Query Match             14.6%;  Score 151.8;  DB 1;  Length 642;
  Best Local Similarity   61.0%;  Pred. No. 1.2e-21;
  Matches  340;  Conservative    0;  Mismatches  172;  Indels   45;  Gaps    4;

Qy     73 GGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCT 132
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Qy    133 GCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTG 192
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Db     63 gcccttcgcgcgcgccgaggacgccgcccgcgccaactcggaccgctacgccgtctactg 122

Qy    193 GAACAGCTCCAACCAGCACCTGCGGCGAGA------------------GGGCTACACCGT 234
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Db    123 gaaccgcagcaaccccaggttccacgcaggcgcgggggacgacggcgggggctacacggt 182

Qy    235 GCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGT 294
          | |||||| | | || ||||| ||||| || ||||||||||||||
Db    183 ggaggtgagcatcaatgactacctggacatctactgcccgcactat-------------- 228

Qy    295 GGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGT 354
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Db    229 -------ggggcgccgctgccgccggccgagcgcatggagcactacgtgctgtacatggt 281

Qy    355 GAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCTTCAAGCGCTGGGAGTG 411
           | | || | ||| ||  | ||||| ||  | |||||   ||||||||||||||||||||
Db    282 caacggcgagggccacgcctcctgcgaccaccgccagcgcggcttcaagcgctgggagtg 341

Qy    412 CAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAG 471
          |||||||||    || ||     | ||  |||||||||||||||||||||||| || ||
Db    342 caaccggcccgcggcgcccggggggccgctcaagttctcggagaagttccagctcttcac 401

Qy    472 CGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCT---CCAC 528
            ||||||| ||||||| ||||||||   ||||||||||||| ||||||||||   ||||
Db    402 gcccttctccctgggcttcgagttccggcccggccacgagtattactacatctctgccac 461

Qy    529 GCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTC 588
          |||  |  |     || || ||   || ||| |  ||||||||| |||  |     ||
Db    462 gcctcccaatgctgtggaccggccctgcctgcgactgaaggtgtacgtgcggccgaccaa 521

Qy    589 CACATCGCACTCCGGGG 605
          |    | |  | || ||
Db    522 cgagaccctgtacgagg 538
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RESULT    7
US-08-920-440B-9
; Sequence 9, Application US/08920440B
; Patent No. 5919905
;  GENERAL INFORMATION:
;    APPLICANT:  Cerretti, Douglas P.
;    TITLE OF INVENTION:  Cytokine Designated LERK-6
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
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;       ZIP:  98101
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  Apple Power Macintosh
;       OPERATING SYSTEM:  System 7.6
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/920,440B
;       FILING DATE:  29-AUG-1997
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Henry, Janis C.
;       REGISTRATION NUMBER:  34,347
;       REFERENCE/DOCKET NUMBER:  2826-B
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 587-0430
;       TELEFAX:  (206) 233-0644
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  642 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1I642
;       NAME/KEY:  Signal Peptide
;       LOCATION:  1-90
US-08-920-440B-9

  Query Match             14.6%;  Score 151.8;  DB 2;  Length 642;
  Best Local Similarity   61.0%;  Pred. No. 1.2e-21;
  Matches  340;  Conservative    0;  Mismatches  172;  Indels   45;  Gaps    4;

Qy         73 GGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCT 132
              ||| || | |  |    ||   |  | ||||||||| |||||| |   ||    |||||
Db          3 GGCGCCCGCGCAGCGCCCGCTGCTCCCGCTGCTGCTCCTGCTGTTACCGCTGCCGCCGCC 62

Qy        133 GCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTG 192
              ||       ||  ||| | |   |||   | ||        ||||  | || || |||||
Db         63 GCCCTTCGCGCGCGCCGAGGACGCCGCCCGCGCCAACTCGGACCGCTACGCCGTCTACTG 122

Qy        193 GAACAGCTCCAACCAGCACCTGCGGCGAGA------------------GGGCTACACCGT 234
              |||| ||  |||||      | |    ||                   ||||||||| ||
Db        123 GAACCGCAGCAACCCCAGGTTCCACGCAGGCGCGGGGGACGACGGCGGGGGCTACACGGT 182

Qy        235 GCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGT 294
              | |||||| | | || ||||| ||||| || ||||||||||||||
Db        183 GGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCGCACTAT-------------- 228

Qy        295 GGGCCCCGGGGCGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGT 354
                     ||||||   | |  ||| |  |   |    ||||| |||||||||||||||||
Db        229 -------GGGGCGCCGCTGCCGCCGGCCGAGCGCATGGAGCACTACGTGCTGTACATGGT 281

Qy        355 GAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCTTCAAGCGCTGGGAGTG 411
               | | || | ||| ||  | ||||| ||  | |||||   ||||||||||||||||||||
Db        282 CAACGGCGAGGGCCACGCCTCCTGCGACCACCGCCAGCGCGGCTTCAAGCGCTGGGAGTG 341

Qy        412 CAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAG 471
              |||||||||    || ||     | ||  |||||||||||||||||||||||| || ||
Db        342 CAACCGGCCCGCGGCGCCCGGGGGGCCGCTCAAGTTCTCGGAGAAGTTCCAGCTCTTCAC 401

Qy        472 CGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCT---CCAC 528
                ||||||| ||||||| ||||||||   ||||||||||||| ||||||||||   ||||
Db        402 GCCCTTCTCCCTGGGCTTCGAGTTCCGGCCCGGCCACGAGTATTACTACATCTCTGCCAC 461

Qy        529 GCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTC 588
              |||  |  |     || || ||   || ||| |  ||||||||| |||  |     ||
Db        462 GCCTCCCAATGCTGTGGACCGGCCCTGCCTGCGACTGAAGGTGTACGTGCGGCCGACCAA 521
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Qy        589 CACATCGCACTCCGGGG 605
              |    | |  | || ||
Db        522 CGAGACCCTGTACGAGG 538

RESULT   8
US-09-173-492-9
; Sequence 9, Application US/09173492
; Patent No. 6194172
;  GENERAL INFORMATION:
;    APPLICANT:  Cerretti, Douglas P.
;    TITLE OF INVENTION:  Cytokine Designated LERK-6
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  System 7.6
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/173,492
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,440
;      FILING DATE:  29-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Henry, Janis C.
;      REGISTRATION NUMBER:  34,347
;      REFERENCE/DOCKET NUMBER:  2826-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  642 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1I642
;      NAME/KEY:  Signal Peptide
;      LOCATION:  1-90
US-09-173-492-9

  Query Match             14.6%;  Score 151.8;  DB 4;  Length 642;
  Best Local Similarity   61.0%;  Pred. No. 1.2e-21;
  Matches  340;  Conservative    0;  Mismatches  172;  Indels   45;  Gaps    4;

Qy         73 GGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCT 132
              ||| || | |  |    ||   |  | ||||||||| |||||| |   ||    |||||
Db          3 GGCGCCCGCGCAGCGCCCGCTGCTCCCGCTGCTGCTCCTGCTGTTACCGCTGCCGCCGCC 62

Qy        133 GCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTG 192
              ||       ||  ||| | |   |||   | ||        ||||  | || || |||||
Db         63 GCCCTTCGCGCGCGCCGAGGACGCCGCCCGCGCCAACTCGGACCGCTACGCCGTCTACTG 122

Qy        193 GAACAGCTCCAACCAGCACCTGCGGCGAGA------------------GGGCTACACCGT 234
              |||| ||  |||||      | |    ||                   ||||||||| ||
Db        123 GAACCGCAGCAACCCCAGGTTCCACGCAGGCGCGGGGGACGACGGCGGGGGCTACACGGT 182
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Qy    235 GCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGT 294
          | |||||| | | || ||||| ||||| || ||||||||||||||
Db    183 GGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCGCACTAT-------------- 228

Qy    295 GGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGT 354
                 ||||||   | |  ||| |  |   |    ||||| |||||||||||||||||
Db    229 -------GGGGCGCCGCTGCCGCCGGCCGAGCGCATGGAGCACTACGTGCTGTACATGGT 281

Qy    355 GAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCTTCAAGCGCTGGGAGTG 411
           | | || | ||| ||  | ||||| ||  | |||||   ||||||||||||||||||||
Db    282 CAACGGCGAGGGCCACGCCTCCTGCGACCACCGCCAGCGCGGCTTCAAGCGCTGGGAGTG 341

Qy    412 CAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAG 471
          |||||||||    || ||     | ||  |||||||||||||||||||||||| || ||
Db    342 CAACCGGCCCGCGGCGCCCGGGGGGCCGCTCAAGTTCTCGGAGAAGTTCCAGCTCTTCAC 401

Qy    472 CGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCT---CCAC 528
            ||||||| ||||||| ||||||||   ||||||||||||| ||||||||||   ||||
Db    402 GCCCTTCTCCCTGGGCTTCGAGTTCCGGCCCGGCCACGAGTATTACTACATCTCTGCCAC 461

Qy    529 GCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTC 588
          |||  |  |     || || ||   || ||| |  ||||||||| |||  |     ||
Db    462 GCCTCCCAATGCTGTGGACCGGCCCTGCCTGCGACTGAAGGTGTACGTGCGGCCGACCAA 521

Qy    589 CACATCGCACTCCGGGG 605
          |    | |  | || ||
Db    522 CGAGACCCTGTACGAGG 538

RESULT   9
US-09-173-133-9
; Sequence 9, Application US/09173133
; Patent No. 6232447
;  GENERAL INFORMATION:
;    APPLICANT:  Cerretti, Douglas P.
;    TITLE OF INVENTION:  Cytokine Designated LERK-6
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  System 7.6
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/173,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,440
;      FILING DATE:  29-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Henry, Janis C.
;      REGISTRATION NUMBER:  34,347
;      REFERENCE/DOCKET NUMBER:  2826-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  642 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1I642
;      NAME/KEY:  Signal Peptide
;      LOCATION:  1-90
US-09-173-133-9

  Query Match             14.6%;  Score 151.8;  DB 4;  Length 642;
  Best Local Similarity   61.0%;  Pred. No. 1.2e-21;
  Matches  340;  Conservative    0;  Mismatches  172;  Indels   45;  Gaps    4;

Qy     73 GGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCT 132
          ||| || | |  |    ||   |  | ||||||||| |||||| |   ||    |||||
Db      3 GGCGCCCGCGCAGCGCCCGCTGCTCCCGCTGCTGCTCCTGCTGTTACCGCTGCCGCCGCC 62

Qy    133 GCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTG 192
          ||       ||  ||| | |   |||   | ||        ||||  | || || |||||
Db     63 GCCCTTCGCGCGCGCCGAGGACGCCGCCCGCGCCAACTCGGACCGCTACGCCGTCTACTG 122

Qy    193 GAACAGCTCCAACCAGCACCTGCGGCGAGA------------------GGGCTACACCGT 234
          |||| ||  |||||      | |    ||                   ||||||||| ||
Db    123 GAACCGCAGCAACCCCAGGTTCCACGCAGGCGCGGGGGACGACGGCGGGGGCTACACGGT 182

Qy    235 GCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGT 294
          | |||||| | | || ||||| ||||| || ||||||||||||||
Db    183 GGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCGCACTAT-------------- 228

Qy    295 GGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGT 354
                 ||||||   | |  ||| |  |   |    ||||| |||||||||||||||||
Db    229 -------GGGGCGCCGCTGCCGCCGGCCGAGCGCATGGAGCACTACGTGCTGTACATGGT 281

Qy    355 GAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCTTCAAGCGCTGGGAGTG 411
           | | || | ||| ||  | ||||| ||  | |||||   ||||||||||||||||||||
Db    282 CAACGGCGAGGGCCACGCCTCCTGCGACCACCGCCAGCGCGGCTTCAAGCGCTGGGAGTG 341

Qy    412 CAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAG 471
          |||||||||    || ||     | ||  |||||||||||||||||||||||| || ||
Db    342 CAACCGGCCCGCGGCGCCCGGGGGGCCGCTCAAGTTCTCGGAGAAGTTCCAGCTCTTCAC 401

Qy    472 CGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCT---CCAC 528
            ||||||| ||||||| ||||||||   ||||||||||||| ||||||||||   ||||
Db    402 GCCCTTCTCCCTGGGCTTCGAGTTCCGGCCCGGCCACGAGTATTACTACATCTCTGCCAC 461

Qy    529 GCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTC 588
          |||  |  |     || || ||   || ||| |  ||||||||| |||  |     ||
Db    462 GCCTCCCAATGCTGTGGACCGGCCCTGCCTGCGACTGAAGGTGTACGTGCGGCCGACCAA 521

Qy    589 CACATCGCACTCCGGGG 605
          |    | |  | || ||
Db    522 CGAGACCCTGTACGAGG 538

RESULT  10
US-08-455-001-3
; Sequence 3, Application US/08455001
; Patent No. 5795734
;  GENERAL INFORMATION:
;    APPLICANT:  Flanagan, John G.
;    APPLICANT:  Cheng, Hwai-Jong
;    TITLE OF INVENTION:  EPH Receptor Ligands, and Uses Related
;    TITLE OF INVENTION:  Thereto
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/455,001
;      FILING DATE:  31 MAY 1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMI-011CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  783 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  86..685
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..85
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  686..783
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  86..148
US-08-455-001-3


  Query Match             14.4%;  Score 149.2;  DB 1;  Length 783;
  Best Local Similarity   63.3%;  Pred. No. 4e-21;
  Matches  276;  Conservative    0;  Mismatches  133;  Indels   27;  Gaps    2;

Qy     112 GCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGG 171
           ||||||||   |  |        |     ||  |  | | |  |||||    | | |
Db     109 GCTGCTCGCCGCGATCGTCGGCGTCTGCGTGTGGAGCGACGACCCCGGCAAAGTGATCTC 168

Qy     172 AAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACAC 231
             ||||  | || || || |||||| ||  |||||      | |  || | ||  |||||
Db     169 GGACCGCTACGCCGTCTATTGGAACCGCAGCAACCCCAGGTTCCACCGCGGGGATTACAC 228

Qy     232 CGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGG 291
           |||| |||||| | | || ||||| ||||| || |||||||| |||||| |
Db     229 CGTGGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCTCACTACGA--------- 279

Qy     292 GGTGGGCCCCGGGGCGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACAT 351
                          ||  |||  |||||  |   |    ||||  ||||| || |||||
Db     280 ---------------GGAGCCGCTGCCCGCCGAGCGCATGGAGCGCTACGTCCTCTACAT 324

Qy     352 GGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCC---AGGGCTTCAAGCGCTGGGA 408
           ||| | |  | | ||| ||    ||||| ||  | | |   |||||||||| || |||||
Db     325 GGTCAACTACGAGGGCCACGCGTCCTGCGACCACCGGCAGAAGGGCTTCAAACGTTGGGA 384

Qy     409 GTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTA 468
           ||||||||||||  || ||||   | | ||| |||||||||| ||||||||||||| ||
Db     385 GTGCAACCGGCCCGACTCCCCCAGCGGACCCCTCAAGTTCTCAGAGAAGTTCCAGCTCTT 444

Qy     469 CAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCAC 528
           || | |||||||| |||||| ||||||||   ||||||||||||| |||||||||||  |
Db     445 CACCCCCTTCTCTTTGGGCTTCGAGTTCCGTCCCGGCCACGAGTATTACTACATCTCTGC 504

Qy     529 GCCCACTCACAACCTG 544
           | |  | |  |||  ||
Db     505 GTCTCCCCCGAACGTG 520


RESULT  11
PCT-US95-11869-3
; Sequence 3, Application PC/TUS9511869
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  EPH Receptor Ligands, and Uses Related
;    TITLE OF INVENTION:  Thereto
;    NUMBER OF SEQUENCES:  5
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11869
;      FILING DATE:  19-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMI-011CPPC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  783 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  86..685
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..85
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  686..783
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  86..148
PCT-US95-11869-3


  Query Match             14.4%;  Score 149.2;  DB 5;  Length 783;
  Best Local Similarity   63.3%;  Pred. No. 4e-21;
  Matches  276;  Conservative    0;  Mismatches  133;  Indels   27;  Gaps    2;

Qy     112 GCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGG 171
           ||||||||   |  |        |     ||  |  | | |  |||||    | | |
Db     109 GCTGCTCGCCGCGATCGTCGGCGTCTGCGTGTGGAGCGACGACCCCGGCAAAGTGATCTC 168

Qy     172 AAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACAC 231
             ||||  | || || || |||||| ||  |||||      | |  || | ||  |||||
Db     169 GGACCGCTACGCCGTCTATTGGAACCGCAGCAACCCCAGGTTCCACCGCGGGGATTACAC 228

Qy     232 CGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGG 291
           |||| |||||| | | || ||||| ||||| || |||||||| |||||| |
Db     229 CGTGGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCTCACTACGA--------- 279

Qy     292 GGTGGGCCCCGGGGCGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACAT 351
                          ||  |||  |||||  |   |    ||||  ||||| || |||||
Db     280 ---------------GGAGCCGCTGCCCGCCGAGCGCATGGAGCGCTACGTCCTCTACAT 324

Qy     352 GGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCC---AGGGCTTCAAGCGCTGGGA 408
           ||| | |  | | ||| ||    ||||| ||  | | |   |||||||||| || |||||
Db     325 GGTCAACTACGAGGGCCACGCGTCCTGCGACCACCGGCAGAAGGGCTTCAAACGTTGGGA 384

Qy     409 GTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTA 468
           ||||||||||||  || ||||   | | ||| |||||||||| ||||||||||||| ||
Db     385 GTGCAACCGGCCCGACTCCCCCAGCGGACCCCTCAAGTTCTCAGAGAAGTTCCAGCTCTT 444

Qy     469 CAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCAC 528
           || | |||||||| |||||| ||||||||   ||||||||||||| |||||||||||  |
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Db    445 CACCCCCTTCTCTTTGGGCTTCGAGTTCCGTCCCGGCCACGAGTATTACTACATCTCTGC 504

Qy    529 GCCCACTCACAACCTG 544
          | |  | |  ||| ||
Db    505 GTCTCCCCCGAACGTG 520


RESULT 12
US-08-455-001-1
; Sequence 1, Application US/08455001
; Patent No. 5795734
;  GENERAL INFORMATION:
;    APPLICANT:  Flanagan, John G.
;    APPLICANT:  Cheng, Hwai-Jong
;    TITLE OF INVENTION:  EPH Receptor Ligands, and Uses Related
;    TITLE OF INVENTION:  Thereto
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/455,001
;      FILING DATE:  31 MAY 1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMI-011CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1809 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  265..891
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..264
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  892..1809
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  255..324
US-08-455-001-1


  Query Match             14.4%;  Score 149.2;  DB 1;  Length 1809;
  Best Local Similarity   62.6%;  Pred. No. 4.5e-21;
  Matches  322;  Conservative    0;  Mismatches  148;  Indels   44;  Gaps    4;

Qy     53 CGGGGGGCGGCGGCGGCGGCGGCTCCGGGG--ATGGCGGCGGCTCCGCTGCTGCTGCTGC 110
          || |||   | |   ||||| || ||||||  |||||| | || | ||  | ||||||||
Db    233 CGAGGGAGCGAGCGCGCGGCAGCACCGGGGCCATGGCGCCCGCGCAGCGCCCGCTGCTGC 292

Qy    111 TGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGG 170
           ||||||  |||   ||| || |||||    ||    | | |  || |   ||||    |
Db    293 CGCTGCTGCTGCTGCTGCTGCCGCTGCGTGCGCGCAACGAGGACCCGGCCCGGGCCAACG 352
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Qy    171 GAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGC------------ 218
             ||||  | || || ||||||||| |   |||||      | | |
Db    353 CTGACCGATACGCAGTCTACTGGAACCGTAGCAACCCCAGGTTTCAGGTGAGCGCTGTGG 412

Qy    219 ------GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCC 272
                | |  ||||| |||||| |||||| | | |||||||| |||||||| |||||||
Db    413 GTGATGGCGGCGGCTATACCGTGGAGGTGAGCATCAACGACTACCTGGATATCTACTGCC 472

Qy    273 CGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAG 332
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Db    473 CACACTA---------------------CGGGGCGCCGCTGCCCCCGGCTGAGCGCATGG 511

Qy    333 AGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG- 391
          ||| |||| | |||||||||||||   |  | ||| ||  | ||||  ||  | | |||
Db    512 AGCGGTACATCCTGTACATGGTGAATGGTGAGGGCCACGCCTCCTGTGACCACCGGCAGC 571

Qy    392 --GGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCT 449
            ||||||||||||||||| |||||||||||    || ||     | ||| |||||||||
Db    572 GAGGCTTCAAGCGCTGGGAATGCAACCGGCCCGCAGCGCCCGGGGGACCCCTCAAGTTCT 631

Qy    450 CGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACG 509
          | ||||||||||| | || || | |||| || |||||||  |||||||   | |||||||
Db    632 CAGAGAAGTTCCAACTCTTCACCCCCTTTTCCCTGGGCTTTGAGTTCCGGCCTGGCCACG 691

Qy    510 AGTACTACTACATCTCCACGCCCACTCACAACCT 543
          | ||||||||||||||  |  |  ||| ||||||
Db    692 AATACTACTACATCTCTGCCACACCTCCCAACCT 725


RESULT 13
PCT-US95-11869-1
; Sequence 1, Application PC/TUS9511869
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  EPH Receptor Ligands, and Uses Related
;    TITLE OF INVENTION:  Thereto
;    NUMBER OF SEQUENCES:  5
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11869
;      FILING DATE:  19-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMI-011CPPC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1809 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  265..891
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..264
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  892..1809
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  255..324
PCT-US95-11869-1
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  Query Match             14.4%;  Score 149.2;  DB 5;  Length 1809;
  Best Local Similarity   62.6%;  Pred. No. 4.5e-21;
  Matches  322;  Conservative    0;  Mismatches  148;  Indels   44;  Gaps    4;

Qy     53 CGGGGGGCGGCGGCGGCGGCGGCTCCGGGG--ATGGCGGCGGCTCCGCTGCTGCTGCTGC 110
          || |||   | |   ||||| || ||||||  |||||| | || | ||  | ||||||||
Db    233 CGAGGGAGCGAGCGCGCGGCAGCACCGGGGCCATGGCGCCCGCGCAGCGCCCGCTGCTGC 292

Qy    111 TGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGG 170
           ||||||  |||   ||| || |||||    ||    | | |  || |   ||||    |
Db    293 CGCTGCTGCTGCTGCTGCTGCCGCTGCGTGCGCGCAACGAGGACCCGGCCCGGGCCAACG 352

Qy    171 GAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGC------------ 218
             ||||  | || || ||||||||| |   |||||      | | |
Db    353 CTGACCGATACGCAGTCTACTGGAACCGTAGCAACCCCAGGTTTCAGGTGAGCGCTGTGG 412

Qy    219 ------GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCC 272
                | |  ||||| |||||| |||||| | | |||||||| |||||||| |||||||
Db    413 GTGATGGCGGCGGCTATACCGTGGAGGTGAGCATCAACGACTACCTGGATATCTACTGCC 472

Qy    273 CGCACTACAACAGCTCGGGGGGTGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAG 332
          | |||||                     |||||||   | |   || |  |   |    |
Db    473 CACACTA---------------------CGGGGCGCCGCTGCCCCCGGCTGAGCGCATGG 511

Qy    333 AGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG- 391
          ||| |||| | |||||||||||||   |  | ||| ||  | ||||  ||  | | |||
Db    512 AGCGGTACATCCTGTACATGGTGAATGGTGAGGGCCACGCCTCCTGTGACCACCGGCAGC 571

Qy    392 --GGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCT 449
            ||||||||||||||||| |||||||||||    || ||     | ||| |||||||||
Db    572 GAGGCTTCAAGCGCTGGGAATGCAACCGGCCCGCAGCGCCCGGGGGACCCCTCAAGTTCT 631

Qy    450 CGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACG 509
          | ||||||||||| | || || | |||| || |||||||  |||||||   | |||||||
Db    632 CAGAGAAGTTCCAACTCTTCACCCCCTTTTCCCTGGGCTTTGAGTTCCGGCCTGGCCACG 691

Qy    510 AGTACTACTACATCTCCACGCCCACTCACAACCT 543
          | ||||||||||||||  |  |  ||| ||||||
Db    692 AATACTACTACATCTCTGCCACACCTCCCAACCT 725


RESULT 14
US-08-308-814-1
; Sequence 1, Application US/08308814
; Patent No. 6268476
;  GENERAL INFORMATION:
;    APPLICANT:  Flanagan, John G.
;    APPLICANT:  Cheng, Hwai-Jong
;    TITLE OF INVENTION:  EPH Receptor Ligands, and Uses Related
;    TITLE OF INVENTION:  Thereto
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(txt)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/308,814
;      FILING DATE:  19-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36.709
;      REFERENCE/DOCKET NUMBER:  HMI-011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1615 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  10..636
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  10..69
US-08-308-814-1

  Query Match             14.3%;  Score 148;  DB 4;  Length 1615;
  Best Local Similarity   62.6%;  Pred. No. 7.7e-21;
  Matches  304;  Conservative    0;  Mismatches  140;  Indels   42;  Gaps    3;

Qy     79 GGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCC 138
          ||  |||||| | || | ||  | |||||||| ||||||  |||   |||  || |||||
Db      6 GGCCATGGCGCCCGCGCAGCGCCCGCTGCTGCCGCTGCTGCTGCTGCTGCTGCCGCTGCG 65

Qy    139 GCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAG 198
             ||    | | |  || |   ||||    |   ||||  | || || ||||||||| |
Db     66 TGCGCGCAACGAGGACCCGGCCCGGGCCAACGCTGACCGATACGCAGTCTACTGGAACCG 125

Qy    199 CTCCAACCAGCACCTGCGGC------------------GAGAGGGCTACACCGTGCAGGT 240
             |||||      | | |                   | |  ||||| |||||| ||||
Db    126 TAGCAACCCCAGGTTTCAGGTGAGCGCTGTGGGTGATGGCGGCGGCTATACCGTGGAGGT 185

Qy    241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGGTGGCCC 300
          || | | |||||||| |||||||| |||||||| |||||
Db    186 GAGCATCAACGACTACCTGGATATCTACTGCCCACACTA--------------------- 224

Qy    301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360
          |||||||   | |   || |  |   |    |||| |||| | |||||||||||||   |
Db    225 CGGGGCGCCGCTGCCCCCGGCTGAGCGCATGGAGCGGTACATCCTGTACATGGTGAATGG 284

Qy    361 CAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCTTCAAGCGCTGGGAGTGCAACCG 417
            | ||| ||  | ||||  ||  | | |||   ||||||||||||||||| ||||||||
Db    285 TGAGGGCCACGCCTCCTGTGACCACCGGCAGCGAGGCTTCAAGCGCTGGGAATGCAACCG 344

Qy    418 GCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTT 477
          |||    || ||     | ||| |||||||||| ||||||||||| | || || | ||||
Db    345 GCCCGCAGCGCCCGGGGGACCCCTCAAGTTCTCAGAGAAGTTCCAACTCTTCACCCCCTT 404

Qy    478 CTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCA 537
           || |||||||  |||||||   | |||||||| ||||||||||||||  |  |  |||
Db    405 TTCCCTGGGCTTTGAGTTCCGGCCTGGCCACGAATACTACTACATCTCTGCCACACCTCC 464

Qy    538 CAACCT 543
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Db    465 CAACCT 470


RESULT 15
US-09-609-324A-7
; Sequence 7, Application US/09609324A
; Patent No. RE37582
; GENERAL INFORMATION:
;  APPLICANT: CERRETTI, Douglas P.
;  TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
;  FILE REFERENCE: A7772
;  CURRENT APPLICATION NUMBER: US/09/609,324A
;  CURRENT FILING DATE:  2000-06-30
;  PRIOR APPLICATION NUMBER: 08/920,440
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/538,709
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;  PRIOR FILING DATE: 1995-10-03
;  PRIOR APPLICATION NUMBER: 08/318,393
;  PRIOR FILING DATE: 1994-10-05
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 314
;   TYPE: DNA
;   ORGANISM: LERK-6
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(313)
US-09-609-324A-7

  Query Match            13.1%;  Score 135.4;  DB 1;  Length 314;
  Best Local Similarity  70.9%;  Pred. No. 1.8e-18;
  Matches  219;  Conservative    0;  Mismatches   66;  Indels   24;  Gaps    2;

Qy     219 GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACT 278
           | | ||||||||| ||| |||||| | | || ||||| ||||| || |||||||||||||
Db      27 gcgggggctacacggtggaggtgagcatcaatgactacctggacatctactgcccgcact 86

Qy     279 ACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGT 338
           |                      ||||||   | |  ||| |  |   |    ||||| |
Db      87 at---------------------ggggcgccgctgccgccggccgagcgcatggagcact 125

Qy     339 ACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG---GGCT 395
           |||||||||||||||| | | || | ||| ||  | ||||| ||  | |||||   ||||
Db     126 acgtgctgtacatggtcaacggcgagggccacgcctcctgcgaccaccgccagcgcggct 185

Qy     396 TCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGA 455
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Db     186 tcaagcgctgggagtgcaaccggcccgcggcgcccggggggccgctcaagttctcggaga 245

Qy     456 AGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACT 515
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Qy     516 ACTACATCT 524
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Db     306 actacatct 314


Search completed: September 27, 2002, 22:42:54
Job time: 8650 sec
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                    GenCore version 4.5
             Copyright (c) 1993 - 2000  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          September 27, 2002, 21:26:30 ; Search time 3673.16 Seconds
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Title:           US-09-904-954-1
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters:      43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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  Pred. No. is the number of results predicted by chance to have a
  score greater than or equal to the result being printed,
  and is derived by analysis of the total score distribution.

                                SUMMARIES
                      %
Result              Query
  No.     Score     Match  Length DB  ID                              Description
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    2      1037     100.0    1037 34  US-09-904-954-1                  Sequence 1, Appli
    3    1033.8      99.7    1037  5  US-08-109-745-1                  Sequence 1, Appli
    4    1033.8      99.7    1037  5  US-08-161-132-1                  Sequence 1, Appli
    5     988.8      95.4    1761 56  US-60-172-373-10727              Sequence 10727, A
    6     988.8      95.4    1761 66  US-60-278-258-13410              Sequence 13410, A
    7       987      95.2     987 18  US-09-440-302A-838               Sequence 838, App
    8     917.8      88.5    1743 29  US-09-733-756-1                  Sequence 1, Appli
    9     907.4      87.5    1070  6  US-08-229-402-8                  Sequence 8, Appli
   10     907.4      87.5    1070  7  US-08-327-423-8                  Sequence 8, Appli
   11       773      74.5     818 27  US-09-698-010-11586              Sequence 11586, A
   12       717      69.1     717 35  US-09-948-941-53                 Sequence 53, Appl
   13       717      69.1     717 35  US-09-948-941-98                 Sequence 98, Appl
   14     411.8      39.7     421 16  US-09-287-618-6642               Sequence 6642, Ap
   15       392      37.8     392 16  US-09-221-481-182                Sequence 182, App
   16       392      37.8     392 18  US-09-440-302-241                Sequence 241, App
   17       391      37.7     391 18  US-09-440-302A-241               Sequence 241, App
   18     351.2      33.9     497 33  US-09-880-093-649                Sequence 649, App
   19     350.8      33.8     442 16  US-09-235-076-27387              Sequence 27387, A
   20     350.8      33.8     442 16  US-09-289-768-28196              Sequence 28196, A
   21     350.8      33.8     442 17  US-09-332-782-27387              Sequence 27387, A
   22     350.8      33.8     442 29  US-09-737-223-27387              Sequence 27387, A
   23     350.8      33.8     442 35  US-09-939-397-28196              Sequence 28196, A
   24     346.8      33.4   11602 35  US-09-948-941-577                Sequence 577, App
   25     346.8      33.4   11603 35  US-09-948-941-622                Sequence 622, App
c  26     346.8      33.4   22453 60  US-60-212-656-70                 Sequence 70, Appl
   27     345.8      33.3     665 27  US-09-699-997-10319              Sequence 10319, A
c  28     335.8      32.4     627 55  US-60-169-868-3231               Sequence 3231, Ap
   29       334      32.2     468 27  US-09-699-997-3157               Sequence 3157, Ap
   30       334      32.2    2332 60  US-60-212-656-600                Sequence 600, App
   31     308.8      29.8     339 20  US-09-534-853-8616               Sequence 8616, Ap
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    32   304.2   29.3    600  18  US-09-404-549-2399          Sequence 2399, Ap
    33   304.2   29.3    600  18  US-09-404-549A-2399         Sequence 2399, Ap
c   34   292.2   28.2    575  18  US-09-474-434-253           Sequence 253, App
c   35   292.2   28.2    575  18  US-09-474-434-715           Sequence 715, App
c   36   292.2   28.2    575  56  US-60-173-686-253           Sequence 253, App
c   37   292.2   28.2    575  56  US-60-173-686-715           Sequence 715, App
c   38   284.4   27.4    429  58  US-60-194-508-1189          Sequence 1189, Ap
    39   282.2   27.2    390  27  US-09-698-010-7881          Sequence 7881, Ap
    40   253.6   24.5    454  16  US-09-287-618-31308         Sequence 31308, A
    41   251.2   24.2    276  20  US-09-534-853-8650          Sequence 8650, Ap
    42   246.2   23.7    288  5  US-08-104-507A-756          Sequence 756, App
    43   246.2   23.7    288  5  US-08-104-507C-756          Sequence 756, App
    44   239.4   23.1    258  23  US-09-605-784A-440          Sequence 440, App
    45   234.6   22.6    279  6  US-08-222-075-5             Sequence 5, Appli
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ALIGNMENTS

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RESULT   1
PCT-US94-09282-1
; Sequence 1, Application PC/TUS9409282
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09282
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1037 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  hek-L A2
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  83..799
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  83..139
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  140..796
PCT-US94-09282-1


  Query Match             100.0%;  Score 1037;  DB 1;  Length 1037;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-160;
  Matches 1037;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGC 60
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Db        1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGC 60

Qy       61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120

Qy      121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180

Qy      181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240

Qy      241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300

Qy      301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360

Qy      361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420

Qy      421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480

Qy      481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540

Qy      541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600

Qy      601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGCCCCAATGTGAAGATCAA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGCCCCAATGTGAAGATCAA 660

Qy      661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720

Qy      721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780

Qy      781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGGGCGGGGCT 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGGGCGGGGCT 840

Qy      841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900

Qy     901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960

Qy     961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020

Qy    1021 GTCTCGTTCCAAGATCC 1037
           |||||||||||||||||
Db    1021 GTCTCGTTCCAAGATCC 1037


RESULT   2
US-09-904-954-1
; Sequence 1, Application US/09904954
;  GENERAL INFORMATION:
;       APPLICANT: BECKMANN, M. P.
;                  CERRETTI, DOUGLAS P.
;       TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
;                           RECEPTOR HEK
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: IMMUNEX CORPORATION
;            STREET: 51 UNIVERSITY STREET
;            CITY: SEATTLE
;            STATE: WASHINGTON
;            COUNTRY: USA
;            ZIP: 98101
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: Apple Macintosh
;            OPERATING SYSTEM: Apple System 7.1
;            SOFTWARE: Microsoft Word for Apple, Version 5.1a
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/904,954
;            FILING DATE: 12-Jul-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/240,124
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: US 08/114,426
;            FILING DATE: 30-AUG-1993
;            APPLICATION NUMBER: US 08/109,745
;            FILING DATE: 20-AUG-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SEESE, KATHRYN A.
;            REGISTRATION NUMBER: 32,172
;            REFERENCE/DOCKET NUMBER: 2814-C
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 587-0430
;            TELEFAX: (206) 233-0644
;            TELEX: 756822
;  INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1037 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA to mRNA
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       IMMEDIATE SOURCE:
;            CLONE: hek-L A2
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  83..799
;       FEATURE:
;            NAME/KEY:  sig_peptide
;            LOCATION:  83..139
;       FEATURE:
;            NAME/KEY:  mat_peptide
;            LOCATION:  140..796
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-904-954-1


  Query Match             100.0%;  Score 1037;  DB 34;  Length 1037;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-160;
  Matches 1037;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGC 60

Qy      61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120

Qy     121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180

Qy     181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240

Qy     241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300

Qy     301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360

Qy     361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420

Qy     421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480

Qy     481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540

Qy     541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600

Qy     601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660

Qy     661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720

Qy     721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780

Qy     781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCT 840

Qy     841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900

Qy     901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960
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Qy     961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGTCCCGAGCAGGTC 1020
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Db     961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGTCCCGAGCAGGTC 1020

Qy    1021 GTCTCGTTCCAAGATCC 1037
           |||||||||||||||||
Db    1021 GTCTCGTTCCAAGATCC 1037


RESULT   3
US-08-109-745-1
; Sequence 1, Application US/08109745
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.1
;      SOFTWARE:  Microsoft Word, Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/109,745
;      FILING DATE:  20-AUG-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1037 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  hek-L A2
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  83..799
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  83..139
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  140..796
US-08-109-745-1


  Query Match             99.7%;  Score 1033.8;  DB 5;  Length 1037;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-159;
  Matches 1035;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db       1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGC 60

Qy      61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120

Qy     121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180

Qy     181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240

Qy     241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300

Qy     301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360

Qy     361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGCCC 420

Qy     421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480
           |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCACGCGCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480

Qy     481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540

Qy     541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600

Qy     601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660

Qy     661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720

Qy     721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780

Qy     781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGGGCGGGGCT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGGGCGGGGCT 840

Qy     841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900

Qy     901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960

Qy     961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGTCCCGAGCAGGTC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGTCCCGAGCAGGTC 1020

Qy    1021 GTCTCGTTCCAAGATCC 1037
           |||||||||||||||||
Db    1021 GTCTCGTTCCAAGATCC 1037


RESULT   4
US-08-161-132-1
; Sequence 1, Application US/08161132
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;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES: . 4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/161,132
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1037 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  hek-L A2
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  83..799
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  83..139
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  140..796
US-08-161-132-1

  Query Match             99.7%;  Score 1033.8;  DB 5;  Length 1037;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-159;
  Matches 1035;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGATCTTGGAACGAGACGACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGC 60

Qy       61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGT 120

Qy      121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db      121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180

Qy      181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240

Qy      241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300

Qy      301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360

Qy      361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGCCC 420

Qy      421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCACGCGCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480

Qy      481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAA 540

Qy      541 CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541.CCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTC 600

Qy      601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAA 660

Qy      661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAG 720

Qy      721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780

Qy      781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGGGCGGGGCT 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGGGCGGGGCT 840

Qy      841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 TGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCC 900

Qy      901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 TCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCC 960

Qy      961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 CCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTC 1020

Qy     1021 GTCTCGTTCCAAGATCC 1037
            |||||||||||||||||
Db     1021 GTCTCGTTCCAAGATCC 1037


RESULT   5
US-60-172-373-10727
; Sequence 10727, Application US/60172373
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT: Lal, Preeti
;  APPLICANT: Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
;  FILE REFERENCE: GX-0006 P
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;  CURRENT APPLICATION NUMBER: US/60/172,373
;  CURRENT FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 25,772
;  SOFTWARE: PERL Program
; SEQ ID NO 10727
;   LENGTH: 1761
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 406106.1
US-60-172-373-10727

  Query Match             95.4%;  Score 988.8;  DB 56;  Length 1761;
  Best Local Similarity   99.8%;  Pred. No. 3.7e-152;
  Matches  990;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      26 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATG 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ggagaagccgggagcgcggggctcagtcggggggcggcggcggcggcggctccggggatg 60

Qy      86 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 gcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgctg 120

Qy     146 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaac 180

Qy     206 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 265
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 cagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatatt 240

Qy     266 TACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGGC 325
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 tactgcccgcactacaacagctcgggggtggccccggggcggaccggggcccggaggc 300

Qy     326 GGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCC 385
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgcc 360

Qy     386 AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAG 445
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 agccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaag 420

Qy     446 TTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGC 505
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgccggc 480

Qy     506 CACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATG 565
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 cacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggatg 540

Qy     566 AAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTC 625
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 aaggtgttcgtctgctgcgcctccacatcgcactccggggagaagccggtccccactctc 600

Qy     626 CCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAG 685
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ccccagttcaccatgggccccaatgtgaagatcaacgtgctggaagactttgagggagag 660

Qy     686 AACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACAC 745
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 aaccctcaggtgcccaagcttgagaagagcatcagcgggaccagccccaaacgggaacac 720

Qy     746 CTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGC 805
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ctgcccctggccgtgggcatcgccttcttcctcatgacgttcttggcctcctagctctgc 780

Qy     806 CCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCC 865
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 cccctcccctggggggggagagatggggcggggcttggaaggagcagggagcctttggcc 840

Qy     866 TCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGC 925
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 tctccaagggaagcctagtgggcctagacccctcctcccatggctagaagtggggcctgc 900

Qy     926 ACCATACATCTGTGTCCGCCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGAC 985
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 accatacatctgtgtccgccccctctaccccttccccccacgtagggcactgtagtggac 960

Qy     986 CAAGCACGGGGACAGCCATGGGTCCCGAGCAG 1017
           ||||||||||||||||||||||||||| || |
Db     961 caagcacggggacagccatgggtcccgggcgg 992

RESULT   6
US-60-278-258-13410
; Sequence 13410, Application US/60278258
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION:  Polynucleotide Sequence Databases, and Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms Identified Thereby
;  FILE REFERENCE: GX-0010-1 P
;  CURRENT APPLICATION NUMBER: US/60/278,258
;  CURRENT FILING DATE:  2001-03-23
;  NUMBER OF SEQ ID NOS: 17730
;  SOFTWARE: PERL Program
; SEQ ID NO 13410
;   LENGTH: 1761
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 406106.5
US-60-278-258-13410

  Query Match             95.4%;  Score 988.8;  DB 66;  Length 1761;
  Best Local Similarity   99.8%;  Pred. No. 3.7e-152;
  Matches  990;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      26 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATG 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ggagaagccgggagcgcggggctcagtcggggggcggcggcggcggcggctccggggatg 60

Qy      86 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 gcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgctg 120

Qy     146 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaac 180

Qy     206 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 265
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 cagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatatt 240

Qy     266 TACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGGC 325
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 tactgcccgcactacaacagctcgggggtggccccggggcggaccggggcccggaggc 300

Qy     326 GGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCC 385
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgcc 360

Qy     386 AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAG 445
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 agccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaag 420

Qy     446 TTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGC 505
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        421 ttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgccggc 480

Qy        506 CACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATG 565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 cacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggatg 540

Qy        566 AAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTC 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 aaggtgttcgtctgctgcgcctccacatcgcactccggggagaagccggtccccactctc 600

Qy        626 CCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAG 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ccccagttcaccatgggccccaatgtgaagatcaacgtgctggaagactttgagggagag 660

Qy        686 AACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACAC 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 aaccctcaggtgcccaagcttgagaagagcatcagcgggaccagccccaaacgggaacac 720

Qy        746 CTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGC 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ctgcccctggccgtgggcatcgccttcttcctcatgacgttcttggcctcctagctctgc 780

Qy        806 CCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCC 865
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 cccctcccctggggggggagagatggggcggggcttggaaggagcagggagcctttggcc 840

Qy        866 TCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGC 925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 tctccaagggaagcctagtgggcctagacccctcctcccatggctagaagtggggcctgc 900

Qy        926 ACCATACATCTGTGTCCGCCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGAC 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 accatacatctgtgtccgccccctctaccccttccccccacgtagggcactgtagtggac 960

Qy        986 CAAGCACGGGGACAGCCATGGGTCCCGAGCAG 1017
              ||||||||||||||||||||||||||| || |
Db        961 caagcacggggacagccatgggtcccgggcgg 992

RESULT   7
US-09-440-302A-838
; Sequence 838, Application US/09440302A
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey E.
;  TITLE OF INVENTION: Human Neurobiology Array
;  FILE REFERENCE: CLON-006CIP11
;  CURRENT APPLICATION NUMBER: US/09/440,302A
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 1193
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 838
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-440-302A-838

  Query Match             95.2%;  Score 987;  DB 18;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-152;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATG 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ggagaagccgggagcgcggggctcagtcggggggcggcggcggcggcggctccggggatg 60

Qy         86 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 gcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgctg 120

Qy        146 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 gcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaac 180

Qy        206 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 cagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatatt 240

Qy        266 TACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGC 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 tactgcccgcactacaacagctcgggggtgggccccggggcgggaccggggcccggaggc 300

Qy        326 GGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCC 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgcc 360

Qy        386 AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAG 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 agccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaag 420

Qy        446 TTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGC 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgccggc 480

Qy        506 CACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATG 565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 cacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggatg 540

Qy        566 AAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTC 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 aaggtgttcgtctgctgcgcctccacatcgcactccggggagaagccggtccccactctc 600

Qy        626 CCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAG 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ccccagttcaccatgggccccaatgtgaagatcaacgtgctggaagactttgagggagag 660

Qy        686 AACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACAC 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 aaccctcaggtgcccaagcttgagaagagcatcagcgggaccagccccaaacgggaacac 720

Qy        746 CTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGC 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ctgcccctggccgtgggcatcgccttcttcctcatgacgttcttggcctcctagctctgc 780

Qy        806 CCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCC 865
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 cccctcccctggggggggagagatggggcggggcttggaaggagcagggagcctttggcc 840

Qy        866 TCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGC 925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 tctccaagggaagcctagtgggcctagacccctcctcccatggctagaagtggggcctgc 900

Qy        926 ACCATACATCTGTGTCCGCCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGAC 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 accatacatctgtgtccgccccctctaccccttccccccacgtagggcactgtagtggac 960

Qy        986 CAAGCACGGGGACAGCCATGGGTCCCG 1012
              |||||||||||||||||||||||||||
Db        961 caagcacggggacagccatgggtcccg 987

RESULT   8
US-09-733-756-1
; Sequence 1, Application US/09733756
; GENERAL INFORMATION:
;  APPLICANT: Mack, David
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Wilson, Keith E.
;  TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER AND/OR BREAST CA
;  TITLE OF INVENTION:  COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER
;  TITLE OF INVENTION:  CANCER MODULATORS
;  FILE REFERENCE: A-69439/DJB/JJD
;  CURRENT APPLICATION NUMBER: US/09/733,756
;  CURRENT FILING DATE:  2000-12-08
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;  PRIOR APPLICATION NUMBER: US 09/525,993
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: US 09/493,444
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: US 09/453,850
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US 00/07044
;  PRIOR FILING DATE: 2000-03-15
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1743
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-733-756-1

  Query Match             88.5%;  Score 917.8;  DB 29;  Length 1743;
  Best Local Similarity   99.8%;  Pred. No. 1.5e-140;
  Matches  919;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      97 GCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCC 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 gctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgctggcccaagggcc 60

Qy     157 CGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCG 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 cggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaaccagcacctgcg 120

Qy     217 GCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCA 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatatttactgcccgca 180

Qy     277 CTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCA 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ctacaacagctcgggggtgggccccggggcgggaccggggcccggaggcggggcagagca 240

Qy     337 GTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTT 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 gtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgccagccagggctt 300

Qy     397 CAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAA 456
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 caagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaagttctcggagaa 360

Qy     457 GTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTA 516
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 gttccagcgctacagcgccttctctctgggctacgagttccacgccggccacgagtacta 420

Qy     517 CTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGT 576
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ctacatctccacgcccactcacaacctgcactggaagtgtctgaggatgaaggtgttcgt 480

Qy     577 CTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCAC 636
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ctgctgcgcctccacatcgcactccggggagaagccggtccccactctcccccagttcac 540

Qy     637 CATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGT 696
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 catgggccccaatgtgaagatcaacgtgctggaagactttgagggagagaaccctcaggt 600

Qy     697 GCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGC 756
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 gcccaagcttgagaagagcatcagcgggaccagccccaaacgggaacacctgcccctggc 660

Qy     757 CGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTG 816
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 cgtgggcatcgccttcttcctcatgacgttcttggcctcctagctctgccccctcccctg 720

Qy     817 GGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGA 876
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 gggggggagagatggggcggggcttggaaggagcagggagcctttggcctctccaaggga 780

Qy     877 AGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCATACATCT 936
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 agcctagtgggcctagacccctcctcccatggctagaagtggggcctgcaccatacatct 840

Qy     937 GTGTCCGCCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGG 996
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 gtgtccgcccccctctaccccttccccccacgtagggcactgtagtggaccaagcacgggg 900

Qy     997 ACAGCCATGGGTCCCGAGCAG 1017
           |||||||||||||||| || |
Db     901 acagccatgggtcccgggcgg 921


RESULT   9
US-08-229-402-8
; Sequence 8, Application US/08229402
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, et al.
;    TITLE OF INVENTION:  EPH Family Ligands
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Regeneron Pharmaceuticals, Inc.
;      STREET:  777 Old Saw Mill River Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10591
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/229,402
;      FILING DATE:  12-APR-1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/222,075
;      FILING DATE:  04-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/144,992
;      FILING DATE:  15-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/736,559
;      FILING DATE:  26-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kempler Ph.D., Gail M.
;      REGISTRATION NUMBER:  32,143
;      REFERENCE/DOCKET NUMBER:  REG 280
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  914-345-7400
;      TELEFAX:  914-347-2113
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1070 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA
US-08-229-402-8


  Query Match             87.5%;  Score 907.4;  DB 6;  Length 1070;
  Best Local Similarity   96.3%;  Pred. No. 7.5e-139;
  Matches  939;  Conservative    0;  Mismatches   24;  Indels   12;  Gaps    1;

Qy      44 GGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTG 103
           | | ||  | | |  |    ||||||||||||||||||||||||||||||||||||||||
Db       7 GAGATCCATTGTGCTGGAAAGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTG 66

Qy     104 CTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGG 163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 CTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGG 126
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Qy    164 GCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAG 223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 GCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAG 186

Qy    224 GGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAAC 283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 GGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAAC 246

Qy    284 AGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTG 343
          ||||||            ||||||||||||||||||||||||||||||||||||||||||
Db    247 AGCTCG------------GGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTG 294

Qy    344 CTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGC 403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 CTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGC 354

Qy    404 TGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAG 463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    355 TGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAG 414

Qy    464 CGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATC 523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    415 CGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATC 474

Qy    524 TCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGC 583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    475 TCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGC 534

Qy    584 GCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGC 643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    535 GCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGC 594

Qy    644 CCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAG 703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    595 CCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAG 654

Qy    704 CTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGC 763
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    655 CTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGC 714

Qy    764 ATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGG 823
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    715 ATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGG 774

Qy    824 AGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAG 883
          ||||||||||||||| |||||||||| |||||||||||||||||||||||||||||||||
Db    775 AGAGATGGGGCGGGGNTTGGAAGGAGNAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAG 834

Qy    884 TGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCG 943
          ||||||||||||||||||||||||| ||||||||||||||| ||||||||||||||||||
Db    835 TGGGCCTAGACCCCTCCTCCCATGGTTAGAAGTGGGGCCTGNACCATACATCTGTGTCCG 894

Qy    944 CCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCA 1003
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Db    895 CCCCCTCTACCCCTTCCCCCCANGTAGGGNACTGTAGTGGACCAAGCACGGNGACAGACA 954

Qy   1004 TGGGTCCCGAGCAGG 1018
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Db    955 TGGNTCCCGGGNGGG 969

RESULT  10
US-08-327-423-8
; Sequence 8, Application US/08327423
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, et al.
;    TITLE OF INVENTION:  METHOD OF ENHANCING THE BIOLOGICAL
;    TITLE OF INVENTION:  ACTIVITY OF EPH FAMILY LIGANDS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Regeneron Pharmaceuticals, Inc.
;      STREET:  777 Old Saw Mill River Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10591-6707
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/327,423
;      FILING DATE:  21-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/299,567
;      FILING DATE:  01-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kempler, Gail M.
;      REGISTRATION NUMBER:  32,143
;      REFERENCE/DOCKET NUMBER:  REG 290
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  914-345-7400
;      TELEFAX:  914-345-7721
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1070 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-327-423-8

  Query Match             87.5%;  Score 907.4;  DB 7;  Length 1070;
  Best Local Similarity   96.3%;  Pred. No. 7.5e-139;
  Matches  939;  Conservative    0;  Mismatches   24;  Indels   12;  Gaps    1;

Qy     44 GGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTG 103
          | | ||  | | |  |    ||||||||||||||||||||||||||||||||||||||||
Db      7 GAGATCCATTGTGCTGGAAAGGCGGCGGCGGCTCCGGGGATGGCGGCGGCTCCGCTGCTG 66

Qy    104 CTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGG 163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 CTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGG 126

Qy    164 GCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAG 223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 GCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAG 186

Qy    224 GGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAAC 283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 GGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAAC 246

Qy    284 AGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTG 343
          ||||||            ||||||||||||||||||||||||||||||||||||||||||
Db    247 AGCTCG------------GGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTG 294

Qy    344 CTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGC 403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295 CTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGC 354

Qy    404 TGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAG 463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    355 TGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAG 414

Qy    464 CGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATC 523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    415 CGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATC 474

Qy    524 TCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGC 583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    475 TCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGC 534
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Qy    584 GCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGC 643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    535 GCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGC 594

Qy    644 CCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAG 703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    595 CCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAG 654

Qy    704 CTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGC 763
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    655 CTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGC 714

Qy    764 ATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGG 823
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    715 ATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGG 774

Qy    824 AGAGATGGGGCGGGCTTGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAG 883
          |||||||||||||| |||||||||| ||||||||||||||||||||||||||||||||||
Db    775 AGAGATGGGGCGGGNTTGGAAGGAGNAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAG 834

Qy    884 TGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCG 943
          ||||||||||||||||||||||||| ||||||||||||||| ||||||||||||||||||
Db    835 TGGGCCTAGACCCCTCCTCCCATGGTTAGAAGTGGGGCCTGNACCATACATCTGTGTCCG 894

Qy    944 CCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCA 1003
          |||||||||||||||||||||| |||||| ||||||||||||||||||||| ||||| ||
Db    895 CCCCCTCTACCCCTTCCCCCCANGTAGGGNACTGTAGTGGACCAAGCACGGNGACAGACA 954

Qy   1004 TGGGTCCCGAGCAGG 1018
          ||| ||||| |  ||
Db    955 TGGNTCCCGGGNGGG 969

RESULT  11
US-09-698-010-11586
; Sequence 11586, Application US/09698010
; GENERAL INFORMATION:
;  APPLICANT:  Williamson, Mark
;  APPLICANT:  Shyjan, Andrew W.
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.2029-001
;  CURRENT APPLICATION NUMBER: US/09/698,010
;  CURRENT FILING DATE:  2000-10-27
;  PRIOR APPLICATION NUMBER:  60/162,358
;  PRIOR FILING DATE:  1999-10-29
;  NUMBER OF SEQ ID NOS:  15684
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 11586
;   LENGTH: 818
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(818)
;   OTHER INFORMATION: n = A,T,C or G
US-09-698-010-11586


  Query Match             74.5%;  Score 773;  DB 27;  Length 818;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-117;
  Matches  773;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     26 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCTCCGGGGATG 85
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     46 ggagaagccgggagcgcggggctcagtcggggggcggcggcggcggctccggggatg 105

Qy     86 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    106 gcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgctg 165

Qy    146 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    166 gcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaac 225

Qy    206 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    226 cagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatatt 285

Qy    266 TACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGC 325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    286 tactgcccgcactacaacagctcgggggtgggccccggggcgggaccggggcccggaggc 345

Qy    326 GGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCC 385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346 ggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgcc 405

Qy    386 AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAG 445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    406 agccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaag 465

Qy    446 TTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGC 505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    466 ttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgccggc 525

Qy    506 CACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATG 565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    526 cacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggatg 585

Qy    566 AAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTC 625
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    586 aaggtgttcgtctgctgcgcctccacatcgcactccggggagaagccggtccccactctc 645

Qy    626 CCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAG 685
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    646 ccccagttcaccatgggccccaatgtgaagatcaacgtgctggaagactttgagggagag 705

Qy    686 AACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACAC 745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    706 aaccctcaggtgcccaagcttgagaagagcatcagcgggaccagccccaaacgggaacac 765

Qy    746 CTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTA 798
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 ctgcccctggccgtgggcatcgccttcttcctcatgacgttcttggcctccta 818

RESULT  12
US-09-948-941-53
; Sequence 53, Application US/09948941
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH CANCER, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL000788
;  CURRENT APPLICATION NUMBER: US/09/948,941
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/231,328
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 12618
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Human
US-09-948-941-53


  Query Match             69.1%;  Score 717;  DB 35;  Length 717;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-108;
  Matches  717;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     83 ATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTG 142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 atggcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctg 60

Qy    143 CTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCC 202
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ctggcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctcc 120

Qy    203 AACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGAT 262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 aaccagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggat 180

Qy    263 ATTTACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGA 322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 atttactgcccgcactacaacagctcgggggtggccccggggcggaccggggcccgga 240

Qy    323 GGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAAC 382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ggcggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaac 300

Qy    383 GCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATC 442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 gccagccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatc 360

Qy    443 AAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCC 502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 aagttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgcc 420

Qy    503 GGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGG 562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ggccacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgagg 480

Qy    563 ATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACT 622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 atgaaggtgttcgtctgctgcgcctccacatcgcactccggggagaagccggtccccact 540

Qy    623 CTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGA 682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ctcccccagttcaccatgggccccaatgtgaagatcaacgtgctggaagactttgaggga 600

Qy    683 GAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAA 742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 gagaaccctcaggtgcccaagcttgagaagagcatcagcgggaccagccccaaacgggaa 660

Qy    743 CACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAG 799
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 cacctgcccctggccgtgggcatcgccttcttcctcatgacgttcttggcctcctag 717


RESULT  13
US-09-948-941-98
; Sequence 98, Application US/09948941
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH CANCER, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL000788
;  CURRENT APPLICATION NUMBER: US/09/948,941
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/231,328
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 12618
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Human
US-09-948-941-98


  Query Match             69.1%;  Score 717;  DB 35;  Length 717;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-108;
  Matches  717;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     83 ATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTG 142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 atggcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctg 60

Qy    143 CTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCC 202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ctggcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctcc 120

Qy    203 AACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGAT 262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 aaccagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggat 180

Qy    263 ATTTACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGA 322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 atttactgcccgcactacaacagctcgggggtggccccggggcggaccggggcccgga 240

Qy    323 GGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAAC 382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ggcggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaac 300

Qy    383 GCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATC 442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 gccagccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatc 360

Qy    443 AAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCC 502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 aagttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgcc 420

Qy    503 GGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGG 562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ggccacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgagg 480

Qy    563 ATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACT 622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 atgaaggtgttcgtctgctgcgcctccacatcgcactccggggagaagccggtccccact 540

Qy    623 CTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGA 682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ctcccccagttcaccatgggccccaatgtgaagatcaacgtgctggaagactttgaggga 600

Qy    683 GAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAA 742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 gagaaccctcaggtgcccaagcttgagaagagcatcagcgggaccagccccaaacgggaa 660

Qy    743 CACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAG 799
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 cacctgcccctggccgtgggcatcgccttcttcctcatgacgttcttggcctcctag 717


RESULT  14
US-09-287-618-6642
; Sequence 6642, Application US/09287618
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-768
;  CURRENT APPLICATION NUMBER: US/09/287,618
;  CURRENT FILING DATE: 1999-04-02
;  NUMBER OF SEQ ID NOS: 35865
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6642
;   LENGTH: 421
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(421)
;   OTHER INFORMATION: n = A,T,C or G
US-09-287-618-6642


  Query Match             39.7%;  Score 411.8;  DB 16;  Length 421;
  Best Local Similarity   99.3%;  Pred. No. 7.3e-58;
  Matches  413;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    121 GCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCA 180
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           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5 gtccgtgccgctgctgccgctgctggcccaagggcccggaggggcgctgggaaaccggca 64

Qy     181 TGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65 tgcggtgtactggaacagctccaaccagcacctgcggcgagagggctacaccgtgcaggt 124

Qy     241 GAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     125 gaacgtgaacgactatctggatatttactgcccgcactacaacagctcgggggtgggccc 184

Qy     301 CGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 cggggcgggaccggggcccggaggcggggcagagcagtacgtgctgtacatggtgagccg 244

Qy     361 CAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     245 caacggctaccgcacctgcaacgccagccagggcttcaagcgctgggagtgcaaccggcc 304

Qy     421 GCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTC 480
           |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db     305 gcacgccccgcacagncccatcaagttctcggagaagttccagcgctacagcgccttctc 364

Qy     481 TCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTC 536
           |||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     365 tctgagctacgagttccacgccggccacgagtactactacatctccacgcccactc 420

RESULT  15
US-09-221-481-182
; Sequence 182, Application US/09221481
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey
;  TITLE OF INVENTION: Human Array
;  FILE REFERENCE: CLON-006CIP6
;  CURRENT APPLICATION NUMBER: US/09/221,481
;  CURRENT FILING DATE:  1998-12-28
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 589
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 182
;   LENGTH: 392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-221-481-182


  Query Match            37.8%;  Score 392;  DB 16;  Length 392;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-54;
  Matches  392;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     200 TCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTG 259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 tccaaccagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctg 60

Qy     260 GATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCC 319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 gatatttactgcccgcactacaacagctcgggggtgggccccggggcgggaccggggccc 120

Qy     320 GGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGC 379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ggaggcggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgc 180

Qy     380 AACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCC 439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 aacgccagccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagcccc 240

Qy     440 ATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCAC 499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 atcaagttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccac 300

Qy     500 GCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTG 559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 gccggccacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctg 360

Qy     560 AGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
           ||||||||||||||||||||||||||||||||
Db     361 aggatgaaggtgttcgtctgctgcgcctccac 392


Search completed: September 28, 2002, 01:28:23
Job time: 14513 sec
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                      GenCore version 4.5
           Copyright (c) 1993 - 2000  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          September 27, 2002, 22:03:20 ; Search time 401.97 Seconds
                                                (without alignments)
                                                8379.801 Million cell updates/sec

Title:           US-09-904-954-1
Perfect score:   1037
Sequence:        1 GGATCTTGGAACGAGACGAC..........GTCGTCTCGTTCCAAGATCC 1037

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2167403 seqs, 1624121725 residues

Total number of hits satisfying chosen parameters:      4334806

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_NA_New:*
                1:  /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
                2:  /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
                3:  /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
                4:  /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
                5:  /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
                6:  /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
                7:  /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
                8:  /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                  SUMMARIES
                       %
Result                 Query
  No.     Score   Match Length DB  ID                        Description
-------------------------------------------------------------------------------
    1      987    95.2    987  1  PCT-US02-25766-6624        Sequence 6624, Ap
    2      987    95.2    987  5  US-09-053-375B-186         Sequence 186, App
    3      987    95.2    987  5  US-09-440-302B-838         Sequence 838, App
    4      392    37.8    392  5  US-09-442-366A-292         Sequence 292, App
    5      391    37.7    391  5  US-09-440-302B-241         Sequence 241, App
    6    350.8    33.8    442  5  US-09-918-995-27387        Sequence 27387, A
    7    153.8    14.8   1594  5  US-09-053-375B-1095        Sequence 1095, Ap
    8      117    11.3   1557  5  US-09-919-039-161          Sequence 161, App
    9    116.4    11.2   1480  1  PCT-US02-13644-14          Sequence 14, Appl
   10    116.4    11.2   1480  5  US-09-053-375B-1504        Sequence 1504, Ap
   11    116.4    11.2   1480  5  US-09-442-384B-743         Sequence 743, App
   12    116.4    11.2   1480  5  US-09-440-302B-837         Sequence 837, App
   13    116.4    11.2   1480  7  US-10-007-926A-227         Sequence 227, App
   14    116.4    11.2   1480  7  US-10-136-819-14          Sequence 14, Appl
   15    116.4    11.2   1480  7  US-10-171-311-49          Sequence 49, Appl
   16    116.4    11.2   1480  7  US-10-171-581-190         Sequence 190, App
   17    116.4    11.2   1496  1  PCT-US02-24563-287         Sequence 287, App
   18    116.4    11.2   1496  6  US-10-194-359-287         Sequence 287, App
   19    116.4    11.2   1496  6  US-10-192-007-287         Sequence 287, App
   20    116.4    11.2   1496  6  US-10-210-951-39          Sequence 39, Appl
   21    116.4    11.2   1496  6  US-10-211-858-39          Sequence 39, Appl
   22    116.4    11.2   1496  6  US-10-211-884-39          Sequence 39, Appl
   23    116.4    11.2   1496  6  US-10-230-417-287         Sequence 287, App
   24    116.4    11.2   1496  7  US-10-121-049-287         Sequence 287, App
   25    116.4    11.2   1496  7  US-10-121-050-287         Sequence 287, App
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   26    116.4    11.2   1496  7  US-10-121-053-287         Sequence 287, App
   27    116.4    11.2   1496  7  US-10-121-043-287         Sequence 287, App
   28    116.4    11.2   1496  7  US-10-121-044-287         Sequence 287, App
   29    116.4    11.2   1496  7  US-10-121-047-287         Sequence 287, App
   30    116.4    11.2   1496  7  US-10-121-054-287         Sequence 287, App
   31    116.4    11.2   1496  7  US-10-121-056-287         Sequence 287, App
   32    116.4    11.2   1496  7  US-10-121-057-287         Sequence 287, App
   33    116.4    11.2   1496  7  US-10-121-058-287         Sequence 287, App
   34    116.4    11.2   1496  7  US-10-121-060-287         Sequence 287, App
   35    116.4    11.2   1496  7  US-10-121-063-287         Sequence 287, App
   36    116.4    11.2   1496  7  US-10-123-108-287         Sequence 287, App
   37    116.4    11.2   1496  7  US-10-123-154-287         Sequence 287, App
   38    116.4    11.2   1496  7  US-10-123-156-287         Sequence 287, App
   39    116.4    11.2   1496  7  US-10-123-157-287         Sequence 287, App
   40    116.4    11.2   1496  7  US-10-123-212-287         Sequence 287, App
   41    116.4    11.2   1496  7  US-10-123-213-287         Sequence 287, App
   42    116.4    11.2   1496  7  US-10-123-109-287         Sequence 287, App
   43    116.4    11.2   1496  7  US-10-121-041-287         Sequence 287, App
   44    116.4    11.2   1496  7  US-10-121-045-287         Sequence 287, App
   45    116.4    11.2   1496  7  US-10-121-046-287         Sequence 287, App

                                  ALIGNMENTS


RESULT   1
PCT-US02-25766-6624
; Sequence 6624, Application PC/TUS0225766
; GENERAL INFORMATION:
;  APPLICANT: GENE LOGIC, INC.
;  APPLICANT:  MUNGER, William E
;  APPLICANT:  FAULK, Ronald
;  APPLICANT:  SUN, Hongwei
;  APPLICANT:  SASAI, Hitoshi
;  APPLICANT:  WAGA, Iwao
;  APPLICANT:  YAMAMOTO, Jun
;  TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
;  FILE REFERENCE: 44921-5068-WO
;  CURRENT APPLICATION NUMBER: PCT/US02/25766
;  CURRENT FILING DATE:  2002-08-14
;  PRIOR APPLICATION NUMBER: US 60/311,837
;  PRIOR FILING DATE: 2001-08-14
;  NUMBER OF SEQ ID NOS: 13946
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6624
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. U14187
PCT-US02-25766-6624


  Query Match             95.2%;  Score 987;  DB 1;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-154;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATG 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ggagaagccgggagcgcggggctcagtcggggggcggcggcggcggcggctccggggatg 60

Qy         86 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 gcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgctg 120

Qy        146 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 gcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaac 180

Qy        206 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 cagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatatt 240
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Qy      266 TACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGGC 325
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 tactgcccgcactacaacagctcgggggtggccccggggcggaccggggcccggaggc 300

Qy      326 GGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCC 385
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 ggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgcc 360

Qy      386 AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAG 445
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 agccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaag 420

Qy      446 TTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGC 505
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 ttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgccggc 480

Qy      506 CACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATG 565
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 cacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggatg 540

Qy      566 AAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTC 625
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 aaggtgttcgtctgctgcgcctccacatcgcactccggggagaagccggtccccactctc 600

Qy      626 CCCCAGTTCACCATGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAG 685
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 ccccagttcaccatggccccaatgtgaagatcaacgtgctggaagactttgagggagag 660

Qy      686 AACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACAC 745
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 aaccctcaggtgcccaagcttgagaagagcatcagcgggaccagccccaaacgggaacac 720

Qy      746 CTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGC 805
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 ctgcccctggccgtgggcatcgccttcttcctcatgacgttcttggcctcctagctctgc 780

Qy      806 CCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCC 865
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 cccctcccctggggggggagagatggggcggggcttggaaggagcagggagcctttggcc 840

Qy      866 TCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGC 925
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 tctccaagggaagcctagtgggcctagacccctcctcccatggctagaagtggggcctgc 900

Qy      926 ACCATACATCTGTGTCCGCCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGAC 985
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 accatacatctgtgtccgccccctctaccccttccccccacgtagggcactgtagtggac 960

Qy      986 CAAGCACGGGGACAGCCATGGGTCCCG 1012
            |||||||||||||||||||||||||||
Db      961 caagcacggggacagccatgggtcccg 987

RESULT   2
US-09-053-375B-186
; Sequence 186, Application US/09053375B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Bibilashvilli, Robert
;  TITLE OF INVENTION: Nucleic Acid Arrays
;  FILE REFERENCE: CLON-006
;  CURRENT APPLICATION NUMBER: US/09/053,375B
;  CURRENT FILING DATE:  1998-08-31
;  NUMBER OF SEQ ID NOS: 1543
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 186
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-053-375B-186

  Query Match             95.2%;  Score 987;  DB 5;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-154;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       26 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCTCCGGGGATG 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ggagaagccgggagcgcggggctcagtcggggggcggcggcggcggctccggggatg 60

Qy       86 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 gcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgctg 120

Qy      146 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 gcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaac 180

Qy      206 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 265
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 cagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatatt 240

Qy      266 TACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGGC 325
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 tactgcccgcactacaacagctcgggggtggccccggggcggaccggggcccggaggc 300

Qy      326 GGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCC 385
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 ggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgcc 360

Qy      386 AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAG 445
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 agccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaag 420

Qy      446 TTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGC 505
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 ttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgccggc 480

Qy      506 CACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATG 565
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 cacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggatg 540

Qy      566 AAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTC 625
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 aaggtgttcgtctgctgcgcctccacatcgcactccggggagaagccggtccccactctc 600

Qy      626 CCCCAGTTCACCATGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAG 685
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 ccccagttcaccatggccccaatgtgaagatcaacgtgctggaagactttgagggagag 660

Qy      686 AACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACAC 745
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 aaccctcaggtgcccaagcttgagaagagcatcagcgggaccagccccaaacgggaacac 720

Qy      746 CTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGC 805
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Db      721 ctgcccctggccgtgggcatcgccttcttcctcatgacgttcttggcctcctagctctgc 780

Qy      806 CCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCC 865
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 cccctcccctggggggggagagatggggcggggcttggaaggagcagggagcctttggcc 840

Qy      866 TCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGC 925
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 tctccaagggaagcctagtgggcctagacccctcctcccatggctagaagtggggcctgc 900

Qy      926 ACCATACATCTGTGTCCGCCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGAC 985
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 accatacatctgtgtccgccccctctaccccttccccccacgtagggcactgtagtggac 960

Qy      986 CAAGCACGGGGACAGCCATGGGTCCCG 1012
            |||||||||||||||||||||||||||
Db      961 caagcacggggacagccatgggtcccg 987

RESULT   3
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US-09-440-302B-838
; Sequence 838, Application US/09440302B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey E.
;  TITLE OF INVENTION: Human Neurobiology Array
;  FILE REFERENCE: CLON-006CIP11
;  CURRENT APPLICATION NUMBER: US/09/440,302B
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 1193
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 838
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-440-302B-838

  Query Match             95.2%;  Score 987;  DB 5;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-154;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     26 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATG 85
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ggagaagccgggagcgcggggctcagtcggggggcggcggcggcggcggctccggggatg 60

Qy     86 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgctg 120

Qy    146 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaac 180

Qy    206 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 cagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatatt 240

Qy    266 TACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGC 325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 tactgcccgcactacaacagctcgggggtgggccccggggcgggaccggggcccggaggc 300

Qy    326 GGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCC 385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgcc 360

Qy    386 AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAG 445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 agccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaag 420

Qy    446 TTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGC 505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgccggc 480

Qy    506 CACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATG 565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 cacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggatg 540

Qy    566 AAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTC 625
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 aaggtgttcgtctgctgcgcctccacatcgcactccggggagaagccggtccccactctc 600

Qy    626 CCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAG 685
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ccccagttcaccatgggccccaatgtgaagatcaacgtgctggaagactttgagggagag 660

Qy    686 AACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACAC 745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 aaccctcaggtgcccaagcttgagaagagcatcagcgggaccagccccaaacgggaacac 720

Qy    746 CTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGC 805
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ctgcccctggccgtgggcatcgccttcttcctcatgacgttcttggcctcctagctctgc 780

Qy    806 CCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCC 865
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 cccctcccctggggggggagagatggggcggggcttggaaggagcagggagcctttggcc 840

Qy    866 TCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGC 925
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 tctccaagggaagcctagtgggcctagacccctcctcccatggctagaagtggggcctgc 900

Qy    926 ACCATACATCTGTGTCCGCCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGAC 985
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 accatacatctgtgtccgccccctctaccccttccccccacgtagggcactgtagtggac 960

Qy    986 CAAGCACGGGGACAGCCATGGGTCCCG 1012
          |||||||||||||||||||||||||||
Db    961 caagcacggggacagccatgggtcccg 987

RESULT   4
US-09-442-366A-292
; Sequence 292, Application US/09442366A
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey E.
;  TITLE OF INVENTION: Human Array
;  FILE REFERENCE: CLON-006CIP13
;  CURRENT APPLICATION NUMBER: US/09/442,366A
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 2216
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292
;   LENGTH: 392
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic gene fragment
US-09-442-366A-292

  Query Match             37.8%;  Score 392;  DB 5;  Length 392;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-56;
  Matches  392;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    200 TCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTG 259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 tccaaccagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctg 60

Qy    260 GATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCC 319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gatatttactgcccgcactacaacagctcgggggtgggccccggggcgggaccggggccc 120

Qy    320 GGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGC 379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ggaggcggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgc 180

Qy    380 AACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCC 439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 aacgccagccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagcccc 240

Qy    440 ATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCAC 499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 atcaagttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccac 300

Qy    500 GCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTG 559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 gccggccacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctg 360

Qy    560 AGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
          ||||||||||||||||||||||||||||||||
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```
Db    361 aggatgaaggtgttcgtctgctgcgcctccac 392

RESULT   5
US-09-440-302B-241
; Sequence 241, Application US/09440302B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey E.
;  TITLE OF INVENTION: Human Neurobiology Array
;  FILE REFERENCE: CLON-006CIP11
;  CURRENT APPLICATION NUMBER: US/09/440,302B
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 1193
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 241
;   LENGTH: 391
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302B-241

  Query Match             37.7%;  Score 391;  DB 5;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-56;
  Matches  391;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    200 TCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTG 259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 tccaaccagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctg 60

Qy    260 GATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCC 319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gatatttactgcccgcactacaacagctcgggggtgggccccggggcgggaccggggccc 120

Qy    320 GGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGC 379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ggaggcggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgc 180

Qy    380 AACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCC 439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 aacgccagccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagcccc 240

Qy    440 ATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCAC 499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 atcaagttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccac 300

Qy    500 GCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTG 559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 gccggccacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctg 360

Qy    560 AGGATGAAGGTGTTCGTCTGCTGCGCCTCCA 590
          |||||||||||||||||||||||||||||||
Db    361 aggatgaaggtgttcgtctgctgcgcctcca 391

RESULT   6
US-09-918-995-27387
; Sequence 27387, Application US/09918995
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27387
;   LENGTH: 442
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(442)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27387

  Query Match             33.8%;  Score 350.8;  DB 5;  Length 442;
  Best Local Similarity   93.8%;  Pred. No. 2.1e-49;
  Matches  364;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy    630 AGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACC 689
          | |  |||||  |  |  | |  ||    || | ||||||||||||||||||||||||||
Db      6 actggaccatccganctgagggcaatcgaaangcgctggaagactttgagggagagaacc 65

Qy    690 CTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGC 749
          ||||||||||||||||||||  |||||||||||||  |||||||||||||||||||||||
Db     66 ctcaggtgcccaagcttgagttgagcatcagcgggttcagccccaaacgggaacacctgc 125

Qy    750 CCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCC 809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 ccctggccgtgggcatcgccttcttcctcatgacgttcttggcctcctagctctgccccc 185

Qy    810 TCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCCTCTC 869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 tcccctgggggggagagatggggcggggcttggaaggagcagggagcctttggcctctc 245

Qy    870 CAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCA 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 caagggaagcctagtgggcctagacccctcctcccatggctagaagtggggcctgcacca 305

Qy    930 TACATCTGTGTCCGCCCCCTCTACCCCTTCCCCCACGTAGGGCACTGTAGTGGACCAAG 989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 tacatctgtgtccgcccccctctaccccttcccccacgtagggcactgtagtggaccaag 365

Qy    990 CACGGGGACAGCCATGGGTCCCGAGCAG 1017
          ||||||||||||||||||||||| || |
Db    366 cacggggacagccatgggtcccgggcgg 393

RESULT   7
US-09-053-375B-1095
; Sequence 1095, Application US/09053375B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Bibilashvilli, Robert
;  TITLE OF INVENTION: Nucleic Acid Arrays
;  FILE REFERENCE: CLON-006
;  CURRENT APPLICATION NUMBER: US/09/053,375B
;  CURRENT FILING DATE:  1998-08-31
;  NUMBER OF SEQ ID NOS: 1543
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1095
;   LENGTH: 1594
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-053-375B-1095

  Query Match             14.8%;  Score 153.8;  DB 5;  Length 1594;
  Best Local Similarity   63.1%;  Pred. No. 6e-17;
  Matches  326;  Conservative    0;  Mismatches  147;  Indels   44;  Gaps    4;

Qy     50 AGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGG--ATGGCGGCGGCTCCGCTGCTGCTGC 107
          ||   ||| |||   |||||||| || ||||||  |||||| | || | ||  |  |||||
Db     20 agcgagggagcgagcgcggcggcagcaccggggccatggcgcccgcgcagcgcccgctgc 79

Qy    108 TGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGC 167
          ||| ||||||  |||   ||| || |||||    ||    | | |  || |   ||||
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Db     80 tgccgctgctgctgctgctgctgccgctgcgtgcgcgcaacgaggacccggcccgggcca 139

Qy    168 TGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGC--------- 218
            |   ||||  | || || ||||||||| |   |||||      | | |
Db    140 acgctgaccgatacgcagtctactggaaccgtagcaaccccaggtttcaggtgagcgctg 199

Qy    219 ---------GAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACT 269
                   | |  ||||| |||||| |||||| | | ||||||| |||||||| ||||
Db    200 tgggtgatggcggcggctataccgtggaggtgagcatcaacgactacctggatatctact 259

Qy    270 GCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGG 329
          |||| |||||                     |||||||   | |   || |  |   |
Db    260 gcccacacta---------------------cggggcgccgctgcccccggctgagcgca 298

Qy    330 CAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCC 389
            |||| |||| | ||||||||||||||   |  | ||| ||  | |||| ||  | | |
Db    299 tggagcggtacatcctgtacatggtgaatggtgagggccacgcctcctgtgaccaccggc 358

Qy    390 AG---GGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGT 446
          ||   ||||||||||||||||| |||||||||||    || ||     | ||| ||||||
Db    359 agcgaggcttcaagcgctgggaatgcaaccggcccgcagcgcccgggggacccctcaagt 418

Qy    447 TCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCC 506
          |||| ||||||||||| | || || | |||| || |||||||  ||||||||   | ||||
Db    419 tctcagagaagttccaactcttcaccccctttccctgggctttgagttccggcctggcc 478

Qy    507 ACGAGTACTACTACATCTCCACGCCCACTCACAACCT 543
          |||| |||||||||||||  |  |  ||| ||||||
Db    479 acgaatactactacatctctgccacacctcccaacct 515

RESULT    8
US-09-919-039-161
; Sequence 161, Application US/09919039
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 401
;  SOFTWARE: PERL Program
; SEQ ID NO 161
;   LENGTH: 1557
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 405844.22
US-09-919-039-161


  Query Match             11.3%;  Score 117;  DB 5;  Length 1557;
  Best Local Similarity   53.4%;  Pred. No. 7.2e-11;
  Matches  308;  Conservative    0;  Mismatches  245;  Indels   24;  Gaps    2;

Qy     18 GACCTGCTGGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTC 77
          || |||   |   |||   ||  |||  ||  ||   |   | ||   |   | |   |
Db     14 gatctgtgagcccagcgctgactgcgccgcggagaaagccagtgggaacccagacccata 73

Qy     78 CGGGGATGGCGGCGGCTCCGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGC 137
           | |    ||| |  | |     |||     ||  |      ||    | |    |   |
Db     74 ggagacccgcgtccccgctcggcctggccaggccccgcgctatggagttcctctgggccc 133

Qy    138 CGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACA 197
          | ||  |||  |   |   | |   |||    |   | || ||  | || | ||||||||
Db    134 ctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccgtcttctggaaca 193

Qy    198 GCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATC 257
          | || || |   |  | |||   |||| ||||||| | || ||| |  ||| |||||
Db    194 gttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactacg 253
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Qy    258 TGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGC 317
          |||| ||   ||| ||||||||||  |          ||||    ||  ||
Db    254 tggacatcatctgtccgcactatgaagatcactctgtggcagacgctgcca--------- 304

Qy    318 CCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCT 377
                        ||||||||| | |||||| |||||   |   | |  ||||     |
Db    305 ------------tggagcagtacatactgtacctggtggagcatgaggagtaccagctgt 352

Qy    378 GCAACGCC---AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACA 434
          || |  ||     | ||| |      |||||| |||||||||||||    |||  |||
Db    353 gccagccccagtccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcatg 412

Qy    435 GCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGT 494
          ||||    ||| | || |||||||||||||||| ||   | ||| | |||||| | ||||
Db    413 gcccggagaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggagt 472

Qy    495 TCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGT 554
          || | |  || |||   |||||||||||||||  ||||  ||| | |   |       |
Db    473 tcaaagaaggacacagctactactacatctccaaacccatccaccagcatgaagaccgct 532

Qy    555 GTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
          |  ||||| ||||||||   ||| |  ||     |||
Db    533 gcttgaggttgaaggtgactgtcagtggcaaaatcac 569

RESULT    9
PCT-US02-13644-14
; Sequence 14, Application PC/TUS0213644
; GENERAL INFORMATION:
;  APPLICANT: Chien, Kenneth
;  APPLICANT:  Hoshijima, Masahiko
;  TITLE OF INVENTION: Non-viral vesicle vector for cardiac specific gene delivery
;  FILE REFERENCE: 6627-PA1198
;  CURRENT APPLICATION NUMBER: PCT/US02/13644
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: 60/287,423
;  PRIOR FILING DATE: 2001-04-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 1480
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-13644-14


  Query Match             11.2%;  Score 116.4;  DB 1;  Length 1480;
  Best Local Similarity   57.4%;  Pred. No. 9.1e-11;
  Matches  263;  Conservative    0;  Mismatches  171;  Indels   24;  Gaps    2;

Qy    137 CCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAAC 196
          || ||  |||  |   |   | |   |||    |   | || ||  | ||  | |||||||
Db     92 cctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccgtcttctggaac 151

Qy    197 AGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTAT 256
          || || || |   |  | ||| |   |||| |||||| | || ||| |  |||| |||||
Db    152 agttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactac 211

Qy    257 CTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGG 316
           |||| ||   ||| ||||||||||  |          ||||    ||  ||
Db    212 gtggacatcatctgtccgcactatgaagatcactctgtggcagacgctgccatg------ 265

Qy    317 CCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACC 376
                         ||||||||| | |||||| |||||   |   | |  ||||
Db    266 ---------------gagcagtacatactgtacctggtggagcatgaggagtaccagctg 310

Qy    377 TGCAACGCCAG---CCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCAC 433
          ||| |  ||     | ||| |      |||||| |||||||||||||    |||  |||
Db    311 tgccagccccagtccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcat 370

Qy    434 AGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAG 493
           ||||    ||| | || |||||||||||||||| ||   | ||| | |||||| | |||
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Db    371 ggcccggagaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggag 430

Qy    494 TTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAG 553
          ||| | |  || |||   ||||||||||||||||  ||||  ||| | |   |
Db    431 ttcaaagaaggacacagctactactacatctccaaacccatccaccagcatgaagaccgc 490

Qy    554 TGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
          ||  ||||| ||||||||   ||| |  ||     |||
Db    491 tgcttgaggttgaaggtgactgtcagtggcaaaatcac 528

RESULT  10
US-09-053-375B-1504
; Sequence 1504, Application US/09053375B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Bibilashvilli, Robert
;  TITLE OF INVENTION: Nucleic Acid Arrays
;  FILE REFERENCE: CLON-006
;  CURRENT APPLICATION NUMBER: US/09/053,375B
;  CURRENT FILING DATE:  1998-08-31
;  NUMBER OF SEQ ID NOS: 1543
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1504
;   LENGTH: 1480
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-053-375B-1504


  Query Match             11.2%;  Score 116.4;  DB 5;  Length 1480;
  Best Local Similarity   57.4%;  Pred. No. 9.1e-11;
  Matches  263;  Conservative    0;  Mismatches  171;  Indels   24;  Gaps    2;

Qy    137 CCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAAC 196
          || ||  |||  |   |   | |   |||    |   | || ||  | || | |||||||
Db     92 cctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccgtcttctggaac 151

Qy    197 AGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTAT 256
          || || || |   |  | |||   |||| ||||||| | || ||| |  |||| |||||
Db    152 agttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactac 211

Qy    257 CTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGG 316
           |||| ||   ||| ||||||||  |          ||||    ||  ||
Db    212 gtggacatcatctgtccgcactatgaagatcactctgtggcagacgctgccatg------ 265

Qy    317 CCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACC 376
                         ||||||||| | |||||| |||||   |   | |  ||||
Db    266 ---------------gagcagtacatactgtacctggtggagcatgaggagtaccagctg 310

Qy    377 TGCAACGCCAG---CCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCAC 433
          ||| |  ||     | ||| |      |||||| |||||||||||||     |||  |||
Db    311 tgccagccccagtccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcat 370

Qy    434 AGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAG 493
           ||||    ||| | || |||||||||||||||| ||   | ||| | ||||||| | |||
Db    371 ggcccggagaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggag 430

Qy    494 TTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAG 553
          ||| | |  || |||   ||||||||||||||||  ||||  ||| | |   |
Db    431 ttcaaagaaggacacagctactactacatctccaaacccatccaccagcatgaagaccgc 490

Qy    554 TGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
          ||  ||||| ||||||||   ||| |  ||     |||
Db    491 tgcttgaggttgaaggtgactgtcagtggcaaaatcac 528

RESULT  11
US-09-442-384B-743
; Sequence 743, Application US/09442384B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey
;  TITLE OF INVENTION: Hematology/Immunology Array
;  FILE REFERENCE: CLON-006CIP15
;  CURRENT APPLICATION NUMBER: US/09/442,384B
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 830
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 743
;   LENGTH: 1480
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-442-384B-743


  Query Match             11.2%;  Score 116.4;  DB 5;  Length 1480;
  Best Local Similarity   57.4%;  Pred. No. 9.1e-11;
  Matches  263;  Conservative    0;  Mismatches  171;  Indels   24;  Gaps    2;

Qy    137 CCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAAC 196
          || ||  |||  |   |   | |   |||    |   | || ||  | || | |||||||
Db     92 cctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccgtcttctggaac 151

Qy    197 AGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTAT 256
          || || || |   |  | |||   |||| ||||||| | || ||| |  |||| |||||
Db    152 agttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactac 211

Qy    257 CTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGG 316
           |||| ||   ||| ||||||||  |          ||||    ||  ||
Db    212 gtggacatcatctgtccgcactatgaagatcactctgtggcagacgctgccatg------ 265

Qy    317 CCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACC 376
                         ||||||||| | |||||| |||||   |   | |  ||||
Db    266 ---------------gagcagtacatactgtacctggtggagcatgaggagtaccagctg 310

Qy    377 TGCAACGCCAG---CCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCAC 433
          ||| |  ||     | ||| |      |||||| |||||||||||||     |||  |||
Db    311 tgccagccccagtccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcat 370

Qy    434 AGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAG 493
           ||||    ||| | || |||||||||||||||| ||   | ||| | ||||||| | |||
Db    371 ggcccggagaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggag 430

Qy    494 TTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAG 553
          ||| | |  || |||   ||||||||||||||||  ||||  ||| | |   |
Db    431 ttcaaagaaggacacagctactactacatctccaaacccatccaccagcatgaagaccgc 490

Qy    554 TGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
          ||  ||||| ||||||||   ||| |  ||     |||
Db    491 tgcttgaggttgaaggtgactgtcagtggcaaaatcac 528

RESULT  12
US-09-440-302B-837
; Sequence 837, Application US/09440302B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey E.
;  TITLE OF INVENTION: Human Neurobiology Array
;  FILE REFERENCE: CLON-006CIP11
;  CURRENT APPLICATION NUMBER: US/09/440,302B
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 1193
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 837
;   LENGTH: 1480
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-440-302B-837
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  Query Match             11.2%;  Score 116.4;  DB 5;  Length 1480;
  Best Local Similarity   57.4%;  Pred. No. 9.1e-11;
  Matches  263;  Conservative    0;  Mismatches  171;  Indels   24;  Gaps    2;

Qy    137 CCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAAC 196
          || ||  |||  |   |   | |   |||    |   | || ||  | || | |||||||
Db     92 cctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccgtcttctggaac 151

Qy    197 AGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTAT 256
          || || || |   |  | |||   |||| ||||||| | || ||| |  |||| |||||
Db    152 agttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactac 211

Qy    257 CTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGACCGGGG 316
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Db    212 gtggacatcatctgtccgcactatgaagatcactctgtggcagacgctgccatg------ 265

Qy    317 CCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACC 376
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Db    266 ---------------gagcagtacatactgtacctggtggagcatgaggagtaccagctg 310

Qy    377 TGCAACGCCAG---CCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCAC 433
          ||| |  ||     | ||| |      |||||| |||||||||||||    |||  |||
Db    311 tgccagccccagtccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcat 370

Qy    434 AGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAG 493
           ||||    ||| | || |||||||||||||||| ||   | ||| | |||||| | |||
Db    371 ggcccggagaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggag 430

Qy    494 TTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAG 553
          ||| | |  || |||   ||||||||||||||||  ||||  ||| | |   |
Db    431 ttcaaagaaggacacagctactactacatctccaaacccatccaccagcatgaagaccgc 490

Qy    554 TGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
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Db    491 tgcttgaggttgaaggtgactgtcagtggcaaaatcac 528

RESULT  13
US-10-007-926A-227
; Sequence 227, Application US/10007926A
; GENERAL INFORMATION:
;  APPLICANT: BERTUCCI, FRANCOIS
;  APPLICANT:  HOULGATTE, REMI
;  APPLICANT:  BIRNBAUM, DANIEL
;  APPLICANT:  NGUYEN, CATHERINE
;  APPLICANT:  VIENS, PATRICE
;  APPLICANT:  FERT, VINCENT
;  TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
;  TITLE OF INVENTION:  USING ARRAYS OF CANDIDATE GENES
;  FILE REFERENCE: 1546-R-00
;  CURRENT APPLICATION NUMBER: US/10/007,926A
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: 60/254,090
;  PRIOR FILING DATE: 2000-12-08
;  NUMBER OF SEQ ID NOS: 468
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 227
;   LENGTH: 1480
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: ephrin-a1 (EFNA1) gene.
US-10-007-926A-227

  Query Match             11.2%;  Score 116.4;  DB 7;  Length 1480;
  Best Local Similarity   57.4%;  Pred. No. 9.1e-11;
  Matches  263;  Conservative    0;  Mismatches  171;  Indels   24;  Gaps    2;

Qy    137 CCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAAC 196
          || ||  |||  |   |   | |   |||    |   | || ||  | || | |||||||
Db     92 cctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccgtcttctggaac 151

Qy    197 AGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTAT 256
          || || || |   |  | |||   |||| ||||||| | || ||| |  |||| |||||
Db    152 agttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactac 211

Qy    257 CTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGACCGGGG 316
           |||| ||   ||| ||||||||  |          ||||    ||  ||
Db    212 gtggacatcatctgtccgcactatgaagatcactctgtggcagacgctgccatg------ 265

Qy    317 CCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACC 376
                         ||||||||| | |||||| |||||   |   | |  ||||
Db    266 ---------------gagcagtacatactgtacctggtggagcatgaggagtaccagctg 310

Qy    377 TGCAACGCCAG---CCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCAC 433
          ||| |  ||     | ||| |      |||||| |||||||||||||    |||  |||
Db    311 tgccagccccagtccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcat 370

Qy    434 AGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAG 493
           ||||    ||| | || |||||||||||||||| ||   | ||| | |||||| | |||
Db    371 ggcccggagaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggag 430

Qy    494 TTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAG 553
          ||| | |  || |||   ||||||||||||||||  ||||  ||| | |   |
Db    431 ttcaaagaaggacacagctactactacatctccaaacccatccaccagcatgaagaccgc 490

Qy    554 TGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
          ||  ||||| ||||||||   ||| |  ||     |||
Db    491 tgcttgaggttgaaggtgactgtcagtggcaaaatcac 528

RESULT  14
US-10-136-819-14
; Sequence 14, Application US/10136819
; GENERAL INFORMATION:
;  APPLICANT: Chien, Kenneth
;  APPLICANT:  Hoshijima, Masahiko
;  TITLE OF INVENTION: Non-viral vesicle vector for cardiac specific gene delivery
;  FILE REFERENCE: 6627-PA1198
;  CURRENT APPLICATION NUMBER: US/10/136,819
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: 60/287,423
;  PRIOR FILING DATE: 2001-04-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 1480
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-136-819-14

  Query Match             11.2%;  Score 116.4;  DB 7;  Length 1480;
  Best Local Similarity   57.4%;  Pred. No. 9.1e-11;
  Matches  263;  Conservative    0;  Mismatches  171;  Indels   24;  Gaps    2;

Qy    137 CCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAAC 196
          || ||  |||  |   |   | |   |||    |   | || ||  | || | |||||||
Db     92 cctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccgtcttctggaac 151

Qy    197 AGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTAT 256
          || || || |   |  | |||   |||| ||||||| | || ||| |  |||| |||||
Db    152 agttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactac 211

Qy    257 CTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGACCGGGG 316
           |||| ||   ||| ||||||||  |          ||||    ||  ||
Db    212 gtggacatcatctgtccgcactatgaagatcactctgtggcagacgctgccatg------ 265

Qy    317 CCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACC 376
                         ||||||||| | |||||| |||||   |   | |  ||||
Db    266 ---------------gagcagtacatactgtacctggtggagcatgaggagtaccagctg 310

Qy    377 TGCAACGCCAG---CCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCAC 433
          ||| |  ||     | ||| |      |||||| |||||||||||||    |||  |||
Db    311 tgccagccccagtccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcat 370
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Qy    434 AGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAG 493
           ||||    ||| | || |||||||||||||||| ||   | ||| | |||||| | |||
Db    371 ggcccggagaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggag 430

Qy    494 TTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAG 553
          ||| | |  || |||   ||||||||||||||||  ||||  ||| | |   |
Db    431 ttcaaagaaggacacagctactactacatctccaaacccatccaccagcatgaagaccgc 490

Qy    554 TGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
          ||  ||||| ||||||||   ||| |  ||     |||
Db    491 tgcttgaggttgaaggtgactgtcagtggcaaaatcac 528


RESULT  15
US-10-171-311-49
; Sequence 49, Application US/10171311
; GENERAL INFORMATION:
;  APPLICANT: Schlegel, Robert
;  APPLICANT:  Chen, Yan
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Monahan, John
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Gannavarapu, Manjula
;  APPLICANT:  Hoersh, Sebastian
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
;  TITLE OF INVENTION:  OF CERVICAL CANCER
;  FILE REFERENCE: MRI-035
;  CURRENT APPLICATION NUMBER: US/10/171,311
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US 60/298,159
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,155
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/335,936
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 238
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
;   LENGTH: 1480
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-171-311-49


  Query Match             11.2%;  Score 116.4;  DB 7;  Length 1480;
  Best Local Similarity   57.4%;  Pred. No. 9.1e-11;
  Matches  263;  Conservative    0;  Mismatches  171;  Indels   24;  Gaps    2;

Qy    137 CCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAAC 196
          || ||  |||  |   |   | |   |||    |   | || ||  | || | |||||||
Db     92 cctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccgtcttctggaac 151

Qy    197 AGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTAT 256
          || || || |   |  | |||   |||| ||||||| | || ||| |  |||| |||||
Db    152 agttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctgaatgactac 211

Qy    257 CTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGG 316
           |||| ||   ||| ||||||||  |          ||||    ||  ||
Db    212 gtggacatcatctgtccgcactatgaagatcactctgtggcagacgctgccatg------ 265

Qy    317 CCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACC 376
                         ||||||||| | |||||| |||||   |   | |  ||||
Db    266 ---------------gagcagtacatactgtacctggtggagcatgaggagtaccagctg 310

Qy    377 TGCAACGCCAG---CCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCAC 433
          ||| |  ||     | ||| |      |||||| |||||||||||||    |||  |||
Db    311 tgccagccccagtccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcat 370

Qy    434 AGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAG 493
           ||||    ||| | || |||||||||||||||| ||   | ||| | |||||| | |||
Db    371 ggcccggagaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggag 430

Qy    494 TTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAG 553
          ||| | |  || |||   ||||||||||||||||  ||||  ||| | |   |
Db    431 ttcaaagaaggacacagctactactacatctccaaacccatccaccagcatgaagaccgc 490

Qy    554 TGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
          ||  ||||| ||||||||   ||| |  ||     |||
Db    491 tgcttgaggttgaaggtgactgtcagtggcaaaatcac 528


Search completed: September 28, 2002, 01:35:23
Job time: 12723 sec
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                    GenCore version 4.5
           Copyright (c) 1993 - 2000  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:         September 27, 2002, 20:13:14 ; Search time 2180.79 Seconds
                                               (without alignments)
                                               6418.015 Million cell updates/sec

Title:          US-09-904-954-1
Perfect score:  1037
Sequence:       1 GGATCTTGGAACGAGACGAC..........GTCGTCTCGTTCCAAGATCC 1037

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters:      27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      EST:*
                1:  em_estba:*
                2:  em_esthum:*
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                4:  em_estmu:*
                5:  em_estov:*
                6:  em_estpl:*
                7:  em_estro:*
                8:  em_htc:*
                9:  gb_est1:*
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                11:  gb_htc:*
                12:  gb_gss:*
                13:  em_gss_hum:*
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                15:  em_gss_pln:*
                16:  em_gss_vrt:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                 %
Result          Query
  No.   Score   Match Length DB  ID                              Description
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    1     901    86.9   1030  9  AL533153                        AL533153 AL533153
    2   649.6    62.6    804 10  BF983120                        BF983120 602305829
    3   615.6    59.4    684  9  AL527972                        AL527972 AL527972
    4   553.2    53.3    902  9  AL546822                        AL546822 AL546822
c   5   438.2    42.3    496 10  BF953157                        BF953157 CM3-NN118
    6   421.4    40.6    884 10  BG705182                        BG705182 602688106
    7     409    39.4    535  9  AW786993                        AW786993 120664 MA
    8   363.8    35.1    702 10  BG743158                        BG743158 602634316
    9   322.2    31.1    848 10  BF542148                        BF542148 602068243
   10   289.6    27.9    552  9  AL628407                        AL628407 AL628407
   11   268.4    25.9    879 10  BF977204                        BF977204 602146759
   12   257.8    24.9    460  9  AW200648                        AW200648 da24c06.y
   13   247.8    23.9   1013 10  BF969747                        BF969747 602272160
   14   246.2    23.7    288  9  AA338749                        AA338749 EST43752
   15   220.2    21.2    258 10  BF950361                        BF950361 CM3-NN118
c  16   217.4    21.0    750  9  AW199923                        AW199923 da24c06.x
   17   217.4    21.0    906 10  BF240606                        BF240606 601875729
   18   210.4    20.3    553 10  BE663141                        BE663141 126832 MA
   19   205.2    19.8    762 10  BG698896                        BG698896 602703313
c  20   203.6    19.6    435  9  BB833304                        BB833304 BB833304
   21   199.6    19.2    374 10  BF394888                        BF394888 UI-R-CA0-
c  22     198    19.1    431  9  BB830682                        BB830682 BB830682
   23   187.4    18.1   1141 12  CNS03W6J                        AL263332 Tetraodon
   24   180.6    17.4    353  9  AA389416                        AA389416 mp12g10.r
c  25     177    17.1   1008  9  AL565095                        AL565095 AL565095
   26   165.4    15.9    307  9  AA389014                        AA389014 mp13c10.r
   27   165.2    15.9   1085 11  AK020438                        AK020438 Mus muscu
   28   153.8    14.8    939 12  CNS02SNV                        AL212116 Tetraodon
   29   151.2    14.6    523 10  BE648416                        BE648416 UI-M-BH2.
   30   146.6    14.1    676  9  AL661297                        AL661297 AL661297
c  31   143.8    13.9    798  9  AL563020                        AL563020 AL563020
   32     136    13.1    593  9  AA170896                        AA170896 ms49f07.r
   33     132    12.7    677  9  AL630156                        AL630156 AL630156
   34   130.6    12.6    494 10  BE753526                        BE753526 206699 MA
   35   128.4    12.4    646 10  BJ030542                        BJ030542 BJ030542
   36   128.4    12.4    656 10  BJ075270                        BJ075270 BJ075270
   37   127.4    12.3    516 10  BG892797                        BG892797 de55h10.y
   38   127.2    12.3    586 10  BJ074808                        BJ074808 BJ074808
   39   125.6    12.1    592 10  BJ031724                        BJ031724 BJ031724
   40   125.6    12.1    623 10  BJ074739                        BJ074739 BJ074739
   41   125.2    12.1    532 10  BJ065530                        BJ065530 BJ065530
   42   124.8    12.0    594 10  BJ096950                        BJ096950 BJ096950
   43   124.8    12.0    597 10  BJ094859                        BJ094859 BJ094859
c  44   123.6    11.9    701  9  BB643986                        BB643986 BB643986
   45     120    11.6    582  9  AW918015                        AW918015 EST349319


                              ALIGNMENTS


RESULT   1
AL533153
LOCUS       AL533153                1030 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL533153 LTI_FL015_Brn1 Homo sapiens cDNA clone CS0DN003YL19 5
            prime, mRNA sequence.
ACCESSION   AL533153
VERSION     AL533153.1  GI:12796646
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1030)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1..1030
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DN003YL19"
                     /clone_lib="LTI_FL015_Brn1"
                     /sex="male"
                     /tissue_type="Adult brain"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was constructed by Life Technologies.
                     Contact : Feng Liang Life Technologies, a division of
                     Invitrogen 9800 Medical Center Drive Rockville, Maryland
                     20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      183 a    333 c    338 g    173 t      3 others
ORIGIN
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  Query Match             86.9%;  Score 901;  DB 9;  Length 1030;
  Best Local Similarity   98.0%;  Pred. No. 2e-136;
  Matches  963;  Conservative    2;  Mismatches   12;  Indels    6;  Gaps    5;

Qy       32 GCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCTCCGGGGATGGCGGCG 91
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Db        1 GCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCTCCGGGGATGGCGGCG 60

Qy       92 GCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAA 151
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAA 120

Qy      152 GGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCAC 211
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Db      121 GGGCCCGGA-GGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCAC 179

Qy      212 CTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGC 271
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      180 CTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGC 239

Qy      272 CCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGGCGGGGCA 331
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      240 CCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGGCGGGGCA 299

Qy      332 GAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG 391
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      300 GAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG 359

Qy      392 GGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCG 451
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Db      360 GGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCG 419

Qy      452 GAGAAGTTCCAGCGCTACAGCGCCTTCTCTCT-GGGCTACGAGTTCCACGCCGGCCACGA 510
            |||||||||||||||||||||:|||||||||| |||||||||||||||||||||||||||
Db      420 GAGAAGTTCCAGCGCTACAGCSCCTTCTCTCTGGGGCTACGAGTTCCACGCCGGCCACGA 479

Qy      511 GTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGT 570
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Db      480 GTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGT 539

Qy      571 GTTCGTCTGCTGCGCCTCCACATCGCACTCC-GGGGAGAAGCCGGTCCCCACTCTCCCCC 629
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      540 GTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGGAGAAGCCGGTCCCCACTCTCCCCC 599

Qy      630 AGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACC 689
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Db      600 AGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACC 659

Qy      690 CTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGC 749
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      660 CTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGC 719

Qy      750 CCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCC 809
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Db      720 CCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCC 779

Qy      810 TCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCCTCTC 869
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      780 TCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCCTCTC 839

Qy      870 CAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCA 929
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      840 CAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCA 899

Qy      930 TACATCTGTGTCCGCCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTGGACCAAG 989
            ||||||||||||||||||      ||| | ||||||||||||||||||||||||| |||:
Db      900 TACATCTGTGTCCGCCCC--TCTACCCCTTCCCCCACGTAGGGCACTGTAGTGGA-CAAR 956

Qy      990 CACGGGGACAGCCATGGGTCCCG 1012
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Db      957 CACGGGGACAGCATGGGTCCCGG 979
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RESULT   2
BF983120
LOCUS       BF983120                 804 bp    mRNA    linear   EST 23-JAN-2001
DEFINITION  602305829F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4397263 5',
            mRNA sequence.
ACCESSION   BF983120
VERSION     BF983120.1  GI:12386017
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 804)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10097  row: i  column: 08
            High quality sequence stop: 766.
FEATURES             Location/Qualifiers
     source          1. .804
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4397263"
                     /clone_lib="NIH_MGC_88"
                     /tissue_type="duodenal adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: small intestine; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
                     oligo-dT primed. Average insert size 1.767 kb. Library
                     enriched for full-length clones and constructed by Life
                     Technologies. Note: this is a NIH_MGC Library."
BASE COUNT      150 a    256 c    265 g    133 t
ORIGIN


  Query Match             62.6%;  Score 649.6;  DB 10;  Length 804;
  Best Local Similarity   94.6%;  Pred. No. 8.5e-96;
  Matches  749;  Conservative    0;  Mismatches   34;  Indels    9;  Gaps    7;

Qy       26 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCTCCGGGGATG 85
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Db       13 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCTCCGGGGATG 72

Qy       86 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 145
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Db       73 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 132

Qy      146 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      133 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 192

Qy      206 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 265
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Db      193 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATT 252

Qy      266 TACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGGC 325
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Db      253 TACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGGC 312

Qy      326 GGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCC 385
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Qy    386 AGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAG 445
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Db    372 AGCCAGGTCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCG-ACAGCCCCATCAAG 430

Qy    446 TTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAG-TTCCACGCCGG 504
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Db    431 TTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTTCCACGCCGG 490

Qy    505 CCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGAT 564
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Db    491 CCACGAGTACTACTACATCTCCACGCCCA-TCACAAGCTGCACTGGAAGTGTCTGAGGAT 549

Qy    565 GAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCT 624
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Db    550 GAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCATCTC 609

Qy    625 CCCCCAGTTCACCATGGGCCCCAATGTG-AAGATCAACGTGCTGG---AAGACTTTGAGG 680
          |||||||||||||||||||||||||||| |||||||||||||| |    |   ||   ||
Db    610 CCCCCAGTTCACCATGGGCCCCAATGTGAAAGATCAACGTGCTTGGAAGAACTTTGAGGG 669

Qy    681 GAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGG 740
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Db    670 GAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCCAGCCCAAACGGG 729

Qy    741 AACACCTGCCCCTGGCCGTGGGCATC-GCCTTCTTCCTCATGACGTTCTTGGCCTCCTAG 799
          ||||||||||||||| |||||||||| || ||||||||||  |   | |||| || |||
Db    730 AACACCTGCCCCTGGGCGTGGGCATCGGCTTTCTTCCTCAATAACGTTTTGGGCTTCTAA 789

Qy    800 CTCTGCCCCCTC 811
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Db    790 ATTGCCCCTCCC 801


RESULT   3
AL527972
LOCUS       AL527972                  684 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL527972 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC027YP19 5
            prime, mRNA sequence.
ACCESSION   AL527972
VERSION     AL527972.1  GI:12791465
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1..684
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                     /db_xref="taxon:9606"
                     /clone="CS0DC027YP19"
                     /clone_lib="LTI_NFL003_NBC3"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
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BASE COUNT      146 a    203 c    199 g     94 t     42 others
ORIGIN

  Query Match             59.4%;  Score 615.6;  DB 9;  Length 684;
  Best Local Similarity   89.3%;  Pred. No. 2.6e-90;
  Matches  609;  Conservative   42;  Mismatches   31;  Indels    0;  Gaps    0;

Qy    112 GCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGG 171
          |||||||||||:|||||||||||||||       | || | || || |  |||||  |||
Db      1 GCTGCTCGTGCMCGTGCCGCTGCTGCCAGCTGCTGGCCCAAGGGCCCGGAGGGCGAAGGG 60

Qy    172 AAACCGGCATGCGGTGTACTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACAC 231
          ||||:|||||||||||||||||||||:|:||||||||||||||||||||||||||:|||:
Db     61 AAACMGGCATGCGGTGTACTGGAACARCWCCAACCAGCACCTGCGGCGAGAGGGCWACAM 120

Qy    232 CGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGG 291
          :  |:||||||||||||||||||||:||||||:::|  || ||:|:|| ||:|||:||||
Db    121 MAAGMAGGTGAACGTGAACGACTATMTGGATAWWWAAAGCACGMAMTAAAAMAGCWCGGG 180

Qy    292 GGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACAT 351
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Db    181 GGTRGGCCCCGGGGCGGGAMCGGGGCCCGGAGGCGGGGCARARCAGTACGTGCTGTACAT 240

Qy    352 GGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTG 411
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Db    241 GGWGAGCMGCAACGGCWACMGCACCTGCAACGCCAGCAAGGGCTTMAAGCGCTGGGAGTG 300

Qy    412 CAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAG 471
          |||||||||||||||:|||||:||||||||:||||||||||||||||||||||||:| |:
Db    301 CAACCGGCCGCACGCMCCGCAMAGCCCCATMAAGTTCTCGGAGAAGTTCCAGCGCWAAAR 360

Qy    472 CGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCC 531
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Db    361 CGCCTTCWMTCTGGGCWACGARTWCCACGCMGGCCACGAGTACTACWAMATCTCCACGCC 420

Qy    532 CACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCAC 591
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Db    421 CACTCAMAACCTGCACTGGAAGTGTCTGARGATGAAGGTGTTCGTCTGCAGCGCCTCCAC 480

Qy    592 ATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGCCCCAATGT 651
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Db    481 ATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGCCCCAATGT 540

Qy    652 GAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAA 711
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Db    541 GAAGATMAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAA 600

Qy    712 GAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTT 771
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Db    601 GAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTT 660

Qy    772 CTTCCTCATGACGTTCTTGGCC 793
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Db    661 CTTCCTCMCGACGTATCTTGGC 682


RESULT   4
AL546822
LOCUS       AL546822                  902 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL546822 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI026YI24 5
            prime, mRNA sequence.
ACCESSION   AL546822
VERSION     AL546822.1  GI:12880311
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 902)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
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COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1..902
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                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      161 a    297 c    278 g    156 t     10 others
ORIGIN


  Query Match             53.3%;  Score 553.2;  DB 9;  Length 902;
  Best Local Similarity   91.1%;  Pred. No. 3.3e-80;
  Matches  749;  Conservative    8;  Mismatches   37;  Indels   28;  Gaps   15;

Qy    201 CCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAA--------CGA 252
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Db     67 CCCACAGCCTGCGGCGACGCAGCGGCTACACCGTGCAGGTGAACGTGCAGACGAGCTCAC 126

Qy    253 CTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGG---G 309
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Db    127 TCGTGGATATGTTAGCTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGCGAC 186

Qy    310 ACCGGGGCCCGGAGGCGGGGCAGA-GCAGTACG-TGCTGTAC-ATGGTGAGCCGCAACGG 366
            || ||||||||||||||||||| |||||||| |||||||| |||||||||||||||||
Db    187 CGCGCGGCCCGGAGGCGGGGCAGACGCAGTACGCTGCTGTACGATGGTGAGCCGCAACGG 246

Qy    367 CTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGC 426
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Db    247 CTACCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGC 306

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Qy    484 GGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCT 543
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Db    367 GGGCTACGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCT 426

Qy    544 GCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGG 603
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Db    427 GCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGG 486

Qy    604 G-GAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACG 662
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Db    487 GCGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACG 546

Qy    663 TGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCAT--CAG 720
          |||||||||||||||||||||:|||||||||||||||||||||||||||||||||    |
Db    547 TGCTGGAAGACTTTGAGGGAGRGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATGCAGG 606

Qy    721 CGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCAT 780
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Qy    781 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCT-GGGGGGGGAGAGATGGGGCGGGGC 839
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Db    667 GACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCYGGGGGGGGGAGAGATGGGGCGGGGC 726
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Qy    900 CTCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTC 959
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Db    785 CTCCCATGGCTAGAAGTGGGGSCTGCACCATACATCTGTGTCCGSCC---CTSTACCCYT 841

Qy    960 CCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGC 1001
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Db    842 CCCCCACGTA-GGCACTGTAGTGGA-CAAGCACGGGGACABC 881


RESULT   5
BF953157/c
LOCUS       BF953157                 496 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION  CM3-NN1187-111100-478-a06 NN1187 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF953157
VERSION     BF953157.1  GI:12370432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 496)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-NN1187-
            111100-478-a06&t3=2000-11-11&t4=1)
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            High quality sequence start: 19
            High quality sequence stop: 495.
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                     /dev_stage="Adult"
                     /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
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                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       94 a    144 c    162 g     96 t
ORIGIN


  Query Match             42.3%;  Score 438.2;  DB 10;  Length 496;
  Best Local Similarity   97.9%;  Pred. No. 1.2e-61;
  Matches  465;  Conservative    0;  Mismatches    8;  Indels    2;  Gaps    2;

Qy    539 AACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCC-ACATCGCA 597
          |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
```

```
Db      496 AACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCTTCTGCTGCGCCTCCAACATCGCA 437

Qy      598 CTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGAT 657
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db      436 CTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATATGAAGAT 377

Qy      658 CAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCAT 717
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      376 CAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCAT 317

Qy      718 CAGCGGACCAGCCCCAAACGGGAACACCTGCCCCCTGGCCGTGGGCATCGCCTTCTTCCT 777
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      316 CAGCGGACCAGCCCCAAACGGGAACACCTGCCCCCTGGCCGTGGGCATCGCCTTCTTCCT 257

Qy      778 CATGACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGGGCGGG 837
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      256 CATGACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATGGCCGGG 197

Qy      838 GCTTGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCC 897
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      196 GCTTGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCC 137

Qy      898 TCCTCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCT 957
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      136 TCCTCCCATGGCTAGAAGT-GGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCT 78

Qy      958 TCCCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCG 1012
            ||||||||||||||||||||||||||||||||||||||||||  |   |||||||
Db       77 TCCCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACATACCGTGGTCCCG 23


RESULT   6
BG705182
LOCUS       BG705182                 884 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602688106F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4820496 5',
            mRNA sequence.
ACCESSION   BG705182
VERSION     BG705182.1  GI:13979264
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 884)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10725  row: 1  column: 01
            High quality sequence stop: 587.
FEATURES             Location/Qualifiers
     source          1..884
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4820496"
                     /clone_lib="NIH_MGC_95"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.5 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for  full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health).  Note: this is a NIH_MGC Library."
BASE COUNT      152 a    338 c    289 g    105 t
ORIGIN

  Query Match              40.6%;  Score 421.4;  DB 10;  Length 884;
  Best Local Similarity    83.2%;  Pred. No. 6.8e-59;
  Matches  655;  Conservative    0;  Mismatches   96;  Indels   36;  Gaps   14;

Qy       26 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATG 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       49 GGAGAAGCCGGGAGCGCGGGGCTCAGTCGGGGGGCGGCGGCGGCGGCGGCTCCGGGGATG 108

Qy       86 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      109 GCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCTG 168

Qy      146 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      169 GCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAAC 228

Qy      206 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGG-TGAACGTGAACGACTATCTGGA-TA 263
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||| ||
Db      229 CAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGCTGAACGTGAACGACTATCTGGACTA 288

Qy      264 TTTACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAG 323
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      289 TTTACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAG 348

Qy      324 GCGGGGCAGAGCAGTACGTGCTGTACA-TGGTGAGCCGCA-ACGGCTACCGCACCTGCAA 381
            ||||||||||||||||||||||||||| |||||||||||| |||||||||||||||||||
Db      349 GCGGGGCAGAGCAGTACGTGCTGTACACTGGTGAGCCGCACACGGCTACCGCACCTGCAA 408

Qy      382 CGCCAGCCAGGGCTTCAAGCGC---TGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCC 438
            ||||||||||||| |  | |||    ||   ||||||||||||||||||||||     ||
Db      409 CGCCAGCCAGGGCCTTCAACGCGCTGGGAGCTGCAACCGGCCGCACGCCCCGCCACAGCC 468

Qy      439 CATCAAGTTCTCGGAG------AAGTTCCAGCGCTACAGCGCCTT--CTCTCTGGGCTAC 490
            |  |     |||   |      |  ||||||||||||||||||||  |||||||||||||
Db      469 CCACTCAAGCTCCTCGAGCAGAAGCTTCCAGCGCTACAGCGCCTTTCCTCTCTGGGCTAC 528

Qy      491 --GAGTTCCACGCCGGC---CACGAGTACTACTACATCTCCACGCCCACTCACAACCTGC 545
                 ||||||||||||   | |   ||||||||||||||||||||||||||||||||||
Db      529 CGAGCTTCCACGCCGGCCCACCCAGCTACTACTACATCTCCACGCCCACTCACAACCTGC 588

Qy      546 ACTGGAAGTGTCTGAGGATGA-----AGGTGTTCGTCTGCTGCGCCTCCACA-TCGCACT 599
            ||||| |  |      || |      |||||| || |||||||||||||||| |||||||
Db      589 ACTGGCACAGCGCTCTGACGGATGACAGGTGTCCGCCTGCTGCGCCTCCACACTCGCACT 648

Qy      600 CCGGGGAGAAGCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAA--TGTGAAGAT 657
            |||||||||||||||||||||||||||||    ||||||  || |||||      | |||
Db      649 CCGGGGAGAAGCCGGTCCCCACTCTCCCCAGCATCACCAATGGGCCCAACCGTGCACGAT 708

Qy      658 CAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTC--AGGTGCCCAAGCTTGAGAAGAG- 714
            | ||| || || | |||  || ||| ||||||| |    ||||||||||      |  |
Db      709 CCACGCGCCGGGACACTCGGACGGACAGAACCCCCCAGCGTGCCCAAGCGCCGCCACCGA 768

Qy      715 -----CATCAGCGGACCAGCCCCAAACGGGAACACCTGCCCCCTGGCCGTGGGCATCGCC 769
                 || | |         |||||| |||||||||||||||| | ||| | ||||||||
Db      769 GCACTCAGCGGGCACCAGGCCCCCAACCGGGAACACCTGCCCCGGCCCGCGCGCATCGCC 828

Qy      770 TTCTTCC 776
            | |  ||
Db      829 TCCCCCC 835


RESULT   7
AW786993
LOCUS       AW786993                 535 bp    mRNA    linear   EST 09-JUL-2000
DEFINITION  120664 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   AW786993
```

```
VERSION     AW786993.1  GI:7843769
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 44  row: E  column: 17
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .535
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 1PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
BASE COUNT      100 a    169 c    166 g    100 t
ORIGIN


  Query Match             39.4%;  Score 409;  DB 9;  Length 535;
  Best Local Similarity   94.4%;  Pred. No. 6.4e-57;
  Matches  424;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy    205 CCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 264
          |||   ||||||||||||||||||||| ||||||||||| |||||||| |||||||||||
Db     87 CCACAGCCTGCGGCGAGAGGGCTACACGGTGCAGGTGAATGTGAACGATTATCTGGATAT 146

Qy    265 TTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGG 324
          ||||||||| |||||||||||||| |||||||||||||||||||| ||·||||| |||||
Db    147 TTACTGCCCTCACTACAACAGCTCAGGGGTGGGCCCCGGGGCGGGGCCAGGGCCTGGAGG 206

Qy    325 CGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGC 384
          |||||| ||||||||||||||||| |||||||||||    ||||||||||||||||||||
Db    207 CGGGGCGGAGCAGTACGTGCTGTATATGGTGAGCCGGGCGGGCTACCGCACCTGCAACGC 266

Qy    385 CAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAA 444
          |||||| |||||||||||||||||||||||||| ||||||||||| || |||||||||||
Db    267 CAGCCAAGGCTTCAAGCGCTGGGAGTGCAACCGACCGCACGCCCCTCATAGCCCCATCAA 326

Qy    445 GTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGG 504
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    327 GTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCGCTGGGCTACGAGTTCCACGCCGG 386

Qy    505 CCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGAT 564
          |||||||||||||||||||||||||||||| || |||||||| |||||||||||||||||
Db    387 CCACGAGTACTACTACATCTCCACGCCCACCCATAACCTGCATTGGAAGTGTCTGAGGAT 446

Qy    565 GAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCT 624
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    447 GAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCT 506
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Qy    625 CCCCCAGTTCACCATGGCCCCAATGTGA 653
          ||||||||||||||||||||||||||||
Db    507 CCCCCAGTTCACCATGGCCCCAATGTGA 535


RESULT  8
BG743158
LOCUS       BG743158                 702 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602634316F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4779506 5',
            mRNA sequence.
ACCESSION   BG743158
VERSION     BG743158.1  GI:14053811
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 702)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10636  row: p  column: 03
            High quality sequence stop: 702.
FEATURES             Location/Qualifiers
     source          1. .702
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4779506"
                     /clone_lib="NCI_CGAP_Skn3"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      139 a    226 c    201 g    136 t
ORIGIN


  Query Match             35.1%;  Score 363.8;  DB 10;  Length 702;
  Best Local Similarity   99.5%;  Pred. No. 1.4e-49;
  Matches  365;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    651 TGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGA 710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGA 60

Qy    711 AGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCT 770
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCT 120

Qy    771 TCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATG 830
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TCTTCCTCATGACGTTCTTGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGAGAGATG 180

Qy    831 GGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCT 890
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCT 240

Qy    891 AGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTC 950
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTC 300

Qy    951 TACCCCTTCCCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGTCC 1010
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    301 TACCCCTTCCCCCCACGTAGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCC 360

Qy   1011 CGAGCAG 1017
          || || |
Db    361 CGGGCGG 367


RESULT   9
BF542148
LOCUS       BF542148                 848 bp    mRNA    linear   EST 11-DEC-2000
DEFINITION  602068243F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067314 5',
            mRNA sequence.
ACCESSION   BF542148
VERSION     BF542148.1  GI:11629529
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM906  row: e  column: 11
            High quality sequence stop: 511.
FEATURES             Location/Qualifiers
     source          1..848
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4067314"
                     /clone_lib="NIH_MGC_58"
                     /tissue_type="hypernephroma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
                     Double-stranded cDNA was prepared from cell line RNA.  5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C,  G, or T).   Average
                     insert size 1.35 kb (range 0.9-4.0 kb).  15/15 colonies
                     contained  inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA)."
BASE COUNT      175 a    238 c    282 g    153 t
ORIGIN


  Query Match             31.1%;  Score 322.2;  DB 10;  Length 848;
  Best Local Similarity   89.0%;  Pred. No. 7.4e-43;
  Matches  462;  Conservative    0;  Mismatches   43;  Indels   14;  Gaps   10;

Qy    509 GAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAG 568
          ||| |   ||   ||||||||||||||||||| |||||||||||||||||||||||||||
Db    105 GAGAATCGCTGTTTCTCCACGCCCACTCACAAGCTGCACTGGAAGTGTCTGAGGATGAAG 164

Qy    569 GTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCC 628
          ||| ||||||||||||||||||||||||||||| |||||||||||||||||| |||||||
Db    165 GTG-TCGTCTGCTGCGCCTCCACATCGCACTCC-GGGAGAAGCCGGTCCCCA-TCTCCCC 221

Qy    629 CAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAAC 688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    222 CAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAAC 281

Qy    689 CCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGAACACCTG 748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    282 CCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGAACACCTG 341

Qy    749 CCCCTGGCCGTGGGCATCG-CCTTCTTCCTCATGACGTTCT-TGGCCTCCTAGCTCT-GC 805
          ||||||||||||||||||| |||||||||||||||||||||  |||||||||||||| ||
Db    342 CCCCTGGCCGTGGGCATCGCCCTTCTTCCTCATGACGTTCTAGGGCCTCCTAGCTCTGGC 401

Qy    806 CCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGAGCAGGGA-GCCTTTGGC 864
          ||||||||||||||||||||||||||||||||  | | |||||||| ||| ||||||||
Db    402 CCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGTTTGGAAAGGAGCAAGGATGCCTTTGGG 461

Qy    865 CTCTCCAAGGGAAGCCTAGTGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTG 924
          |||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||
Db    462 CTCTCCAAGGGAAGCCTAGTGGCCTAGAGCCCTCCTCCCATGG-TAGAAGTGGGGCCTG 520

Qy    925 CACCATACA---TCTGTGTCCGCCCCCTCTACCCCTTCCCCCCACGTAGGGCAC---TGT 978
           ||||||||   | |||  |  |||  |  |||  ||| |||||||||||||||     |
Db    521 AACCATACAATCTGTGTTCCGCCCCTTTTAACCATTTCACCCCACGTAGGGCACCTTGTT 580

Qy    979 AGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAG 1017
          |||||||| |     |||||||| ||||   |||  || |
Db    581 AGTGGACCCACGCACGGGACAGCAATGGTGTCCGGGCGG 619


RESULT  10
AL628407
LOCUS       AL628407                 552 bp    mRNA    linear   EST 02-NOV-2001
DEFINITION  AL628407 XGC-gastrula Silurana tropicalis cDNA clone TGas008p08 5',
            mRNA sequence.
ACCESSION   AL628407
VERSION     AL628407.1  GI:16597890
KEYWORDS    EST.
SOURCE      western clawed frog.
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 552)
  AUTHORS   Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (10_2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Huckle E
            Sanger Centre
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TGas008p08.sp6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
FEATURES             Location/Qualifiers
     source          1..552
                     /organism="Silurana tropicalis"
                     /db_xref="taxon:8364"
                     /clone="TGas008p08"
                     /clone_lib="XGC-gastrula"
                     /dev_stage="gastrula (stages 10.5-13 mixed)"
                     /lab_host="Escherichia coli XL1-blue"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from stages
                     10-13 gastrulae.  EcoRI-NotI cut cDNA was then ligated
                     into pCS107 with EcoRI at the 5' end and NotI at the 3'
                     end."
BASE COUNT      123 a    186 c    138 g    104 t      1 others
ORIGIN


  Query Match             27.9%;  Score 289.6;  DB 9;  Length 552;
  Best Local Similarity   72.9%;  Pred. No. 1.3e-37;
  Matches  398;  Conservative    0;  Mismatches  124;  Indels   24;  Gaps    1;

Qy    130 GCTGCTGCCGCTGCTGGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTA 189
```

```
           ||||||    | ||||  |     |  |    |  |    |  ||||||||  |||| ||
Db      25 GCTGCTCTTCCCGCTGCTCTCCCTGTTCCCCCGCTCCGGAGCCAACCGGCACTCGGTCTA 84

Qy     190 CTGGAACAGCTCCAACCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAA 249
            ||||||||||||||| | ||||||||||| || |||||||| ||||||||||| |||||
Db      85 TTGGAACAGCTCCAACTACCACCTGCGGCGGGACGGCTACACGGTGCAGGTGAATGTGAA 144

Qy     250 CGACTATCTGGATATTTACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCCGGGGCGGG 309
           ||| || ||||| ||||| ||||| ||||||||     |   || ||  | |  |  |
Db     145 CGATTACCTGGACATTTATTGCCCCCACTACAATGAGACCCCGGGGGAGCACAAGATG-- 202

Qy     310 ACCGGGGCCCGGAGGCGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTA 369
                                 ||||||||| | |||||||||||||||  | | |||||
Db     203 ----------------------GAGCAGTACATCCTGTACATGGTGAGCTACGAGGGCTA 240

Qy     370 CCGCACCTGCAACGCCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCC 429
           ||| |||||||||  ||||||||||||||||||||||||||||||||| || ||||||||
Db     241 CCGGACCTGCAACATCAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGCCCCCACGCCCC 300

Qy     430 GCACAGCCCCATCAAGTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTA 489
            ||||| || ||||| ||||| ||||||||||||||||||||||||||||| ||||||||
Db     301 CCACAGTCCAATCAAATTCTCCGAGAAGTTCCAGCGCTACAGCGCCTTCTCCCTGGGCTA 360

Qy     490 CGAGTTCCACGCCGGCCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTG 549
           |||||||||||||||||||||||||||||| ||||| || || || |||||||      |
Db     361 CGAGTTCCACGCCGGCCACGAGTACTACTATATCTCAACACCGACCCACAACCACAGGCG 420

Qy     550 GAAGTGTCTGAGGATGAAGGTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAA 609
               || || | |||||| ||||| || ||||| |||  |||  | || || || |||||
Db     421 CTCCTGCCTCAAGATGAAAGTGTTTGTGTGCTGTGCCAGCACTGCCCATTCAGGAGAGAA 480

Qy     610 GCCGGTCCCCACTCTCCCCCAGTTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGA 669
           ||    ||| || |||||||||||||| || |||||  | ||||||||  | |   | ||
Db     481 GCACTCCCCGACCCTCCCCCAGTTCACGATAGGCCCAGAGGTGAAGATAGAGGATTTAGA 540

Qy     670 AGACTT 675
             ||||
Db     541 TCACTT 546


RESULT  11
BF977204
LOCUS       BF977204                 879 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION  602146759F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4305782 5',
            mRNA sequence.
ACCESSION   BF977204
VERSION     BF977204.1  GI:12344419
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 879)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1173  row: e  column: 15
            High quality sequence stop: 494.
FEATURES             Location/Qualifiers
     source          1..879
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4305782"
                     /clone_lib="NIH_MGC_62"
                     /tissue_type="melanotic melanoma, high MDR"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
                     Double-stranded cDNA was prepared from cell line RNA.  5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C,  G, or T).   Average
                     insert size 1.75 kb (range 0.9-4.0 kb).  15/15 colonies
                     contained  inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA)."
BASE COUNT      161 a    256 c    289 g    172 t    1 others
ORIGIN

  Query Match             25.9%;  Score 268.4;  DB 10;  Length 879;
  Best Local Similarity   90.4%;  Pred. No. 3.7e-34;
  Matches  320;  Conservative    0;  Mismatches   31;  Indels    3;  Gaps    3;

Qy     669 AAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCA 728
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 AAGACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCA 253

Qy     729 GCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCT 788
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 GCCCCAAACGGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCT 313

Qy     789 TGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGA 848
           |||||||||||||||||||||||||||||||||||   ||    || | ||   | | | |
Db     314 TGGCCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGGGAGGAGATGGGGCGGGCTTGGAAGG 373

Qy     849 GCAGGGAGCCTTTGGCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGG 908
               ||||||||  | ||||||||||||||||||||| ||||||| ||||||||||||||
Db     374 AGCAGGAGCCTTGTGGCTCTCCAAGGGAAGCCTAGTGCGCCTAGA-CCCTCCTCCCATGG 432

Qy     909 CTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCCCCCCACGT 968
           |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db     433 CTAGAAGTGGGGCCTGCACCATACATCTGTGTCCGCCCCCTCTA-CCCTTCCCCCCACGT 491

Qy     969 AGGGCACTGTAGTGGACCAAGCACGGGGACAGCCATGGGTCCCGAGCAGGTCGT 1022
           ||||||||||||||| || ||||||||||  | ||||||| ||| || ||  ||
Db     492 AGGGCACTGTAGTGG-CCCAGCACGGGGAACGGCATGGGTTCCGGGCGGGCTGT 544


RESULT  12
AW200648
LOCUS       AW200648                 460 bp    mRNA    linear   EST 22-JUN-2000
DEFINITION  da24c06.y1 normalized Xenopus laevis gastrula Xenopus laevis cDNA
            clone XENOPUS_SOURCE_ID:xlnga003n11 5' similar to SW:EFA3_HUMAN
            P52797 EPHRIN-A3 PRECURSOR ;, mRNA sequence.
ACCESSION   AW200648
VERSION     AW200648.1  GI:6481217
KEYWORDS    EST.
SOURCE      African clawed frog.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 460)
  AUTHORS   Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
            , Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
            ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Xenopus EST project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: da24c06.x1
            Contact: Sandy Clifton, Ph.D.
            WashU Xenopus EST project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
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                Fax: 314 286 1810
                Email: est@watson.wustl.edu
                Library constructed by Bruce Blumberg
                 Library normalized by Jihwan Song
                 DNA Sequencing by: Washington University Genome Sequencing Center.
                 Clone distribution: Xenopus clone distribution information for
                this library can be found through Research Genetics, visit their
                web page at: http://www.resgen.com/
                Seq primer: -40RP from Gibco
                High quality sequence stop: 423.
FEATURES             Location/Qualifiers
     source          1..460
                     /organism="Xenopus laevis"
                     /db_xref="taxon:8355"
                     /clone="XENOPUS_SOURCE_ID:xlnga003n11"
                     /clone_lib="normalized Xenopus laevis gastrula"
                     /tissue_type="gastrula (stages 10.5, 11.5 mixed)"
                     /lab_host="Top-10 F'"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; cDNA was prepared from 2ug of poly A+ RNA (equal
                     parts from stage 10.5 and stage 11.5 gastrulae).
                     EcoRI-XhoI cut cDNA was then ligated into UniZap-XR
                     (Stratagene) with EcoRI at the 5' end and XhoI at the 3'
                     end. SS-library phagemids were prepared by mass excision
                     from the original library and normalized by hybridization
                     to biotinylated driver (prepared from the same library by
                     PCR) to Cot-omega of 11. After removal of hybrids and
                     excess driver by streptavidin sepharose chromatography,
                     the ss-phagemids were made double stranded and
                     electroporated into Top-10 F'. Original library
                     contruction by Bruce Blumberg (Cho et al. 1991 Cell 67,
                     1111-1120). Normalized by Jihwan Song (Song, Cho and
                     Blumberg, unpublished). Note: This is a Xenopus Gene
                     Collection (XGC) library."
BASE COUNT      118 a    139 c    110 g     93 t
ORIGIN


  Query Match             24.9%;  Score 257.8;  DB 9;  Length 460;
  Best Local Similarity   74.0%;  Pred. No. 1.7e-32;
  Matches  344;  Conservative    0;  Mismatches  112;  Indels    9;  Gaps    1;

Qy        332 GAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAG 391
              ||||||||| | || || |||||||||  | | |||||||| |||||||||  |||||||
Db          5 GAGCAGTACATCCTCTATATGGTGAGCTACGAGGGCTACCGGACCTGCAACATCAGCCAG 64

Qy        392 GGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCG 451
              |||||||||||||||||||| ||||| || ||||  || ||||| || ||||| |||||
Db         65 GGCTTCAAGCGCTGGGAGTGTAACCGCCCCCACGTACCCCACAGTCCAATCAAATTCTCC 124

Qy        452 GAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAG 511
              |||||||||||||| ||||||||||||||  |||||||||||||||||||||||||||||
Db        125 GAGAAGTTCCAGCGGTACAGCGCCTTCTCCTTGGGCTACGAGTTCCACGCCGGCCACGAG 184

Qy        512 TACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTG 571
              |||||||| ||||| || || || ||||| |      |    ||||||| || ||| |||
Db        185 TACTACTATATCTCGACACCGACGCACAATCACAGGCGCTCCTGTCTGAAGAAGAAAGTG 244

Qy        572 TTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCCCAG 631
              || || |||||||||  ||| || |||||||| ||||| |    ||| || || ||||||
Db        245 TTTGTGTGCTGCGCCAGCACCTCCCACTCCGGAGAGAAACATTCCCCGACCCTGCCCCAG 304

Qy        632 TTCACCATGGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAACCCT 691
              ||||| || |||||  | || || ||  | |   | ||  ||||          |||||
Db        305 TTCACGATAGGCCCAGAGGTCAACATAGAGGATTTAGATAACTT---------CAACCCG 355

Qy        692 CAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGGACCAGCCCCAAACGGGAACACCTGCCC 751
              .|| | || ||| | ||||||||| |||| |||| ||| |||||| || | ||| | | |
Db        356 GAGATCCCAAAGTTGGAGAAGAGCGTCAGTGGGAGCAGTCCCAAAAGGAAGCACTTACAC 415

Qy        752 CTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCC 796
               |  | || |   |     || |  | |||||| || |||| |||
Db        416 TTAACAGTTGCAGTTTGTCTCCTTATAATGACGCTCCTGGCTTCC 460
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RESULT 13
BF969747
LOCUS       BF969747                1013 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION  602272160F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4360358 5',
            mRNA sequence.
ACCESSION   BF969747
VERSION     BF969747.1  GI:12336962
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1013)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10001  row: g  column: 15
            High quality sequence stop: 715.
FEATURES             Location/Qualifiers
     source          1..1013
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4360358"
                     /clone_lib="NIH_MGC_84"
                     /tissue_type="adrenal cortex carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
                     primed. Average insert size 1.229 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      234 a    293 c    285 g    200 t      1 others
ORIGIN


  Query Match             23.9%;  Score 247.8;  DB 10;  Length 1013;
  Best Local Similarity   98.5%;  Pred. No. 8.2e-31;
  Matches  271;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

Qy        744 ACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCT 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGGCCTCCTAGCTCT 60

Qy        804 GCCCCCTCCCCT-GGGGGGGAGAGATGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTG 862
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCCCCTCCCCTGGGGGGGGAGAGATGGGCGGGGCTTGGAAGGAGCAGGGAGCCTTTG 120

Qy        863 GCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCC 922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCTCTCCAAGGGAAGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCC 180

Qy        923 TGCACCATACATCTGTGTCCGCCCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTG 982
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        181 TGCACCATACATCTGTGTCCG-CCCCTCTACCCCTTCCCCCCACGTAGGGCACTGTAGTG 239

Qy        983 GACCAAGCACGGGGACAGCCATGGGTCCCGAGCAG 1017
              |||||||||||||||||||||||||||||| || |
Db        240 GACCAAGCACGGGGACAGCCATGGGTCCCGGGCGG 274


RESULT 14
AA338749
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LOCUS       AA338749                 288 bp    mRNA    linear   EST 21-APR-1997
DEFINITION  EST43752 Fetal brain I Homo sapiens cDNA 5' end similar to similar
            to tyrosine kinase receptor, mRNA sequence.
ACCESSION   AA338749
VERSION     AA338749.1  GI:1991007
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 288)
  AUTHORS   Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C.
  TITLE     Rapid cDNA sequencing (expressed sequence tags) from a
            directionally cloned human infant brain cDNA library
  JOURNAL   Nature Genet. 4, 373-380 (1993)
  MEDLINE   94004965
COMMENT     Other_ESTs: EST43751
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD,20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1..288
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):102467"
                     /db_xref="taxon:9606"
                     /clone_lib="Fetal brain I"
                     /sex="female"
                     /dev_stage="fetus, 24 wks"
                     /note="Organ: brain; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI"
BASE COUNT       63 a     89 c     82 g     54 t
ORIGIN


  Query Match            23.7%;  Score 246.2;  DB 9;  Length 288;
  Best Local Similarity  96.9%;  Pred. No. 1.2e-30;
  Matches  251;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    509 GAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAG 568
          ||| |   ||   |||||||||||||||||||||||||||||||||||||||||||||||
Db     30 GAGAATCGCTGTTTCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAG 89

Qy    569 GTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCC 628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     90 GTGTTCGTCTGCTGCGCCTCCACATCGCACTCCGGGGAGAAGCCGGTCCCCACTCTCCCC 149

Qy    629 CAGTTCACCATGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAAC 688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    150 CAGTTCACCATGGCCCCAATGTGAAGATCAACGTGCTGGAAGACTTTGAGGGAGAGAAC 209

Qy    689 CCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGACCAGCCCCAAACGGAACACCTG 748
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    210 CCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGACCAGCCCCAAACGGAACAACTG 269

Qy    749 CCCCTGGCCGTGGGCATCG 767
          |||||||||||||||||||
Db    270 CCCCTGGCCGTGGGCATCG 288


RESULT 15
BF950361
LOCUS       BF950361                 258 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION  CM3-NN1187-041100-465-c09 NN1187 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF950361
VERSION     BF950361.1  GI:12367636
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 258)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-NN1187-
            041100-465-c09&t3=2000-11-04&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 12
            High quality sequence stop: 258.
FEATURES             Location/Qualifiers
     source          1..258
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NN1187"
                     /dev_stage="Adult"
                     /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       51 a     85 c     78 g     43 t      1 others
ORIGIN


  Query Match            21.2%;  Score 220.2;  DB 10;  Length 258;
  Best Local Similarity  98.3%;  Pred. No. 1.9e-26;
  Matches  233;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy    612 CGGTCCCCACTCTCCCCCAGTTCACCATGGCCCCAATGTGAAGATCAACGTGCTGGAAG 671
          |||||||||||||||||||| |||||||||||||||| ||||||||||||||||||||||
Db     23 CGGTCCCCACTCTCCCCCAG-TCACCATGGCCCCAATATGAAGATCAACGTGCTGGAAG 81

Qy    672 ACTTTGAGGGAGAGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGACCAGCC 731
          |||| ||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db     82 ACTTCGAGGGAGGGAACCCTCAGGTGCCCAAGCTTGAGAAGAGCATCAGCGGACCAGCC 141

Qy    732 CCAAACGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGG 791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 CCAAACGGAACACCTGCCCCTGGCCGTGGGCATCGCCTTCTTCCTCATGACGTTCTTGG 201

Qy    792 CCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGA 848
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 CCTCCTAGCTCTGCCCCCTCCCCTGGGGGGGGAGAGATGGGGCGGGGCTTGGAAGGA 258


Search completed: September 27, 2002, 22:03:08
Job time: 6594 sec
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                    GenCore version 4.5
             Copyright (c) 1993 - 2000  Compugen Ltd.


OM protein - protein search, using sw model

Run on:          September 27, 2002, 22:43:05 ; Search time 74.08 Seconds
                                                 (without alignments)
                                                 356.852 Million cell updates/sec

Title:           US-09-904-954-2
Perfect score:   1301
Sequence:        1 MAAAPLLLLLLLVPVPLLPL..........REHLPLAVGIAFFLMTFLAS 238

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:      747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_032802:*
                 1:  /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                 SUMMARIES
                       %
Result                Query
  No.     Score   Match Length DB  ID                       Description
 ---------------------------------------------------------------------------
    1      1301   100.0    238 16  AAR71481                 Human hek-L protei
    2      1266    97.3    234 16  AAR82605                 Eph transmembrane
    3       437    33.6    209 17  AAR94766                 Mouse EPH receptor
    4       437    33.6    209 19  AAW71006                 Amino acid sequenc
    5       437    33.6    213 20  AAY06822                 Human LERK-6 polyp
    6     426.5    32.8    335 22  ABG27837                 Novel human diagno
    7       421    32.4    200 17  AAR94767                 Chicken EPH recept
    8       421    32.4    200 19  AAW71007                 Amino acid sequenc
    9     415.5    31.9    228 17  AAR97854                 Human AL-1, a liga
   10     415.5    31.9    228 17  AAW02586                 Lerk-7 protein.  H
   11     415.5    31.9    228 17  AAW00035                 HEK4 binding prote
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   12       403    31.0    184 17  AAW02587                 Lerk-6 protein.  M
   13       403    31.0    184 17  AAR91283                 LERK-6 protein.  M
   14       403    31.0    184 20  AAY06820                 Murine LERK-6 poly
   15       390    30.0    205 13  AAR23895                 B61 protein sequen
   16       390    30.0    205 15  AAR53634                 EBP.  Homo sapiens
   17       390    30.0    205 16  AAR82604                 Eph transmembrane
   18       390    30.0    205 18  AAW04632                 eck receptor bindi
   19       386    29.7    205 22  AAB50990                 Human PRO202 prote
   20       386    29.7    218 21  AAB54058                 Human pancreatic c
   21       384    29.5    180 18  AAW18082                 Truncated eck rece
   22       382    29.4    171 18  AAW18081                 Truncated eck rece
   23       380    29.2    167 18  AAW18080                 Truncated eck rece
   24     379.5    29.2    160 18  AAW18079                 Truncated eck rece
   25     377.5    29.0    151 18  AAW18078                 Truncated eck rece
   26     377.5    29.0    204 22  AAU12315                 Human PRO202 polyp
   27     377.5    29.0    204 22  AAB50974                 Human PRO202 prote
   28     364.5    28.0    179 17  AAR94768                 EPH receptor ligan
   29     364.5    28.0    179 19  AAW71008                 Generic sequence f
   30     364.5    28.0    201 16  AAR71482                 Human hek-L protei
   31       334    25.7    104 17  AAR91284                 LERK-6 exon polype
   32       334    25.7    104 20  AAY06821                 Amino acid sequenc
   33       295    22.7     58 21  AAG03418                 Human secreted pro
   34       180    13.8    340 18  AAW17081                 EPH family ligand
   35       180    13.8    340 19  AAW46615                 Human transmembran
   36       179    13.8    340 18  AAW33699                 AL-2-short (AL-2s)
   37       179    13.8    340 18  AAW31544                 Human cytokine Ler
   38       179    13.8    340 18  AAW10637                 NLERK2 ligand for
   39       179    13.8    455 18  AAW33698                 AL-2-long (AL-21)
   40       177    13.6    658 21  AAY96782                 Ephrin-B2-Ephrin-B
   41     171.5    13.2    308 17  AAW06334                 Ligand #2 for rece
   42     171.5    13.2    308 17  AAR94656                 Ligand for recepto
   43     171.5    13.2    333 17  AAW06337                 Full length ligand
   44     171.5    13.2    333 17  AAR94655                 Ligand for recepto
   45     171.5    13.2    333 17  AAR92743                 Human hepatoma tra


                                 ALIGNMENTS


RESULT   1
AAR71481
ID   AAR71481 standard; Protein; 238 AA.
XX
AC   AAR71481;
XX
DT   03-OCT-1995  (first entry)
XX
DE   Human hek-L protein.
XX
KW   Ligand; cell surface; tyrosine kinase receptor; tumorigenesis;
KW   immunogen.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Protein         20..238
XX
PN   WO9506065-A.
XX
PD   02-MAR-1995.
XX
PF   17-AUG-1994;   94WO-US09282.
XX
PR   20-AUG-1993;   93US-0109745.
PR   30-AUG-1993;   93US-0114426.
PR   03-DEC-1993;   93US-0161132.
PR   09-MAY-1994;   94US-0240124.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Beckmann MP,  Cerretti DP;
```

```
XX
DR   WPI; 1995-106811/14.
DR   N-PSDB; AAQ85887.
XX
PT   New isolated DNA encoding hek-L protein or its fusion products  -
PT   useful as assay reagent or for carrying therapeutic and
PT   diagnostic compounds to leukaemia cells.
XX
PS   Claim 21; Page 36; 45pp; English.
XX
CC   The sequence is that of a novel protein designated hek-L, a protein
CC   that can bind hek (a cell surface receptor tyrosine kinase).  Hek-L
CC   is the first known ligand for hek and can be used to study cellular
CC   processes regulated by hek (which may be involved in tumorigenesis).
CC   It is also an immunogen for antibody production, as a reagent for
CC   detecting hek or hek-L in in vitro assays, to determine binding of
CC   hek proteins, to purify hek proteins, and to carry diagnostic or
CC   cytotoxic agents to particular leukaemia cells that express the hek
CC   antigen.  Hek-L also binds the elk tyrosine kinase receptors.
CC   See also AAR71482.
XX
SQ   Sequence   238 AA;


  Query Match             100.0%;  Score 1301;  DB 16;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-124;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 maaapllllllvpvpllpllaqgpggalgnrhavywnssnqhlrregytvqvnvndyld 60

Qy       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 iycphynssgvgpgagpgpgggaeqyvlymvsrngyrtcnasqgfkrwecnrphaphspi 120

Qy      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 kfsekfqrysafslgyefhagheyyyistpthnlhwkclrmkvfvccastshsgekpvpt 180

Qy      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 lpqftmgpnvkinvledfegenpqvpkleksisgtspkrehlplavgiafflmtflas 238


RESULT   2
AAR82605
ID   AAR82605 standard; Protein; 234 AA.
XX
AC   AAR82605;
XX
DT   16-MAY-1996  (first entry)
XX
DE   Eph transmembrane tyrosine kinase family ligand, Efl-2.
XX
KW   Efl-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand;
KW   neurological disorder; identification; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT                   /label= signal_peptide
FT   Region          218..235
FT                   /note= "carboxy terminal hydrophobic
FT                          GPI-recognition tail"
FT   Misc-difference 158
FT                   /note= "residue borders main conserved regions"
XX
PN   WO9527060-A2.
XX
PD   12-OCT-1995.
XX
```

```
PF   04-APR-1995;   95WO-US04208.
XX
PR   21-OCT-1994;   94US-0327423.
PR   04-APR-1994;   94US-0222075.
PR   12-APR-1994;   94US-0229402.
PR   01-SEP-1994;   94US-0299567.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Aldrich TH,  Davis S,  Gale N,  Goldfarb M,  Maisonpierre PC;
PI   Yancopoulos GD;
XX
DR   WPI; 1995-358635/46.
DR   N-PSDB; AAT03883.
XX
PT   Ligands which bind Eph family receptors - used in the diagnosis of
PT   neurological disorders
XX
PS   Disclosure; Fig 2; 58pp; English.
XX
CC   Efl-2 (also known as EHK-1L) is an Eph transmembrane tyrosine kinase
CC   family ligand. It has homology with B61 (Efl-1) (see AAR82604). Efl-2
CC   ends in a C-terminal hydrophobic sequence that appears to to be a
CC   recognition sequence allowing it to be GPI-linked and thus lacking in
CC   an intracellular domain. Efl-2 is useful for identifying other ligands
CC   for Ehk-1, -2, -3, Eck and Elk receptors.  The ligands are useful in
CC   promoting a differential function and/or influencing the phenotye,
CC   such as growth and/or proliferation, of receptor bearing cells. They
CC   may be used in the diagnosis, and treatment of neurological disorders.
XX
SQ   Sequence   234 AA;


  Query Match             97.3%;  Score 1266;  DB 16;  Length 234;
  Best Local Similarity   98.3%;  Pred. No. 2.8e-120;
  Matches  234;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    1;

Qy        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 maaapllllllvpvpllpllaqgpggalgnrhavywnssnqhlrregytvqvnvndyld 60

Qy       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
            |||||||||    |||||||||||||||||||||||||||||||||||||||||||||||
Db       61 iycphynss----gagpgpgggaeqyvlymvsrngyrtcnasqgfkrwecnrphaphspi 116

Qy      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      117 kfsekfqrysafslgyefhagheyyyistpthnlhwkclrmkvfvccastshsgekpvpt 176

Qy      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      177 lpqftmgpnvkinvledfegenpqvpkleksisgtspkrehlplavgiafflmtflas 234


RESULT   3
AAR94766
ID   AAR94766 standard; Protein; 209 AA.
XX
AC   AAR94766;
XX
DT   02-JUL-1996  (first entry)
XX
DE   Mouse EPH receptor ligand Elf-1.
XX
KW   Elf-1; EPH receptor ligand; dementia; tachycardia; therapy;
KW   diagnosis; transgenic animal.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Sig_peptide
FT   Protein         21..209
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FT                   /label= Mat_protein
FT   Region          69..159
FT                   /label= Cys4_motif
FT   Region          35..166
FT                   /label= Core_sequence_motif
FT   Modified-site   38
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   170
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   184
FT                   /note= "potential N-glycosylation site"
XX
PN   WO9609384-A1.
XX
PD   28-MAR-1996.
XX
PF   19-SEP-1995;   95WO-US11869.
XX
PR   27-FEB-1995;   95US-0393462.
PR   19-SEP-1994;   94US-0308814.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1996-188446/19.
DR   N-PSDB; AAT15008.
XX
PT   Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis
PT   and treatment of disorders associated with the Elf-1 gene, e.g.
PT   dementia, tachycardia , etc.
XX
PS   Claim 1; Page 86; 107pp; English.
XX
CC   A novel mouse EPH receptor ligand, Elf-1 (AAR94766), is involved in
CC   the formation and maintenance of ordered spatial arrangements of
CC   differentiated tissue.  It is the product of a cDNA clone (AAT15008)
CC   obtd. from an embryo mid- and hind-brain cDNA expression library.
CC   This cDNA is used for the prodn. of recombinant Elf-1, which can
CC   be used to modulate proliferation, survival and/or differentiation
CC   of cells and tissues, and to stimulate or antagonise intracellular
CC   signal transduction pathways mediated by the EPH-type receptor.
XX
SQ   Sequence   209 AA;

  Query Match             33.6%;  Score 437;  DB 17;  Length 209;
  Best Local Similarity   50.5%;  Pred. No. 3.6e-36;
  Matches   96;  Conservative   25;  Mismatches   47;  Indels   22;  Gaps    7;

Qy      2 AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE------GYTVQV 53
          |  ||| ||||    |||| |  : |  |  :|:|||||| ||   :        ||||:|
Db      4 aqrpllpllll----llplrarnedparanadryavywnrsnprfqvsavgdgggytvev 59

Qy     54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
          ::|||||||||||       ||   |    |:|:||||:  |: :|:  | |||||||||
Db     60 sindyldiycphy-------gaplppaermeryilymvngeghascdhrqrgfkrwecnr 112

Qy    113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
          | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db    113 paapggplkfsekfqlftpfslgfefrpgheyyyisatppnlvdrpclrlkvyvrptnet 172

Qy    171 SHSGEKPVPT 180
           :   :|: |
Db    173 lyeapepift 182


RESULT   4
AAW71006
ID   AAW71006 standard; Protein; 209 AA.
XX
AC   AAW71006;
XX
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```
DT   20-OCT-1998  (first entry)
XX
DE   Amino acid sequence of a mammalian Elf-1 protein.
XX
KW   Mouse; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand;
KW   B61; LERK-2; proliferation; differentiation; intracellular signalling;
KW   increased; survival; neuronal cell; neuron survival; treatment;
KW   Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage;,
KW   bone formation.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /note= "signal peptide"
FT   Protein         21..209
FT                   /note= "mature protein"
FT   Modified-site   38
FT                   /note= "potential N-linked glycosylation site"
FT   Misc-difference 35..166
FT                   /note= "contains core sequence motif"
FT   Misc-difference 69..159
FT                   /note= "contains a Cys4 motif"
FT   Modified-site   170
FT                   /note= "potential N-linked glycosylation site"
FT   Modified-site   184
FT                   /note= "potential N-linked glycosylation site"
XX
PN   US5795734-A.
XX
PD   18-AUG-1998.
XX
PF   31-MAY-1995;   95US-0455001.
XX
PR   31-MAY-1995;   95US-0455001.
PR   19-SEP-1994;   94US-0308814.
PR   27-FEB-1995;   95US-0393462.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1998-466665/40.
DR   N-PSDB; AAV42926.
XX
PT   Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor
PT   - for production of Elf-1 protein, useful for regulating
PT   proliferation, differentiation, and survival of cells
XX
PS   Claim 1; Fig 2A; 53pp; English.
XX
CC   The present sequence represents a mammalian EPH receptor ligand
CC   designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is
CC   a tyrosine kinase ligand, which is linked to the membrane through a
CC   phosphatidylinositol linkage. It shares some homology to 2 other EPH
CC   receptor ligands, B61 and LERK-2. The Elf-1 protein modulates
CC   proliferation, differentiation and survival of EPH receptor-expressing
CC   cells by stimulating or antagonising intracellular signalling mediated
CC   by the EPH receptor. Typical of many potential applications are
CC   increasing survival of neuronal cells in culture (e.g. where intended for
CC   transplantation), also therapeutically in increase neuron survival
CC   (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent
CC   nervous system and lymphatic tumours, to induce differentiation of
CC   hepatocytes to form an artificial liver, to induce cartilage and bone
CC   formation.
XX
SQ   Sequence   209 AA;

  Query Match             33.6%;  Score 437;  DB 19;  Length 209;
  Best Local Similarity   50.5%;  Pred. No. 3.6e-36;
  Matches   96;  Conservative   25;  Mismatches   47;  Indels   22;  Gaps    7;
```

```
Qy      2 AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE------GYTVQV 53
          |  ||| ||||    |||| |  : |  |  :|:||||| ||   :        ||||:|
Db      4 aqrpllpllll----llplrarnedparanadryavywnrsnprfqvsavgdgggytvev 59

Qy     54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
          ::|||||||||||       ||   |    |:|:||||:  |: :|:  | |||||||||
Db     60 sindyldiycphy-------gaplppaermeryilymvngeghascdhrqrgfkrwecnr 112

Qy    113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
          | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db    113 paapggplkfsekfqlftpfslgfefrpgheyyyisatppnlvdrpclrlkvyvrptnet 172

Qy    171 SHSGEKPVPT 180
           :   :|: |
Db    173 lyeapepift 182


RESULT   5
AAY06822
ID   AAY06822 standard; Protein; 213 AA.
XX
AC   AAY06822;
XX
DT   24-JUN-1999  (first entry)
XX
DE   Human LERK-6 polypeptide.
XX
KW   LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury;
KW   cell proliferation; neural growth; neural tissue; neurological disease;
KW   neurodegenerative; excitotoxicity.
XX
OS   Homo sapiens.
XX
PN   WO9910495-A1.
XX
PD   04-MAR-1999.
XX
PF   27-AUG-1998;   98WO-US17772.
XX
PR   29-AUG-1997;   97US-0920440.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1999-243567/20.
DR   N-PSDB; AAX32767.
XX
PT   New cytokine designated LERK-6
XX
PS   Claim 6; Page 42; 46pp; English.
XX
CC   The invention relates murine and human LERK-6 polypeptides that bind to
CC   hek/elk receptors. Host cells transfected or transformed with vectors
CC   comprising the LERK-6 nucleic acid sequences are used for the recombinant
CC   production of the proteins. LERK-6 polypeptides may be useful in the
CC   enhancement, stimulation, proliferation or growth of cells expressing the
CC   hek or elk receptor. The ligand and receptor complex may be involved in
CC   neural growth, development and/or maintenance. LERK-6 can be used for
CC   treating disorders of neural tissue such as injury or neurological
CC   diseases, either chronic or acute. LERK-6 may be employed in treating
CC   neurodegenerative conditions where there is neural death, excitotoxicity.
CC   In addition, they may be administered to a mammal to exert a trophic
CC   effect on neural tissue. They can also be used as reagents for those
CC   conducting quality assurance studies e.g. to monitor shelf life and
CC   stability of elk protein under different conditions. The polypeptides can
CC   also be used as carriers for delivering agents attached to cells bearing
CC   the elk or hek cell surface receptor. The present sequence represents a
CC   human LERK-6 polypeptide.
XX
SQ   Sequence   213 AA;
```

```
  Query Match             33.6%;  Score 437;  DB 20;  Length 213;
  Best Local Similarity   50.5%;  Pred. No. 3.7e-36;
  Matches   96;  Conservative   24;  Mismatches   52;  Indels   18;  Gaps    7;

Qy      2 AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR------EGYTVQV 53
          |  ||| |||||:|:|  |   |:    |  :|:||||| ||            ||||:|
Db      4 aqrpllplllllllplppppfaraedaaransdryavywnrsnprfhagagddgggytvev 63

Qy     54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
          ::|||||||||||       ||   |    | ||||||:  |: :|:  | |||||||||
Db     64 sindyldiycphy-------gaplppaermehyvlymvngeghascdhrqrgfkrwecnr 116

Qy    113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
          | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db    117 paapggplkfsekfqlftpfslgfefrpgheyyyisatppnavdrpclrlkvyvrptnet 176

Qy    171 SHSGEKPVPT 180
           :   :|: |
Db    177 lyeapepift 186


RESULT   6
ABG27837
ID   ABG27837 standard; Protein; 335 AA.
XX
AC   ABG27837;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #27828.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS92024.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 58196; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
```

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CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   335 AA;

  Query Match             32.8%;  Score 426.5;  DB 22;  Length 335;
  Best Local Similarity   39.2%;  Pred. No. 7.8e-35;
  Matches  100;  Conservative   39;  Mismatches   69;  Indels   47;  Gaps   11;

Qy          1 MAAAPLLLLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYL 59
              :  ||: :| |:  |  : : :| ||  |: :|:||||||||   :|  | : | :||||
Db        106 lgvapvemltlvflvlwmcvfsqdpgskavadryavywnssnprfqrgdyhidvcindyl 165

Qy         60 DIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHS 118
              |::||||  |         |    |:||||||: :||  | : |:|||||||||||:|:
Db        166 dvfcphyeds--------vpedkteryvlymvnfdgysacdhtskgfkrwecnrphspng 217

Qy        119 PIKFSEKFQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHS 173
              |:||||||| :: ||||:||  | ||:|||:    |    ||::||||     |  |
Db        218 plkfsekfqlftpfslgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigv 277

Qy        174 GEKPVPTLPQFTMGPNVKINVLEDFE-----------GEN-PQVPKLEKSISGTSPKREH 221
               ::       | :   |: | ||  :           |||  | |::        | |
Db        278 hdr------vfdvndkve-nslepaddtvhesaepsrgenaaqtpri--------psr-- 320

Qy        222 LPLAVGIAFFLMTFL 236
                  : |  ||:  |
Db        321 ---llaillfllaml 332


RESULT   7
AAR94767
ID   AAR94767 standard; Protein; 200 AA.
XX
AC   AAR94767;
XX
DT   02-JUL-1996  (first entry)
XX
DE   Chicken EPH receptor ligand Elf-1.
XX
KW   Elf-1; EPH receptor ligand; dementia; tachycardia; therapy;
KW   diagnosis; transgenic animal.
XX
OS   Gallus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..21
FT                   /label= Sig_peptide
FT   Protein         22..200
FT                   /label= Mat_protein
FT   Region          61..150
FT                   /label= Cys4_motif
FT   Region          33..157
FT                   /label= Core_sequence_motif
XX
PN   WO9609384-A1.
XX
PD   28-MAR-1996.
XX
PF   19-SEP-1995;   95WO-US11869.
XX
PR   27-FEB-1995;   95US-0393462.
PR   19-SEP-1994;   94US-0308814.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
```

```
XX
DR   WPI; 1996-188446/19.
DR   N-PSDB; AAT15009.
XX
PT   Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis
PT   and treatment of disorders associated with the Elf-1 gene, e.g.
PT   dementia, tachycardia , etc.
XX
PS   Claim 1; Page 88-89; 107pp; English.
XX
CC   A novel chicken EPH receptor ligand, Elf-1 (AAR94767), is involved in
CC   the formation and maintenance of ordered spatial arrangements of
CC   differentiated tissue.  It is the product of a cDNA clone (AAT15009)
CC   obtd. from an embryo cDNA expression library.  This cDNA is used for
CC   the prodn. of recombinant Elf-1, which can be used to modulate
CC   proliferation, survival and/or differentiation of cells and tissues,
CC   and to stimulate or antagonise intracellular signal transduction
CC   pathways mediated by the EPH-type receptor.
XX
SQ   Sequence   200 AA;

  Query Match             32.4%;  Score 421;  DB 17;  Length 200;
  Best Local Similarity   47.5%;  Pred. No. 1.4e-34;
  Matches   86;  Conservative   29;  Mismatches   50;  Indels   16;  Gaps    5;

Qy          3 AAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
              || ||  :: | |      :  ||  : :|:||||| ||    |  |||:|::|||||||
Db          6 aaallaaivgvcv-----wsddpgkvisdryavywnrsnprfhrgdytvevsindyldiy 60

Qy         63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
              ||||          | |    |:||||||:  |: :|:  | |||||||||| :|  |:|
Db         61 cphyee--------plpaermeryvlymvnyeghascdhrqkgfkrwecnrpdspsgplk 112

Qy        122 FSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
              |||||| :: ||||:||  |||||||| :| : :   ||::||:|   : | :   :|:
Db        113 fsekfqlftpfslgfefrpgheyyyisasppnvvdrpclklkvyvrptndslyespepif 172

Qy        180 T 180
              |
Db        173 t 173


RESULT   8
AAW71007
ID   AAW71007 standard; Protein; 200 AA.
XX
AC   AAW71007;
XX
DT   20-OCT-1998  (first entry)
XX
DE   Amino acid sequence of an avian Elf-1 protein.
XX
KW   Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP;
KW   tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation;
KW   intracellular signalling; increased; survival; neuronal cell;
KW   neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour;
KW   artificial liver; cartilage; bone formation.
XX
OS   Gallus sp.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 61..150
FT                   /note= "contains a Cys4 motif"
FT   Misc-difference 35..157
FT                   /note= "contains a core sequence motif"
XX
PN   US5795734-A.
XX
PD   18-AUG-1998.
XX
PF   31-MAY-1995;   95US-0455001.
XX
```

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PR   31-MAY-1995;   95US-0455001.
PR   19-SEP-1994;   94US-0308814.
PR   27-FEB-1995;   95US-0393462.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1998-466665/40.
DR   N-PSDB; AAV42927.
XX
PT   Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor
PT   - for production of Elf-1 protein, useful for regulating
PT   proliferation, differentiation, and survival of cells
XX
PS   Claim 1; Columns 75-78; 53pp; English.
XX
CC   The present sequence represents an avian EPH receptor ligand designated
CC   Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a
CC   tyrosine kinase ligand, which is linked to the membrane through a
CC   phosphatidylinositol linkage. It shares some homology to 2 other EPH
CC   receptor ligands, B61 and LERK-2. The Elf-1 protein modulates
CC   proliferation, differentiation and survival of EPH receptor-expressing
CC   cells by stimulating or antagonising intracellular signalling mediated
CC   by the EPH receptor. Typical of many potential applications are
CC   increasing survival of neuronal cells in culture (e.g. where intended for
CC   transplantation), also therapeutically in increase neuron survival
CC   (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent
CC   nervous system and lymphatic tumours, to induce differentiation of
CC   hepatocytes to form an artificial liver, to induce cartilage and bone
CC   formation.
XX
SQ   Sequence   200 AA;


  Query Match             32.4%;  Score 421;  DB 19;  Length 200;
  Best Local Similarity   47.5%;  Pred. No. 1.4e-34;
  Matches   86;  Conservative   29;  Mismatches   50;  Indels   16;  Gaps    5;

Qy      3 AAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
          || ||  ::  | |      :  ||  : :|:||||| ||    |  |||:|::|||||||
Db      6 aaallaaivgvcv-----wsddpgkvisdryavywnrsnprfhrgdytvevsindyldiy 60

Qy     63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
          ||||          | |    |:||||||:  |: :|:  | |||||||||| :|  |:|
Db     61 cphyee--------plpaermeryvlymvnyeghascdhrqkgfkrwecnrpdspsgplk 112

Qy    122 FSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
          |||||| :: ||||:||  |||||||| :| : :   ||::||:|   : | :   :|:
Db    113 fsekfqlftpfslgfefrpgheyyyisasppnvvdrpclklkvyvrptndslyespepif 172

Qy    180 T 180
          |
Db    173 t 173


RESULT   9
AAR97854
ID   AAR97854 standard; Protein; 228 AA.
XX
AC   AAR97854;
XX
DT   05-JAN-1997  (first entry)
XX
DE   Human AL-1, a ligand for eph-related tyrosine kinase receptor REK7.
XX
KW   AL-1; REK7; eph-related tyrosine kinase receptor; ligand;
KW   neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Sig_peptide
FT   Modified-site   37..39
FT                   /label= Glycosylation
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   162..164
FT                   /label= Glycosylation
FT                   /note= "potential N-glycosylation site"
FT   Binding-site    203..204
FT                   /label= GPI
FT                   /note= "potential attachment site for
FT                          glycophosphatidyl-inositol"
FT   Domain          214..228
FT                   /label= Hydrophobic_domain
XX
PN   WO9613518-A1.
XX
PD   09-MAY-1996.
XX
PF   26-OCT-1995;   95WO-US14016.
XX
PR   07-JUN-1995;   95US-0486449.
PR   27-OCT-1994;   94US-0330128.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Caras IW,  Winslow JW;
XX
DR   WPI; 1996-239448/24.
DR   N-PSDB; AAT18897.
XX
PT   AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in
PT   treatment and diagnosis of neuronal disorders and
PT   angiogenesis-related conditions.
XX
PS   Claim 1; Page 54; 75pp; English.
XX
CC   Human AL-1 (AAR97854) neurotrophic factor is a ligand for eph-related
CC   tyrosine kinase receptor REK7 (AAR97853).  Its amino acid sequence
CC   was deduced from a cDNA clone (AAT18897) isolated from a human foetal
CC   brain cDNA library.  Recombinant, mature AL-1 can be produced in
CC   transformed host cells.  It may be useful in promoting the
CC   development, maintenance or regeneration of neurons in vivo, and
CC   can be utilised in methods for the diagnosis and/or treatment of
CC   neurological disorders.  It can also be used to promote or enhance
CC   angiogenesis.  Antagonists and agonists of AL-1, as well as
CC   antibodies raised against AL-1, also have therapeutic applns.
XX
SQ   Sequence   228 AA;


  Query Match             31.9%;  Score 415.5;  DB 17;  Length 228;
  Best Local Similarity   39.5%;  Pred. No. 6.1e-34;
  Matches   98;  Conservative   37;  Mismatches   66;  Indels   47;  Gaps   11;

Qy      8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
          :| |:  |  : : :| ||  |: :|:||||||||   :|  | : | :|||||::||||
Db      6 mltlvflvlwmcvfsqdpgskavadryavywnssnprfqrgdyhidvcindyldvfcphy 65

Qy     67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
            |         |    |:||||||: :||  | : |:|||||||||||:|: |:|||||
Db     66 eds--------vpedkteryvlymvnfdgysacdhtskgfkrwecnrphspngplkfsek 117

Qy    126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
          || :: ||||:||  | ||:|||:    |    ||::||||     |  |    ::
Db    118 fqlftpfslgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigvhdr---- 173

Qy    181 LPQFTMGPNVKINVLEDFE-----------GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
             | :   |: | ||  :           |||  | |::        | |      : |
Db    174 --vfdvndkve-nslepaddtvhesaepsrgenaaqtpri--------psr-----llai 217

Qy    229 AFFLMTFL 236
            ||:  |
Db    218 llfllaml 225
```

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RESULT  10
AAW02586
ID   AAW02586 standard; Protein; 228 AA.
XX
AC   AAW02586;
XX
DT   28-NOV-1996  (first entry)
XX
DE   Lerk-7 protein.
XX
KW   Lerk-6; hek; elk; cell surface receptor; culture; reagent;
KW   neuron; disorder; injury; delivery agent; diagnostic; therapeutic;
KW   Lerk-7; probe; cytokine.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= signal_peptide
FT   Protein         1..228
FT                   /label= precursor_protein
FT   Domain          1..133
FT                   /label= extracellular_receptor-binding_domain
FT   Region          134..183
FT                   /label= spacer_region
FT   Region          194..208
FT                   /note= "C-terminal stretch of hydrophobic residues"
FT   Binding-site    183
FT                   /label= GPI_attachment_site
XX
PN   WO9617925-A1.
XX
PD   13-JUN-1996.
XX
PF   05-DEC-1995;   95WO-US15781.
XX
PR   01-MAR-1995;   95US-0396946.
PR   06-DEC-1994;   94US-0351025.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1996-287171/29.
DR   N-PSDB; AAT32699.
XX
PT   New isolated human Lerk-7 cytokine - which binds to cell surface
PT   receptors elk, hek and eck, useful for delivering agents to cells or
PT   for treating neural disorders
XX
PS   Claim 1; Page 37-38; 49pp; English.
XX
CC   The present sequence is that of human Lerk-7 protein. Lerk-7 is
CC   predicted to be anchored to the cell surface via
CC   glycosyl-phosphatidylinositol (GPI) linkage. A GPI anchor attaches to the
CC   exposed C-terminal amino acid of the processed mature protein, usually
CC   after cleavage upstream, often about 10-12 amino acids, of the N-terminus
CC   of the hydrophobic domain. Lerk-7 coding sequence (AAT32699) was isolated
CC   using a probe derived from the murine Lerk-6 DNA (AAT32700). The Lerk-7
CC   gene and protein can be used for studying the role of Lerk-7 in
CC   conjunction with elk, hek and eck receptors. They can also be used for
CC   delivering diagnostic or therapeutic agents to cells, e.g. cancer cells.
CC   The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic
CC   properties and can be used to treat neural tissue disorders.
XX
SQ   Sequence   228 AA;


  Query Match             31.9%;  Score 415.5;  DB 17;  Length 228;
  Best Local Similarity   39.5%;  Pred. No. 6.1e-34;
  Matches   98;  Conservative   37;  Mismatches   66;  Indels   47;  Gaps   11;
```

```
Qy      8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
          :| |:  |  : : :| ||  |: :|:||||||||   :|  | : | :|||||::||||
Db      6 mltlvflvlwmcvfsqdpgskavadryavywnssnprfqrgdyhidvcindyldvfcphy 65

Qy     67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
            |         |    |:||||||: :||  | : |:|||||||||||:|: |:|||||
Db     66 eds--------vpedkteryvlymvnfdgysacdhtskgfkrwecnrphspngplkfsek 117

Qy    126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
          || :: ||||:||  | ||:|||:    |    ||::||||     |  |    ::
Db    118 fqlftpfslgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigvhdr---- 173

Qy    181 LPQFTMGPNVKINVLEDFE-----------GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
             | :   |: | ||  :           |||  | |::        | |      : |
Db    174 --vfdvndkve-nslepaddtvhesaepsrgenaaqtpri--------psr-----llai 217

Qy    229 AFFLMTFL 236
            ||:  |
Db    218 llfllaml 225


RESULT  11
AAW00035
ID   AAW00035 standard; Protein; 228 AA.
XX
AC   AAW00035;
XX
DT   24-OCT-1996  (first entry)
XX
DE   HEK4 binding protein.
XX
KW   HEK4 binding protein; HEK4 receptor; EPH-like receptor;
KW   protein tyrosine kinase; ligand; growth; differentiation; cancer;
KW   nervous system disorder; therapy; antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= Sig_peptide
FT   Protein         20..228
FT                   /label= Mat_protein
XX
PN   WO9623000-A1.
XX
PD   01-AUG-1996.
XX
PF   16-JAN-1996;   96WO-US01079.
XX
PR   27-JAN-1995;   95US-0379802.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Bartley TD,  Fox GM;
XX
DR   WPI; 1996-362633/36.
DR   N-PSDB; AAT34292.
XX
PT   Ligand for EPH-like receptors, partic. the HEK4 receptor - useful to
PT   modulate growth and differentiation of, e.g. liver and kidney cells,
PT   and to treat cancer and nervous system disorders
XX
PS   Claim 8; Page 39-40; 65pp; English.
XX
CC   Human HEK4 binding protein (HEK4 BP) (AAW00035) binds to and activates
CC   HEK4 and ECK receptors.  Its amino acid sequence was deduced from
CC   a cDNA clone (AAT34292) isolated from a human placenta cDNA library.
CC   Expression vectors and host cells can be used for the prodn. of
CC   biologically active HEK BP.  It is useful for modulating the growth
CC   and/or differentiation of EPH sub-family receptor-bearing cells,
CC   esp. in liver, kidney, lung, skin or neural tissues.  It can be
CC   used to treat neural system disorders and in the regeneration of
```

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CC   damaged or depleted tissues.  Antagonists are useful for cancer
CC   treatment.  HEK4 BP can also be used to raise antibodies.
XX
SQ   Sequence   228 AA;

  Query Match             31.9%;  Score 415.5;  DB 17;  Length 228;
  Best Local Similarity   39.5%;  Pred. No. 6.1e-34;
  Matches   98;  Conservative   37;  Mismatches   66;  Indels   47;  Gaps   11;

Qy        8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
            :| |:  |  : : :| ||  |: :|:||||||||   :|  | : | :|||||::||||
Db        6 mltlvflvlwmcvfsqdpgskavadryavywnssnprfqrgdyhidvcindyldvfcphy 65

Qy       67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
              |         |    |:||||||: :||  | : |:|||||||||||:|: |:|||||
Db       66 eds--------vpedkteryvlymvnfdgysacdhtskgfkrwecnrphspngplkfsek 117

Qy      126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
            || :: ||||:||  | ||:|||:    |    ||::||||     |  |    ::
Db      118 fqlftpfslgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigvhdr---- 173

Qy      181 LPQFTMGPNVKINVLEDFE-----------GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
               | :   |: | ||  :           |||  | |::        | |      : |
Db      174 --vfdvndkve-nslepaddtvhesaepsrgenaaqtpri--------psr-----llai 217

Qy      229 AFFLMTFL 236
              ||:  |
Db      218 llfllaml 225


RESULT  12
AAW02587
ID   AAW02587 standard; Protein; 184 AA.
XX
AC   AAW02587;
XX
DT   28-NOV-1996  (first entry)
XX
DE   Lerk-6 protein.
XX
KW   Lerk-6; hek; elk; cell surface receptor; culture; reagent;
KW   neuron; disorder; injury; delivery agent; diagnostic; therapeutic;
KW   Lerk-7; probe; cytokine.
XX
OS   Mus musculus.
XX
PN   WO9617925-A1.
XX
PD   13-JUN-1996.
XX
PF   05-DEC-1995;   95WO-US15781.
XX
PR   01-MAR-1995;   95US-0396946.
PR   06-DEC-1994;   94US-0351025.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1996-287171/29.
DR   N-PSDB; AAT32700.
XX
PT   New isolated human Lerk-7 cytokine - which binds to cell surface
PT   receptors elk, hek and eck, useful for delivering agents to cells or
PT   for treating neural disorders
XX
PS   Example 1; Page 35; 49pp; English.
XX
CC   The present sequence is that of a murine cytokine, Lerk-6, encoded by
CC   AAT32700. A fragment of murine Lerk-6 DNA was isolated by PCR for use as
CC   a probe for a human Lerk-6 homologue. The probe however led to the
CC   identification of a human Lerk-7 gene (see AAT32699). The Lerk-7 gene
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CC   and protein can be used for studying the role of Lerk-7 in conjunction
CC   with elk, hek and eck receptors. They can also be used for delivering
CC   diagnostic or therapeutic agents to cells, e.g. cancer cells.  The
CC   Lerk-7 proteins can also exhibit neuroprotective or neurotrophic
CC   properties and can be used to treat neural tissue disorders.
XX
SQ   Sequence   184 AA;

  Query Match             31.0%;  Score 403;  DB 17;  Length 184;
  Best Local Similarity   50.6%;  Pred. No. 8.5e-33;
  Matches   82;  Conservative   24;  Mismatches   40;  Indels   16;  Gaps    5;

Qy       28 ALGNRHAVYWNSSNQHLRRE------GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGG 81
            |  :|:||||| ||   :        ||||:|::|||||||||||       ||   |
Db        3 anadryavywnrsnprfqvsavgdgggytvevsindyldiycphy-------gaplppae 55

Qy       82 GAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHA 140
              |:|:||||:  |: :|:  | |||||||||| ||  |:||||||| :: ||||:||
Db       56 rmeryilymvngeghascdhrqrgfkrwecnrpaapggplkfsekfqlftpfslgfefrp 115

Qy      141 GHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVPT 180
            |||||||| || : :   |||:||:|   : | :   :|: |
Db      116 gheyyyisatppnlvdrpclrlkvyvrptnetlyeapepift 157


RESULT  13
AAR91283
ID   AAR91283 standard; Protein; 184 AA.
XX
AC   AAR91283;
XX
DT   10-OCT-1996  (first entry)
XX
DE   LERK-6 protein.
XX
KW   LERK-6; hek; elk; cell surface receptors; culture; reagent;
KW   neurons; disorder; injury; delivery agent; diagnostic; therapeutic.
XX
OS   Mus musculus.
XX
PN   WO9610911-A1.
XX
PD   18-APR-1996.
XX
PF   04-OCT-1995;   95WO-US12779.
XX
PR   03-OCT-1995;   95US-0538709.
PR   05-OCT-1994;   94US-0318393.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1996-209575/21.
DR   N-PSDB; AAT14009.
XX
PT   Isolated DNA encoding cytokine designated LERK-6 which binds to hek
PT   and elk cell surface receptors - useful for drug delivery and
PT   screening procedures.
XX
PS   Claim 6; Page 34; 44pp; English.
XX
CC   The LERK-6 polypeptide encoded can be used to isolate cells
CC   expressing hek/elk cell surface receptors, or to measure the
CC   biological activity of such receptors.  The protein may also be used
CC   as a delivery agent, taking diagnostic and therapeutic agents to
CC   cells expressing such receptors. LERK-6 can also be used as a tissue
CC   culture reagent to enhance the viability or prolong the lifespan of
CC   the neurons.  Neural tissue disorders and injuries may be treated by
CC   contact with the polypeptide.
XX
SQ   Sequence   184 AA;
```

```
  Query Match             31.0%;  Score 403;  DB 17;  Length 184;
  Best Local Similarity   50.6%;  Pred. No. 8.5e-33;
  Matches   82;  Conservative   24;  Mismatches   40;  Indels   16;  Gaps    5;

Qy     28 ALGNRHAVYWNSSNQHLRRE------GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGG 81
          |  :|:||||| ||   :        ||||:|::|||||||||||       ||   |
Db      3 anadryavywnrsnprfqvsavgdgggytvevsindyldiycphy-------gaplppae 55

Qy     82 GAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHA 140
            |:|:||||:  |: :|:  | |||||||||| ||  |:||||||| :: ||||:||
Db     56 rmeryilymvngeghascdhrqrgfkrwecnrpaapggplkfsekfqlftpfslgfefrp 115

Qy    141 GHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVPT 180
          |||||||| || : :   |||:||:|   : | :   :|: |
Db    116 gheyyyisatppnlvdrpclrlkvyvrptnetlyeapepift 157


RESULT  14
AAY06820
ID   AAY06820 standard; Protein; 184 AA.
XX
AC   AAY06820;
XX
DT   24-JUN-1999  (first entry)
XX
DE   Murine LERK-6 polypeptide.
XX
KW   LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury;
KW   cell proliferation; neural growth; neural tissue; neurological disease;
KW   neurodegenerative; excitotoxicity.
XX
OS   Mus sp.
XX
PN   WO9910495-A1.
XX
PD   04-MAR-1999.
XX
PF   27-AUG-1998;   98WO-US17772.
XX
PR   29-AUG-1997;   97US-0920440.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1999-243567/20.
DR   N-PSDB; AAX32761.
XX
PT   New cytokine designated LERK-6
XX
PS   Claim 6; Page 37-38; 46pp; English.
XX
CC   The invention relates murine and human LERK-6 polypeptides that bind to
CC   hek/elk receptors. Host cells transfected or transformed with vectors
CC   comprising the LERK-6 nucleic acid sequences are used for the recombinant
CC   production of the proteins. LERK-6 polypeptides may be useful in the
CC   enhancement, stimulation, proliferation or growth of cells expressing the
CC   hek or elk receptor. The ligand and receptor complex may be involved in
CC   neural growth, development and/or maintenance. LERK-6 can be used for
CC   treating disorders of neural tissue such as injury or neurological
CC   diseases, either chronic or acute. LERK-6 may be employed in treating
CC   neurodegenerative conditions where there is neural death, excitotoxicity.
CC   In addition, they may be administered to a mammal to exert a trophic
CC   effect on neural tissue. They can also be used as reagents for those
CC   conducting quality assurance studies e.g. to monitor shelf life and
CC   stability of elk protein under different conditions. The polypeptides can
CC   also be used as carriers for delivering agents attached to cells bearing
CC   the elk or hek cell surface receptor. The present sequence represents a
CC   murine LERK-6 polypeptide.
XX
SQ   Sequence   184 AA;
```

```
  Query Match             31.0%;  Score 403;  DB 20;  Length 184;
  Best Local Similarity   50.6%;  Pred. No. 8.5e-33;
  Matches   82;  Conservative   24;  Mismatches   40;  Indels   16;  Gaps    5;

Qy     28 ALGNRHAVYWNSSNQHLRRE------GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGG 81
          |  :|:||||| ||   :        ||||:|::|||||||||||       ||   |
Db      3 anadryavywnrsnprfqvsavgdgggytvevsindyldiycphy-------gaplppae 55

Qy     82 GAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHA 140
            |:|:||||:  |: :|:  | |||||||||| ||  |:||||||| :: ||||:||
Db     56 rmeryilymvngeghascdhrqrgfkrwecnrpaapggplkfsekfqlftpfslgfefrp 115

Qy    141 GHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVPT 180
          |||||||| || : :   |||:||:|   : | :   :|: |
Db    116 gheyyyisatppnlvdrpclrlkvyvrptnetlyeapepift 157


RESULT  15
AAR23895
ID   AAR23895 standard; Protein; 205 AA.
XX
AC   AAR23895;
XX
DT   06-NOV-1992  (first entry)
XX
DE   B61 protein sequence.
XX
KW   Early inflammatory response; marker; antibody; therapy; induction;
KW   lipopolysaccharides; cytokines; Interleukin-2; IL-2; TNF.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..18
FT                   /note= "signal peptide"
XX
PN   WO9207094-A.
XX
PD   30-APR-1992.
XX
PF   15-OCT-1991;   91WO-US07704.
XX
PR   16-OCT-1990;   90US-0607741.
XX
PA   (UNMI ) UNIV MICHIGAN.
XX
PI   Dixit VM;
XX
DR   WPI; 1992-167172/20.
DR   N-PSDB; AAQ24595.
XX
PT   Gene prod. used as marker to detect inflammatory response - by
PT   detecting the B61 gene in biological fluids or by using
PT   hybridisation probes
XX
PS   Claim 7; Fig 3; 39pp; English.
XX
CC   The B1 protein sequence was deduced from the cDNA sequence obtd. by
CC   screening a cDNA library from human umbilical vein endothelial cells
CC   with radiolabelled cDNA fragments derived from the 5' end of B61 DNA.
CC   The B1 protein has 205 residues (24 kD) comprising a signal
CC   sequence and hydrophobic N- and C- terminal regions.  The B61 gene
CC   is involved in early inflammatory response and serves as a marker.
CC   It may be detected by probes or by antibody-based immunoassay of
CC   biological fluids such as plasma, CSF or urine.  These assays make
CC   it possible to predict a worsening in a disease process and allow
CC   the quantitative assessment of the magnitude of the inflammatory
CC   response.  This information will allow the earlier admin. of
CC   appropriate therapy, thereby shortening the disease process and
CC   limiting the patient's exposure to anti-inflammatory/immuno-
CC   suppressive therapy.  B61 induction is rapid and profound, hence
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CC   it is easily detectable. The B61 response is highly specific to
CC   proinflammatory stimuli, being only made by cells exposed to lipo-
CC   polysaccharides or cytokines such as IL-2 and TNF and not growth
CC   factors or interferon.
XX
SQ   Sequence   205 AA;


  Query Match             30.0%;  Score 390;  DB 13;  Length 205;
  Best Local Similarity   41.8%;  Pred. No. 2.1e-31;
  Matches   87;  Conservative   21;  Mismatches   76;  Indels   24;  Gaps    6;

Qy      19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
           |||      |  :|| |:|||||   | | ||: | :|||:|| ||||    |   |
Db       7 pllglccslaaadrhtvfwnssnpkfrnedytihvqlndyvdiicphyedhsvadaa--- 63

Qy      79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                |||:||:|    |: |   |:   ||:|||| | | | | ||||||:: |:|| |
Db      64 ----meqyilylveheeyqlcqpqskdqvrwqcnrpsakhgpeklsekfqrftpftlgke 119

Qy     138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
           |  || ||||| | |    :|||:|| |     :||        ||  : |  |    :|
Db     120 fkeghsyyyiskpihqhedrclrlkvtv-sgkiths--------pqahvnpqekrlaadd 170

Qy     198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
                |:|  |       :|:    |||
Db     171 -----pevrvlhsighsaaprl--fpla 191


Search completed: September 28, 2002, 01:36:51
Job time: 10426 sec
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                         GenCore version 4.5
              Copyright (c) 1993 - 2000  Compugen Ltd.


OM protein - protein search, using sw model

Run on:          September 27, 2002, 22:50:00 ; Search time 29.18 Seconds
                                                (without alignments)
                                                199.222 Million cell updates/sec

Title:           US-09-904-954-2
Perfect score:   1301
Sequence:        1 MAAAPLLLLLLLVPVPLLPL..........REHLPLAVGIAFFLMTFLAS 238

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters:      231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_AA:*
                 1:  /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
                 2:  /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
                 3:  /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
                 4:  /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
                 5:  /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                 6:  /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                 %
Result          Query
  No.   Score   Match Length DB  ID                        Description
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    1    1301   100.0    238  1  US-08-240-124-2            Sequence 2, Appli
    2    1301   100.0    238  1  US-08-453-943-2            Sequence 2, Appli
    3    1301   100.0    238  2  US-09-057-121-2            Sequence 2, Appli
    4    1301   100.0    238  4  US-09-358-734-2            Sequence 2, Appli
    5    1261    96.9    234  1  US-08-299-567-5            Sequence 5, Appli
    6     437    33.6    209  1  US-08-455-001-2            Sequence 2, Appli
    7     437    33.6    209  4  US-08-308-814-2            Sequence 2, Appli
    8     437    33.6    209  5  PCT-US95-11869-2           Sequence 2, Appli
    9     437    33.6    213  1  US-09-609-324A-10          Sequence 10, Appl
   10     437    33.6    213  2  US-08-920-440B-10          Sequence 10, Appl
   11     437    33.6    213  4  US-09-173-492-10           Sequence 10, Appl
   12     437    33.6    213  4  US-09-173-133-10           Sequence 10, Appl
   13     421    32.4    200  1  US-08-455-001-4            Sequence 4, Appli
   14     421    32.4    200  5  PCT-US95-11869-4           Sequence 4, Appli
   15   415.5    31.9    228  1  US-08-442-248-4            Sequence 4, Appli
   16   415.5    31.9    228  1  US-08-440-815-4            Sequence 4, Appli
   17   415.5    31.9    228  3  US-08-379-802-2            Sequence 2, Appli
   18   415.5    31.9    228  3  US-09-048-129-2            Sequence 2, Appli
   19   415.5    31.9    228  4  US-09-048-079-2            Sequence 2, Appli
   20   415.5    31.9    228  4  US-08-486-449-4            Sequence 4, Appli
   21   415.5    31.9    228  5  PCT-US95-15781-5           Sequence 5, Appli
   22     403    31.0    184  1  US-09-609-324A-2           Sequence 2, Appli
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   24     403    31.0    184  4  US-09-173-492-2            Sequence 2, Appli
   25     403    31.0    184  4  US-09-173-133-2            Sequence 2, Appli
   26     403    31.0    184  4  US-09-165-533-2            Sequence 2, Appli
   27     403    31.0    184  5  PCT-US95-12779-2           Sequence 2, Appli
   28     403    31.0    184  5  PCT-US95-15781-2           Sequence 2, Appli
   29     390    30.0    205  1  US-08-321-162-2            Sequence 2, Appli
   30     390    30.0    205  1  US-08-448-736-1            Sequence 1, Appli
   31     390    30.0    205  1  US-08-441-216-2            Sequence 2, Appli
   32     390    30.0    205  1  US-08-452-779-1            Sequence 1, Appli
   33     390    30.0    205  1  US-08-299-567-4            Sequence 4, Appli
   34     390    30.0    205  2  US-08-445-065-1            Sequence 1, Appli
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   36     390    30.0    205  3  US-08-959-524-1            Sequence 1, Appli
   37     390    30.0    205  3  US-08-959-524-12           Sequence 12, Appl
   38   364.5    28.0    179  1  US-08-455-001-5            Sequence 5, Appli
   39   364.5    28.0    179  5  PCT-US95-11869-5           Sequence 5, Appli
   40   364.5    28.0    201  1  US-08-240-124-4            Sequence 4, Appli
   41   364.5    28.0    201  1  US-08-453-943-4            Sequence 4, Appli
   42   364.5    28.0    201  2  US-09-057-121-4            Sequence 4, Appli
   43   364.5    28.0    201  4  US-09-358-734-4            Sequence 4, Appli
   44     334    25.7    104  1  US-09-609-324A-8           Sequence 8, Appli
   45     334    25.7    104  2  US-08-920-440B-8           Sequence 8, Appli


                              ALIGNMENTS


RESULT   1
US-08-240-124-2
; Sequence 2, Application US/08240124
; Patent No. 5516658
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/240,124
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  238 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-240-124-2
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  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
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Db        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180

Qy      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
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Db      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238


RESULT   2
US-08-453-943-2
; Sequence 2, Application US/08453943
; Patent No. 5738844
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,943
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/240,124
;      FILING DATE:  09-MAY-1994
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  238 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-453-943-2

  Query Match             100.0%;  Score 1301;  DB 1;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-128;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
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Qy       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180

Qy      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
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RESULT   3
US-09-057-121-2
; Sequence 2, Application US/09057121
; Patent No. 5969110
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,121
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,124
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  238 amino acids
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;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-057-121-2

  Query Match            100.0%;  Score 1301;  DB 2;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-128;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy     61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy    121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180

Qy    181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238

RESULT   4
US-09-358-734-2
; Sequence 2, Application US/09358734
; Patent No. 6274117
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/358,734
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,124
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  238 amino acids
```

```
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-358-734-2

  Query Match            100.0%;  Score 1301;  DB 4;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-128;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy     61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy    121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180

Qy    181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238

RESULT   5
US-08-299-567-5
; Sequence 5, Application US/08299567
; Patent No. 5747033
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, et al.
;    TITLE OF INVENTION:  METHOD OF ENHANCING THE BIOLOGICAL
;    TITLE OF INVENTION:  ACTIVITY OF EPH FAMILY LIGANDS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Regeneron Pharmaceuticals, Inc.
;      STREET:  777 Old Saw Mill River Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10591-6707
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/299,567
;      FILING DATE:  01-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kempler, Gail M.
;      REGISTRATION NUMBER:  32,143
;      REFERENCE/DOCKET NUMBER:  REG 290
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  914-345-7400
;      TELEFAX:  914-345-7721
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  234 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-299-567-5

  Query Match             96.9%;  Score 1261;  DB 1;  Length 234;
  Best Local Similarity    97.9%;  Pred. No. 4e-124;
  Matches  233;  Conservative    0;  Mismatches    1;  Indels    4;  Gaps    1;
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Qy      1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy     61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
          |||||||||    |||||||||||||||||||||||||||||||||||||||||||||||
Db     61 IYCPHYNSS----GAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 116

Qy    121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
          |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    117 KFSEKFQRYSAFSLGYEFHAGHSYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 176

Qy    181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    177 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 234

RESULT   6
US-08-455-001-2
; Sequence 2, Application US/08455001
; Patent No. 5795734
;  GENERAL INFORMATION:
;    APPLICANT:  Flanagan, John G.
;    APPLICANT:  Cheng, Hwai-Jong
;    TITLE OF INVENTION:  EPH Receptor Ligands, and Uses Related
;    TITLE OF INVENTION:  Thereto
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/455,001
;      FILING DATE:  31 MAY 1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMI-011CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  209 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-455-001-2


  Query Match             33.6%;  Score 437;  DB 1;  Length 209;
  Best Local Similarity   50.5%;  Pred. No. 5.4e-38;
  Matches   96;  Conservative   25;  Mismatches   47;  Indels   22;  Gaps    7;

Qy      2 AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE------GYTVQV 53
          |  ||| ||||    |||| |  : |  |  :|:||||| ||   :        ||||:|
Db      4 AQRPLLPLLLL----LLPLRARNEDPARANADRYAVYWNRSNPRFQVSAVGDGGGYTVEV 59

Qy     54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
          ::|||||||||||       ||   |    |:|:||||:  |: :|:  | |||||||||
Db     60 SINDYLDIYCPHY-------GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKRWECNR 112

Qy    113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
          | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db    113 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNLVDRPCLRLKVYVRPTNET 172

Qy    171 SHSGEKPVPT 180
           :   :|: |
Db    173 LYEAPEPIFT 182

RESULT   7
US-08-308-814-2
; Sequence 2, Application US/08308814
; Patent No. 6268476
;  GENERAL INFORMATION:
;    APPLICANT:  Flanagan, John G.
;    APPLICANT:  Cheng, Hwai-Jong
;    TITLE OF INVENTION:  EPH Receptor Ligands, and Uses Related
;    TITLE OF INVENTION:  Thereto
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII(txt)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/308,814
;      FILING DATE:  19-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36.709
;      REFERENCE/DOCKET NUMBER:  HMI-011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  209 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-308-814-2


  Query Match             33.6%;  Score 437;  DB 4;  Length 209;
  Best Local Similarity   50.5%;  Pred. No. 5.4e-38;
  Matches   96;  Conservative   25;  Mismatches   47;  Indels   22;  Gaps    7;

Qy      2 AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE------GYTVQV 53
          |  ||| ||||    |||| |  : |  |  :|:||||| ||   :        ||||:|
Db      4 AQRPLLPLLLL----LLPLRARNEDPARANADRYAVYWNRSNPRFQVSAVGDGGGYTVEV 59

Qy     54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
          ::|||||||||||       ||   |    |:|:||||:  |: :|:  | |||||||||
Db     60 SINDYLDIYCPHY-------GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKRWECNR 112

Qy    113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
          | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db    113 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNLVDRPCLRLKVYVRPTNET 172

Qy    171 SHSGEKPVPT 180
           :   :|: |
Db    173 LYEAPEPIFT 182

RESULT   8
PCT-US95-11869-2
; Sequence 2, Application PC/TUS9511869
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;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  EPH Receptor Ligands, and Uses Related
;    TITLE OF INVENTION:  Thereto
;    NUMBER OF SEQUENCES:  5
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11869
;      FILING DATE:  19-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMI-011CPPC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  209 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-11869-2


  Query Match             33.6%;  Score 437;  DB 5;  Length 209;
  Best Local Similarity   50.5%;  Pred. No. 5.4e-38;
  Matches   96;  Conservative   25;  Mismatches   47;  Indels   22;  Gaps    7;

Qy      2 AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE------GYTVQV 53
          |  ||| ||||    |||| |  : |  |  :|:||||| ||   :        ||||:|
Db      4 AQRPLLPLLLL----LLPLRARNEDPARANADRYAVYWNRSNPRFQVSAVGDGGGYTVEV 59

Qy     54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
          ::|||||||||||       ||   |    |:|:||||:  |: :|:  | |||||||||
Db     60 SINDYLDIYCPHY-------GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKRWECNR 112

Qy    113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
          | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db    113 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNLVDRPCLRLKVYVRPTNET 172

Qy    171 SHSGEKPVPT 180
           :   :|: |
Db    173 LYEAPEPIFT 182


RESULT   9
US-09-609-324A-10
; Sequence 10, Application US/09609324A
; Patent No. RE37582
; GENERAL INFORMATION:
;  APPLICANT: CERRETTI, Douglas P.
;  TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
;  FILE REFERENCE: A7772
;  CURRENT APPLICATION NUMBER: US/09/609,324A
;  CURRENT FILING DATE:  2000-06-30
;  PRIOR APPLICATION NUMBER: 08/920,440
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/538,709
;  PRIOR FILING DATE: 1995-10-03
;  PRIOR APPLICATION NUMBER: 08/318,393
;  PRIOR FILING DATE: 1994-10-05
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: LERK-6
US-09-609-324A-10
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  Query Match             33.6%;  Score 437;  DB 1;  Length 213;
  Best Local Similarity   50.5%;  Pred. No. 5.6e-38;
  Matches   96;  Conservative   24;  Mismatches   52;  Indels   18;  Gaps    7;

Qy      2 AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR------EGYTVQV 53
          |  ||| |||||:|:|  |   |:    |  :|:||||| ||            ||||:|
Db      4 AQRPLLPLLLLLLPLPPPPFARAEDAARANSDRYAVYWNRSNPRFHAGAGDDGGGYTVEV 63

Qy     54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
          ::|||||||||||       ||   |    | ||||||:  |: :|:  | |||||||||
Db     64 SINDYLDIYCPHY-------GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR 116

Qy    113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
          | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db    117 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNAVDRPCLRLKVYVRPTNET 176

Qy    171 SHSGEKPVPT 180
           :   :|: |
Db    177 LYEAPEPIFT 186


RESULT  10
US-08-920-440B-10
; Sequence 10, Application US/08920440B
; Patent No. 5919905
;  GENERAL INFORMATION:
;    APPLICANT:  Cerretti, Douglas P.
;    TITLE OF INVENTION:  Cytokine Designated LERK-6
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  System 7.6
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,440B
;      FILING DATE:  29-AUG-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Henry, Janis C.
;      REGISTRATION NUMBER:  34,347
;      REFERENCE/DOCKET NUMBER:  2826-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  213 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-920-440B-10


  Query Match             33.6%;  Score 437;  DB 2;  Length 213;
  Best Local Similarity   50.5%;  Pred. No. 5.6e-38;
  Matches   96;  Conservative   24;  Mismatches   52;  Indels   18;  Gaps    7;

Qy      2 AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR------EGYTVQV 53
          |  ||| |||||:|:|  |   |:    |  :|:||||| ||            ||||:|
Db      4 AQRPLLPLLLLLLPLPPPPFARAEDAARANSDRYAVYWNRSNPRFHAGAGDDGGGYTVEV 63

Qy     54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
          ::|||||||||||       ||   |    | ||||||:  |: :|:  | |||||||||
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Db         64 SINDYLDIYCPHY-------GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR 116

Qy        113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
              | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db        117 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNAVDRPCLRLKVYVRPTNET 176

Qy        171 SHSGEKPVPT 180
               :   :|: |
Db        177 LYEAPEPIFT 186

RESULT  11
US-09-173-492-10
; Sequence 10, Application US/09173492
; Patent No. 6194172
;  GENERAL INFORMATION:
;    APPLICANT:  Cerretti, Douglas P.
;    TITLE OF INVENTION:  Cytokine Designated LERK-6
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  System 7.6
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/173,492
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,440
;      FILING DATE:  29-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Henry, Janis C.
;      REGISTRATION NUMBER:  34,347
;      REFERENCE/DOCKET NUMBER:  2826-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  213 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-173-492-10

  Query Match             33.6%;  Score 437;  DB 4;  Length 213;
  Best Local Similarity   50.5%;  Pred. No. 5.6e-38;
  Matches   96;  Conservative   24;  Mismatches   52;  Indels   18;  Gaps    7;

Qy          2 AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR------EGYTVQV 53
              |  ||| |||||:|:|  |   |:    |  :|:||||| ||            ||||:|
Db          4 AQRPLLPLLLLLLPLPPPPFARAEDAARANSDRYAVYWNRSNPRFHAGAGDDGGGYTVEV 63

Qy         54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
              ::|||||||||||       ||   |    | ||||||:  |: :|:  | |||||||||
Db         64 SINDYLDIYCPHY-------GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR 116

Qy        113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
              | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db        117 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNAVDRPCLRLKVYVRPTNET 176

Qy        171 SHSGEKPVPT 180
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Db        177 LYEAPEPIFT 186
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RESULT  12
US-09-173-133-10
; Sequence 10, Application US/09173133
; Patent No. 6232447
;  GENERAL INFORMATION:
;    APPLICANT:  Cerretti, Douglas P.
;    TITLE OF INVENTION:  Cytokine Designated LERK-6
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Power Macintosh
;      OPERATING SYSTEM:  System 7.6
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/173,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/920,440
;      FILING DATE:  29-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Henry, Janis C.
;      REGISTRATION NUMBER:  34,347
;      REFERENCE/DOCKET NUMBER:  2826-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  213 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-173-133-10

  Query Match             33.6%;  Score 437;  DB 4;  Length 213;
  Best Local Similarity   50.5%;  Pred. No. 5.6e-38;
  Matches   96;  Conservative   24;  Mismatches   52;  Indels   18;  Gaps    7;

Qy          2 AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR------EGYTVQV 53
              |  ||| |||||:|:|  |   |:    |  :|:||||| ||            ||||:|
Db          4 AQRPLLPLLLLLLPLPPPPFARAEDAARANSDRYAVYWNRSNPRFHAGAGDDGGGYTVEV 63

Qy         54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
              ::|||||||||||       ||   |    | ||||||:  |: :|:  | |||||||||
Db         64 SINDYLDIYCPHY-------GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR 116

Qy        113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
              | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db        117 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNAVDRPCLRLKVYVRPTNET 176

Qy        171 SHSGEKPVPT 180
               :   :|: |
Db        177 LYEAPEPIFT 186

RESULT  13
US-08-455-001-4
; Sequence 4, Application US/08455001
; Patent No. 5795734
;  GENERAL INFORMATION:
;    APPLICANT:  Flanagan, John G.
;    APPLICANT:  Cheng, Hwai-Jong
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;    TITLE OF INVENTION:  EPH Receptor Ligands, and Uses Related
;    TITLE OF INVENTION:  Thereto
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/455,001
;      FILING DATE:  31 MAY 1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMI-011CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  200 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-455-001-4


  Query Match             32.4%;  Score 421;  DB 1;  Length 200;
  Best Local Similarity   47.5%;  Pred. No. 2.4e-36;
  Matches   86;  Conservative   29;  Mismatches   50;  Indels   16;  Gaps    5;

Qy        3 AAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
            || ||  :: | |      :  ||  : :|:||||| ||    |  |||:|::|||||||
Db        6 AAALLAAIVGVCV-----WSDDPGKVISDRYAVYWNRSNPRFHRGDYTVEVSINDYLDIY 60

Qy       63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
            ||||          | |    |:||||||:  |: :|:  | |||||||||| :|  |:|
Db       61 CPHYEE--------PLPAERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLK 112

Qy      122 FSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
            |||||| :: ||||:||  |||||||| :| : :   ||::||:|   : | :   :|:
Db      113 FSEKFQLFTPFSLGFEFRPGHEYYYISASPPNVVDRPCLKLKVYVRPTNDSLYESPEPIF 172

Qy      180 T 180
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Db      173 T 173


RESULT  14
PCT-US95-11869-4
; Sequence 4, Application PC/TUS9511869
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  EPH Receptor Ligands, and Uses Related
;    TITLE OF INVENTION:  Thereto
;    NUMBER OF SEQUENCES:  5
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11869
;      FILING DATE:  19-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
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;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMI-011CPPC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  200 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-11869-4

  Query Match             32.4%;  Score 421;  DB 5;  Length 200;
  Best Local Similarity   47.5%;  Pred. No. 2.4e-36;
  Matches   86;  Conservative   29;  Mismatches   50;  Indels   16;  Gaps    5;

Qy        3 AAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
            || ||  :: | |      :  ||  : :|:||||| ||    |  |||:|::|||||||
Db        6 AAALLAAIVGVCV-----WSDDPGKVISDRYAVYWNRSNPRFHRGDYTVEVSINDYLDIY 60

Qy       63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
            ||||          | |    |:||||||:  |: :|:  | |||||||||| :|  |:|
Db       61 CPHYEE--------PLPAERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLK 112

Qy      122 FSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
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Db      113 FSEKFQLFTPFSLGFEFRPGHEYYYISASPPNVVDRPCLKLKVYVRPTNDSLYESPEPIF 172

Qy      180 T 180
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Db      173 T 173


RESULT  15
US-08-442-248-4
; Sequence 4, Application US/08442248
; Patent No. 5759863
;  GENERAL INFORMATION:
;    APPLICANT:  Caras, Ingrid W.
;    APPLICANT:  Winslow, John W.
;    TITLE OF INVENTION:  AL-1 Neurotrophic Factor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,248
;      FILING DATE:  15-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/330128
;      FILING DATE:  27-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  920C4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8674
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  228 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-442-248-4

  Query Match             31.9%;  Score 415.5;  DB 1;  Length 228;
  Best Local Similarity   39.5%;  Pred. No. 1.1e-35;
  Matches   98;  Conservative   37;  Mismatches   66;  Indels   47;  Gaps   11;

Qy      8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
          :| |:  |  : : :| ||  |: :|:||||||||   :|  | : | :|||||::||||
Db      6 MLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCPHY 65

Qy     67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
            |         |    |:||||||: :||  | : |:|||||||||||:|: |:|||||
Db     66 EDS--------VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK 117

Qy    126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
          || :: ||||:||  | ||:|||:    |    ||::||||     |  |    ::
Db    118 FQLFTPFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDR---- 173

Qy    181 LPQFTMGPNVKINVLEDFE-----------GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
             | :   |: | ||  :           |||  | |::        | |      : |
Db    174 --VFDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI--------PSR-----LLAI 217

Qy    229 AFFLMTFL 236
            ||:  |
Db    218 LLFLLAML 225


Search completed: September 28, 2002, 01:37:42
Job time: 10062 sec
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                    GenCore version 4.5
          Copyright (c) 1993 - 2000  Compugen Ltd.


OM protein - protein search, using sw model

Run on:         September 28, 2002, 01:28:35 ; Search time 251.33 Seconds
                                               (without alignments)
                                               333.312 Million cell updates/sec

Title:          US-09-904-954-2
Perfect score:  1301
Sequence:       1 MAAAPLLLLLLLVPVPLLPL..........REHLPLAVGIAFFLMTFLAS 238

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters:      3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Pending_Patents_AA_Main:*
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               2:  /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
               3:  /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
               4:  /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
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               26:  /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
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Result              Query
  No.     Score     Match Length DB  ID                        Description
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    1      1301     100.0    238  1  PCT-US94-09282-2           Sequence 2, Appli
    2      1301     100.0    238  5  US-08-109-745-2            Sequence 2, Appli
    3      1301     100.0    238  5  US-08-161-132-2            Sequence 2, Appli
    4      1301     100.0    238  21  US-09-733-756-2            Sequence 2, Appli
    5      1301     100.0    238  23  US-09-904-954-2            Sequence 2, Appli
    6      1301     100.0    238  23  US-09-948-941-315          Sequence 315, App
    7      1301     100.0    238  23  US-09-948-941-360          Sequence 360, App
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    8  1285.5    98.8    237  11  US-08-730-700A-16         Sequence 16, Appl
    9  1285.5    98.8    237  20  US-09-621-595-16          Sequence 16, Appl
   10    1266    97.3    234  6  US-08-229-402-7           Sequence 7, Appli
   11    1261    96.9    234  7  US-08-327-423-5           Sequence 5, Appli
   12  1250.5    96.1    233  11  US-08-730-700A-15         Sequence 15, Appl
   13  1250.5    96.1    233  20  US-09-621-595-15          Sequence 15, Appl
   14  1227.5    94.4    233  16  US-09-214-631-7           Sequence 7, Appli
   15     739    56.8    776  26  US-60-212-656-335         Sequence 335, App
   16     481    37.0     91  26  US-60-207-216-562         Sequence 562, App
   17   444.5    34.2     93  6  US-08-222-075-6           Sequence 6, Appli
   18   444.5    34.2     93  6  US-08-229-402-6           Sequence 6, Appli
   19     437    33.6    209  7  US-08-393-462-2           Sequence 2, Appli
   20     437    33.6    209  15  US-09-135-129-2           Sequence 2, Appli
   21     437    33.6    209  23  US-09-921-984-2           Sequence 2, Appli
   22     437    33.6    213  19  US-09-580-236A-10         Sequence 10, Appl
   23     435    33.4    209  16  US-09-214-631-6           Sequence 6, Appli
   24   426.5    32.8    335  1  PCT-US01-08631-58196      Sequence 58196, A
   25   421.5    32.4    208  11  US-08-730-700A-14         Sequence 14, Appl
   26   421.5    32.4    208  20  US-09-621-595-14          Sequence 14, Appl
   27     421    32.4    200  7  US-08-393-462-4           Sequence 4, Appli
   28     421    32.4    200  15  US-09-135-129-4           Sequence 4, Appli
   29   415.5    31.9    228  7  US-08-330-128-4           Sequence 4, Appli
   30   415.5    31.9    228  7  US-08-396-946-5           Sequence 5, Appli
   31   415.5    31.9    228  8  US-08-440-567-4           Sequence 4, Appli
   32   415.5    31.9    228  8  US-08-442-245A-4          Sequence 4, Appli
   33   415.5    31.9    228  8  US-08-442-249-4           Sequence 4, Appli
   34   415.5    31.9    228  9  US-08-578-684-4           Sequence 4, Appli
   35   415.5    31.9    228  11  US-08-766-239-4           Sequence 4, Appli
   36   415.5    31.9    228  12  US-08-832-660-5           Sequence 5, Appli
   37   415.5    31.9    228  19  US-09-570-327-2           Sequence 2, Appli
   38   413.5    31.8    228  16  US-09-214-631-9           Sequence 9, Appli
   39     403    31.0    184  7  US-08-318-393A-2          Sequence 2, Appli
   40     403    31.0    184  7  US-08-396-946-2           Sequence 2, Appli
   41     403    31.0    184  9  US-08-538-709-2           Sequence 2, Appli
   42     403    31.0    184  12  US-08-832-660-2           Sequence 2, Appli
   43     403    31.0    184  15  US-09-165-861-2           Sequence 2, Appli
   44     403    31.0    184  19  US-09-580-236A-2          Sequence 2, Appli
   45   401.5    30.9     92  18  US-09-474-434-1651        Sequence 1651, Ap


                              ALIGNMENTS


RESULT   1
PCT-US94-09282-2
; Sequence 2, Application PC/TUS9409282
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5:1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09282
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
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;       FILING DATE:  30-AUG-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/109,745
;       FILING DATE:  20-AUG-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SEESE, KATHRYN A.
;       REGISTRATION NUMBER:  32,172
;       REFERENCE/DOCKET NUMBER:  2814-C
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 587-0430
;       TELEFAX:  (206) 233-0644
;       TELEX:  756822
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  238 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US94-09282-2

  Query Match             100.0%;  Score 1301;  DB 1;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-123;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
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Db          1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy         61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180

Qy        181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238

RESULT   2
US-08-109-745-2
; Sequence 2, Application US/08109745
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.1
;      SOFTWARE:  Microsoft Word, Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/109,745
;      FILING DATE:  20-AUG-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
```

```
;       TELEFAX:  (206) 233-0644
;       TELEX:  756822
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  238 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-109-745-2

  Query Match             100.0%;  Score 1301;  DB 5;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-123;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy         61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy        121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180

Qy        181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238

RESULT   3
US-08-161-132-2
; Sequence 2, Application US/08161132
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/161,132
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  238 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-161-132-2

  Query Match             100.0%;  Score 1301;  DB 5;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-123;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180

Qy      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238


RESULT   4
US-09-733-756-2
; Sequence 2, Application US/09733756
; GENERAL INFORMATION:
;  APPLICANT: Mack, David
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Wilson, Keith E.
;  TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER AND/OR BREAST CANCE
;  TITLE OF INVENTION:  COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER AND
;  TITLE OF INVENTION:  CANCER MODULATORS
;  FILE REFERENCE: A-69439/DJB/JJD
;  CURRENT APPLICATION NUMBER: US/09/733,756
;  CURRENT FILING DATE:  2000-12-08
;  PRIOR APPLICATION NUMBER: US 09/525,993
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: US 09/493,444
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: US 09/453,850
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US 00/07044
;  PRIOR FILING DATE: 2000-03-15
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 238
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-733-756-2

  Query Match             100.0%;  Score 1301;  DB 21;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-123;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
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Qy      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238

RESULT   5
US-09-904-954-2
; Sequence 2, Application US/09904954
;   GENERAL INFORMATION:
;        APPLICANT: BECKMANN, M. P.
;                   CERRETTI, DOUGLAS P.
;        TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
;                            RECEPTOR HEK
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: IMMUNEX CORPORATION
;             STREET: 51 UNIVERSITY STREET
;             CITY: SEATTLE
;             STATE: WASHINGTON
;             COUNTRY: USA
;             ZIP: 98101
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: Apple Macintosh
;             OPERATING SYSTEM: Apple System 7.1
;             SOFTWARE: Microsoft Word for Apple, Version 5.1a
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/904,954
;             FILING DATE: 12-Jul-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/240,124
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 08/114,426
;             FILING DATE: 30-AUG-1993
;             APPLICATION NUMBER: US 08/109,745
;             FILING DATE: 20-AUG-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SEESE, KATHRYN A.
;             REGISTRATION NUMBER: 32,172
;             REFERENCE/DOCKET NUMBER: 2814-C
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 587-0430
;             TELEFAX: (206) 233-0644
;             TELEX: 756822
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 238 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-904-954-2

  Query Match             100.0%;  Score 1301;  DB 23;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-123;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180

Qy      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238

RESULT   6
US-09-948-941-315
; Sequence 315, Application US/09948941
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH CANCER, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL000788
;  CURRENT APPLICATION NUMBER: US/09/948,941
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/231,328
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 12618
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 315
;   LENGTH: 238
;   TYPE: PRT
;   ORGANISM: Human
US-09-948-941-315


  Query Match             100.0%;  Score 1301;  DB 23;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-123;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy        61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy       121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180

Qy       181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238

RESULT   7
US-09-948-941-360
; Sequence 360, Application US/09948941
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH CANCER, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL000788
;  CURRENT APPLICATION NUMBER: US/09/948,941
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/231,328
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 12618
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 360
;   LENGTH: 238
;   TYPE: PRT
;   ORGANISM: Human
US-09-948-941-360


  Query Match             100.0%;  Score 1301;  DB 23;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-123;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy        61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy       121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180

Qy       181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238

RESULT   8
US-08-730-700A-16
; Sequence 16, Application US/08730700A
;  GENERAL INFORMATION:
;    APPLICANT:  Pawson, Anthony
;    APPLICANT:  Henkemeyer, Mark
;    TITLE OF INVENTION:  Method of Activating a Novel Ligand
;    TITLE OF INVENTION:  Regulatory Pathway
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Room 970
;      STREET:  600 University Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1X5
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/730,700A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/005,518
;      FILING DATE:  13-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kurdydyk, Linda M.
;      REGISTRATION NUMBER:  34,971
;      REFERENCE/DOCKET NUMBER:  3153-196
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  416-586-3235
;      TELEFAX:  416-586-3110
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  237 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-730-700A-16


  Query Match             98.8%;  Score 1285.5;  DB 11;  Length 237;
  Best Local Similarity   99.6%;  Pred. No. 9.3e-122;
  Matches  237;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy        61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy       121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
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               |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KFSEKF-RYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 179

Qy        181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 237


RESULT   9
US-09-621-595-16
; Sequence 16, Application US/09621595
;   GENERAL INFORMATION:
;        APPLICANT: Pawson, Anthony
;                   Henkemeyer, Mark
;        TITLE OF INVENTION: Method of Activating a Novel Ligand
;                            Regulatory Pathway
;        NUMBER OF SEQUENCES: 21
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Room 970
;             STREET: 600 University Avenue
;             CITY: Toronto
;             STATE: Ontario
;             COUNTRY: Canada
;             ZIP: M5G 1X5
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/621,595
;             FILING DATE: 21-Jul-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/730,700
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kurdydyk, Linda M.
;             REGISTRATION NUMBER: 34,971
;             REFERENCE/DOCKET NUMBER: 3153-196
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 416-586-3235
;             TELEFAX: 416-586-3110
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 237 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE:-protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-621-595-16

  Query Match              98.8%;  Score 1285.5;  DB 20;  Length 237;
  Best Local Similarity    99.6%;  Pred. No. 9.3e-122;
  Matches  237;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy         61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy        121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KFSEKF-RYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 179

Qy        181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 237
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RESULT  10
US-08-229-402-7
; Sequence 7, Application US/08229402
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, et al.
;    TITLE OF INVENTION:  EPH Family Ligands
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Regeneron Pharmaceuticals, Inc.
;      STREET:  777 Old Saw Mill River Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10591
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/229,402
;      FILING DATE:  12-APR-1994
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/222,075
;      FILING DATE:  04-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/144,992
;      FILING DATE:  15-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/736,559
;      FILING DATE:  26-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kempler Ph.D., Gail M.
;      REGISTRATION NUMBER:  32,143
;      REFERENCE/DOCKET NUMBER:  REG 280
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  914-345-7400
;      TELEFAX:  914-347-2113
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  234 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-229-402-7

  Query Match             97.3%;  Score 1266;  DB 6;  Length 234;
  Best Local Similarity   98.3%;  Pred. No. 8.8e-120;
  Matches  234;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    1;

Qy          1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy         61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
              |||||||||    |||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IYCPHYNSS----GAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 116

Qy        121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 176

Qy        181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 234


RESULT  11
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US-08-327-423-5
; Sequence 5, Application US/08327423
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, et al.
;    TITLE OF INVENTION:  METHOD OF ENHANCING THE BIOLOGICAL
;    TITLE OF INVENTION:  ACTIVITY OF EPH FAMILY LIGANDS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Regeneron Pharmaceuticals, Inc.
;      STREET:  777 Old Saw Mill River Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10591-6707
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/327,423
;      FILING DATE:  21-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/299,567
;      FILING DATE:  01-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kempler, Gail M.
;      REGISTRATION NUMBER:  32,143
;      REFERENCE/DOCKET NUMBER:  REG 290
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  914-345-7400
;      TELEFAX:  914-345-7721
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  234 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-327-423-5


  Query Match             96.9%;  Score 1261;  DB 7;  Length 234;
  Best Local Similarity   97.9%;  Pred. No. 2.8e-119;
  Matches  233;  Conservative    0;  Mismatches    1;  Indels    4;  Gaps    1;

Qy        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
            |||||||||    |||||||||||||||||||||||||||||||||||||||||||||||
Db       61 IYCPHYNSS----GAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 116

Qy      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db      117 KFSEKFQRYSAFSLGYEFHAGHSYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 176

Qy      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      177 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 234

RESULT  12
US-08-730-700A-15
; Sequence 15, Application US/08730700A
;  GENERAL INFORMATION:
;    APPLICANT:  Pawson, Anthony
;    APPLICANT:  Henkemeyer, Mark
;    TITLE OF INVENTION:  Method of Activating a Novel Ligand
;    TITLE OF INVENTION:  Regulatory Pathway
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Room 970
;      STREET:  600 University Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1X5
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/730,700A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/005,518
;      FILING DATE:  13-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kurdydyk, Linda M.
;      REGISTRATION NUMBER:  34,971
;      REFERENCE/DOCKET NUMBER:  3153-196
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  416-586-3235
;      TELEFAX:  416-586-3110
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  233 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-730-700A-15


  Query Match             96.1%;  Score 1250.5;  DB 11;  Length 233;
  Best Local Similarity   97.9%;  Pred. No. 3.3e-118;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    5;  Gaps    2;

Qy        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
            |||||||||    |||||||||||||||||||||||||||||||||||||||||||||||
Db       61 IYCPHYNSS----GAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 116

Qy      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      117 KFSEKF-RYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 175

Qy      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      176 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 233

RESULT  13
US-09-621-595-15
; Sequence 15, Application US/09621595
;  GENERAL INFORMATION:
;       APPLICANT: Pawson, Anthony
;                  Henkemeyer, Mark
;       TITLE OF INVENTION: Method of Activating a Novel Ligand
;                           Regulatory Pathway
;       NUMBER OF SEQUENCES: 21
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Room 970
;            STREET: 600 University Avenue
;            CITY: Toronto
;            STATE: Ontario
;            COUNTRY: Canada
;            ZIP: M5G 1X5
```

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;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/621,595
;              FILING DATE: 21-Jul-2000
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/730,700
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Kurdydyk, Linda M.
;              REGISTRATION NUMBER: 34,971
;              REFERENCE/DOCKET NUMBER: 3153-196
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 416-586-3235
;              TELEFAX: 416-586-3110
;    INFORMATION FOR SEQ ID NO: 15:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 233 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-621-595-15

  Query Match             96.1%;  Score 1250.5;  DB 20;  Length 233;
  Best Local Similarity   97.9%;  Pred. No. 3.3e-118;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    5;  Gaps    2;

Qy      1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy     61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
          |||||||||    |||||||||||||||||||||||||||||||||||||||||||||||
Db     61 IYCPHYNSS----GAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 116

Qy    121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    117 KFSEKF-RYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 175

Qy    181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    176 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 233

RESULT  14
US-09-214-631-7
; Sequence 7, Application US/09214631
; GENERAL INFORMATION:
;  APPLICANT: Holland, Sacha
;  APPLICANT: Mbamalu, Geraldine
;  APPLICANT: Pawson, Tony
;  TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
;  TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
;  TITLE OF INVENTION: TYROSINE KINASES
;  FILE REFERENCE: 11757.23USWO
;  CURRENT APPLICATION NUMBER: US/09/214,631
;  CURRENT FILING DATE: 1999-03-12
;  EARLIER APPLICATION NUMBER: PCT/CA97/00473
;  EARLIER FILING DATE: 1997-07-04
;  EARLIER APPLICATION NUMBER: 60/021,272
;  EARLIER FILING DATE: 1996-07-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-631-7

  Query Match             94.4%;  Score 1227.5;  DB 16;  Length 233;
  Best.Local Similarity   96.2%;  Pred. No. 7.2e-116;
  Matches  229;  Conservative    0;  Mismatches    4;  Indels    5;  Gaps    2;

Qy      1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
          |||||||||||||||||||||| || ||||||||||||||||||||||||||||||||||
Db      1 MAAAPLLLLLLLVPVPLLPLLAGGPAGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy     61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
          |||||||||    ||||||||||| |||||||||||||||||||||||||||||||||||
Db     61 IYCPHYNSS----GAGPGPGGGAE-YVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 115

Qy    121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    116 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 175

Qy    181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
          |||||||||||||||||||||||||||||||||||||||||||  |||||||||||||
Db    176 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPALVGIAFFLMTFLAS 233

RESULT  15
US-60-212-656-335
; Sequence 335, Application US/60212656
; GENERAL INFORMATION:
;  APPLICANT:  Beasley, Ellen
;  TITLE OF INVENTION:  ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE:  CL000673
;  CURRENT APPLICATION NUMBER: US/60/212,656
;  CURRENT FILING DATE:  2000-06-19
;  NUMBER OF SEQ ID NOS:  795
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 335
;   LENGTH: 776
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-212-656-335

  Query Match             56.8%;  Score 739;  DB 26;  Length 776;
  Best Local Similarity   65.0%;  Pred. No. 1.6e-65;
  Matches  145;  Conservative   17;  Mismatches   43;  Indels   18;  Gaps    5;

Qy     23 QGPGGALGNRHAV-YWNSSNQ----HLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGP 77
          :|  | :| :     |:   |     | |    |:: :|||||| ||||         ||
Db    565 KGDWGRVGPQPGTKVWSGKGQTPILKLLRGDAVVELGLNDYLDIVCPHYE--------GP 616

Qy     78 GPGGGAEQYVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLG 135
          ||  | | : ||||   || :| |   : :||| |:    |   ::|||| ||:: ||||
Db    617 GPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRFTPFSLG 673

Qy    136 YEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVL 195
          :||  |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674 FEFLPGETYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVL 733

Qy    196 EDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
          |||||||||||||||||||||||||||||||||||||||||||
Db    734 EDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 776


Search completed: September 28, 2002, 01:43:26
Job time: 891 sec
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                        GenCore version 4.5
               Copyright (c) 1993 - 2000  Compugen Ltd.

OM protein - protein search, using sw model

Run on:          September 28, 2002, 01:35:35 ; Search time 125.93 Seconds
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Title:           US-09-904-954-2
Perfect score:   1301
Sequence:        1 MAAAPLLLLLLLVPVPLLPL..........REHLPLAVGIAFFLMTFLAS 238

Scoring table:   BLOSUM62
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Searched:        962758 seqs, 270212090 residues

Total number of hits satisfying chosen parameters:      962758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_AA_New:*
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                 2:  /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
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                 4:  /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
                 5:  /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
                 6:  /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
                 7:  /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
                       %
Result                Query
   No.    Score       Match Length DB  ID                       Description
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     1  1227.5   94.4    233  6  US-10-138-787-7             Sequence 7, Appli
     2     435   33.4    209  6  US-10-138-787-6             Sequence 6, Appli
     3   413.5   31.8    228  6  US-10-138-787-9             Sequence 9, Appli
     4     390   30.0    205  6  US-10-171-311-50            Sequence 50, Appl
     5     390   30.0    205  6  US-10-138-787-10            Sequence 10, Appl
     6   377.5   29.0    204  1  PCT-US02-24563-288          Sequence 288, App
     7   377.5   29.0    204  6  US-10-121-049-288           Sequence 288, App
     8   377.5   29.0    204  6  US-10-121-050-288           Sequence 288, App
     9   377.5   29.0    204  6  US-10-121-053-288           Sequence 288, App
    10   377.5   29.0    204  6  US-10-121-043-288           Sequence 288, App
    11   377.5   29.0    204  6  US-10-121-044-288           Sequence 288, App
    12   377.5   29.0    204  6  US-10-121-047-288           Sequence 288, App
    13   377.5   29.0    204  6  US-10-121-054-288           Sequence 288, App
    14   377.5   29.0    204  6  US-10-121-056-288           Sequence 288, App
    15   377.5   29.0    204  6  US-10-121-057-288           Sequence 288, App
    16   377.5   29.0    204  6  US-10-121-058-288           Sequence 288, App
    17   377.5   29.0    204  6  US-10-121-060-288           Sequence 288, App
    18   377.5   29.0    204  6  US-10-121-063-288           Sequence 288, App
    19   377.5   29.0    204  6  US-10-123-108-288           Sequence 288, App
    20   377.5   29.0    204  6  US-10-123-154-288           Sequence 288, App
    21   377.5   29.0    204  6  US-10-123-156-288           Sequence 288, App
    22   377.5   29.0    204  6  US-10-123-157-288           Sequence 288, App
    23   377.5   29.0    204  6  US-10-123-212-288           Sequence 288, App
    24   377.5   29.0    204  6  US-10-123-213-288           Sequence 288, App
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    26   377.5   29.0    204  6  US-10-121-041-288           Sequence 288, App
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    29   377.5   29.0    204  6  US-10-121-051-288           Sequence 288, App
    30   377.5   29.0    204  6  US-10-121-040-288           Sequence 288, App
    31   377.5   29.0    204  6  US-10-121-048-288           Sequence 288, App
    32   377.5   29.0    204  6  US-10-121-052-288           Sequence 288, App
    33   377.5   29.0    204  6  US-10-121-061-288           Sequence 288, App
    34   377.5   29.0    204  6  US-10-121-042-288           Sequence 288, App
    35   377.5   29.0    204  6  US-10-121-055-288           Sequence 288, App
    36   377.5   29.0    204  6  US-10-121-059-288           Sequence 288, App
    37   377.5   29.0    204  6  US-10-124-822-288           Sequence 288, App
    38   377.5   29.0    204  6  US-10-123-903-288           Sequence 288, App
    39   377.5   29.0    204  6  US-10-124-817-288           Sequence 288, App
    40   377.5   29.0    204  6  US-10-124-819-288           Sequence 288, App
    41   377.5   29.0    204  6  US-10-124-823-288           Sequence 288, App
    42   377.5   29.0    204  6  US-10-125-704-288           Sequence 288, App
    43   377.5   29.0    204  6  US-10-123-215-288           Sequence 288, App
    44   377.5   29.0    204  6  US-10-123-235-288           Sequence 288, App
    45   377.5   29.0    204  6  US-10-123-236-288           Sequence 288, App

                              ALIGNMENTS

RESULT   1
US-10-138-787-7
; Sequence 7, Application US/10138787
; GENERAL INFORMATION:
;  APPLICANT: Holland, Sacha
;  APPLICANT:  Mbamalu, Geraldine
;  APPLICANT:  Pawson, Tony
;  TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
;  TITLE OF INVENTION:  BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
;  TITLE OF INVENTION:  TYROSINE KINASES
;  FILE REFERENCE: 11757.23USWO
;  CURRENT APPLICATION NUMBER: US/10/138,787
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: US/09/214,631
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: PCT/CA97/00473
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: 60/021,272
;  PRIOR FILING DATE: 1996-07-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-138-787-7


  Query Match             94.4%;  Score 1227.5;  DB 6;  Length 233;
  Best Local Similarity   96.2%;  Pred. No. 2.2e-109;
  Matches  229;  Conservative    0;  Mismatches    4;  Indels    5;  Gaps    2;

Qy          1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
              |||||||||||||||||||||| || ||||||||||||||||||||||||||||||||||
Db          1 MAAAPLLLLLLLVPVPLLPLLAGGPAGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy         61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
              |||||||||    ||||||||||| |||||||||||||||||||||||||||||||||||
Db         61 IYCPHYNSS----GAGPGPGGGAE-YVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 115

Qy        121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 175

Qy        181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
              |||||||||||||||||||||||||||||||||||||||||||  |||||||||||||
Db        176 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPALVGIAFFLMTFLAS 233
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RESULT   2
US-10-138-787-6
; Sequence 6, Application US/10138787
; GENERAL INFORMATION:
;  APPLICANT: Holland, Sacha
;  APPLICANT:  Mbamalu, Geraldine
;  APPLICANT:  Pawson, Tony
;  TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
;  TITLE OF INVENTION:  BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
;  TITLE OF INVENTION:  TYROSINE KINASES
;  FILE REFERENCE: 11757.23USWO
;  CURRENT APPLICATION NUMBER: US/10/138,787
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: US/09/214,631
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: PCT/CA97/00473
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: 60/021,272
;  PRIOR FILING DATE: 1996-07-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 209
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-138-787-6


  Query Match             33.4%;  Score 435;  DB 6;  Length 209;
  Best Local Similarity   50.5%;  Pred. No. 1.7e-33;
  Matches   96;  Conservative   25;  Mismatches   47;  Indels   22;  Gaps    7;

Qy      2 AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE------GYTVQV 53
          |  ||| ||||    |||| |  : |  |  :|:||||| ||   :        ||||:|
Db      4 AQRPLLPLLLL----LLPLRARNEDPARANADRYAVYWNRSNPRFQVSAVGDGGGYTVEV 59

Qy     54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
          ::|||||||||||       ||   |    |:|:||||:  |: :|:  | |||||||||
Db     60 SINDYLDIYCPHY-------GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKRWECNR 112

Qy    113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
          | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db    113 PAAPGGPLKFSEKFQLFTPFSLGFEFPPGHEYYYISATPPNLVDRPCLRLKVYVRPTNET 172

Qy    171 SHSGEKPVPT 180
           :   :|: |
Db    173 LYEAPEPIFT 182

RESULT   3
US-10-138-787-9
; Sequence 9, Application US/10138787
; GENERAL INFORMATION:
;  APPLICANT: Holland, Sacha
;  APPLICANT:  Mbamalu, Geraldine
;  APPLICANT:  Pawson, Tony
;  TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
;  TITLE OF INVENTION:  BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
;  TITLE OF INVENTION:  TYROSINE KINASES
;  FILE REFERENCE: 11757.23USWO
;  CURRENT APPLICATION NUMBER: US/10/138,787
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: US/09/214,631
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: PCT/CA97/00473
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: 60/021,272
;  PRIOR FILING DATE: 1996-07-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 228
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
US-10-138-787-9


  Query Match             31.8%;  Score 413.5;  DB 6;  Length 228;
  Best Local Similarity   39.5%;  Pred. No. 2.1e-31;
  Matches   98;  Conservative   37;  Mismatches   66;  Indels   47;  Gaps   11;

Qy      8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
          :| |:  |  : : :| ||  |: :|:||||||||   :|  | : | :|||||::||||
Db      6 MLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCPHY 65

Qy     67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
            |         |    |:||||||: :||  | : |:|||||||||||:|: |:|||||
Db     66 EDS--------VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK 117

Qy    126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
          || :: ||||:||  | ||:|||:    |    ||::||||     |  |    ::
Db    118 FQLFTPFSLGFEFPPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDR---- 173

Qy    181 LPQFTMGPNVKINVLEDFE-----------GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
             | :   |: | ||  :           |||  | |::        | |      : |
Db    174 --VFDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI--------PSR-----LLAI 217

Qy    229 AFFLMTFL 236
            ||:  |
Db    218 LLFLLAML 225


RESULT   4
US-10-171-311-50
; Sequence 50, Application US/10171311
; GENERAL INFORMATION:
;  APPLICANT: Schlegel, Robert
;  APPLICANT:  Chen, Yan
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Monahan, John
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Gannavarapu, Manjula
;  APPLICANT:  Hoersh, Sebastian
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
;  TITLE OF INVENTION:  OF CERVICAL CANCER
;  FILE REFERENCE: MRI-035
;  CURRENT APPLICATION NUMBER: US/10/171,311
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US 60/298,159
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,155
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/335,936
;  PRIOR FILING DATE: 2001-11-14
;  NUMBER OF SEQ ID NOS: 238
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
;   LENGTH: 205
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-171-311-50


  Query Match             30.0%;  Score 390;  DB 6;  Length 205;
  Best Local Similarity   41.8%;  Pred. No. 3.3e-29;
  Matches   87;  Conservative   21;  Mismatches   76;  Indels   24;  Gaps    6;

Qy     19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
          |||      |  :|| |:|||||   | | ||: | :|||:|| ||||    |   |
Db      7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSVADAA--- 63

Qy     79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
               |||:||:|    |: |   |:   ||:|||| | | | | ||||||:: |:|| |
Db     64 ----MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 119
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Qy    138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
          |  || ||||| | |    :|||:|| |     :||        ||  : |  |    :|
Db    120 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHVNPQEKRLAADD 170

Qy    198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
               |:|  |       :|:    |||
Db    171 -----PEVRVLHSIGHSAAPRL--FPLA 191

RESULT   5
US-10-138-787-10
; Sequence 10, Application US/10138787
; GENERAL INFORMATION:
;  APPLICANT: Holland, Sacha
;  APPLICANT:  Mbamalu, Geraldine
;  APPLICANT:  Pawson, Tony
;  TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
;  TITLE OF INVENTION:  BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
;  TITLE OF INVENTION:  TYROSINE KINASES
;  FILE REFERENCE: 11757.23USWO
;  CURRENT APPLICATION NUMBER: US/10/138,787
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: US/09/214,631
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: PCT/CA97/00473
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: 60/021,272
;  PRIOR FILING DATE: 1996-07-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 205
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-138-787-10


  Query Match             30.0%;  Score 390;  DB 6;  Length 205;
  Best Local Similarity   41.8%;  Pred. No. 3.3e-29;
  Matches   87;  Conservative   21;  Mismatches   76;  Indels   24;  Gaps    6;

Qy     19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
          |||      |  :|| |:|||||   | | ||: | :|||:|| ||||    |   |
Db      7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSVADAA--- 63

Qy     79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
               |||:||:|    |: |   |:   ||:|||| | | | | ||||||:: |:|| |
Db     64 ----MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 119

Qy    138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
          |  || ||||| | |    :|||:|| |     :||        ||  : |  |    :|
Db    120 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHVNPQEKRLAADD 170

Qy    198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
               |:|  |       :|:    |||
Db    171 -----PEVRVLHSIGHSAAPRL--FPLA 191

RESULT   6
PCT-US02-24563-288
; Sequence 288, Application PC/TUS0224563
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
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;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C331
;  CURRENT APPLICATION NUMBER: PCT/US02/24563
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
PCT-US02-24563-288


  Query Match             29.0%;  Score 377.5;  DB 1;  Length 204;
  Best Local Similarity   40.9%;  Pred. No. 5.2e-28;
  Matches   85;  Conservative   20;  Mismatches   78;  Indels   25;  Gaps    6;

Qy     19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
          |||      |  :|| |:|||||   | | ||: | :|||:|| ||||
Db      7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA------- 59

Qy     79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
               |||:||:|    |: |   |:   ||:|||| | | | | ||||||:: |:|| |
Db     60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118

Qy    138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
          |  || ||||| | |    :|||:|| |     :||        ||    |  |    :|
Db    119 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHDNPQEKRLAADD 169

Qy    198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
               |:|  |       :|:    |||
Db    170 -----PEVRVLHSIGHSAAPRL--FPLA 190

RESULT   7
US-10-121-049-288
; Sequence 288, Application US/10121049
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
```

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;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C17
;  CURRENT APPLICATION NUMBER: US/10/121,049
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-049-288


  Query Match             29.0%;  Score 377.5;  DB 6;  Length 204;
  Best Local Similarity   40.9%;  Pred. No. 5.2e-28;
  Matches   85;  Conservative   20;  Mismatches   78;  Indels   25;  Gaps    6;

Qy     19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
          |||      |  :|| |:|||||   | | ||: | :|||:|| ||||
Db      7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA------- 59

Qy     79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
               |||:||:|    |: |   |:   ||:|||| | | | | ||||||:: |:|| |
Db     60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118

Qy    138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
          |  || ||||| | |    :|||:|| |     :||        ||    |  |    :|
Db    119 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHDNPQEKRLAADD 169

Qy    198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
               |:|  |       :|:    |||
Db    170 -----PEVRVLHSIGHSAAPRL--FPLA 190


RESULT   8
US-10-121-050-288
; Sequence 288, Application US/10121050
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C20
;  CURRENT APPLICATION NUMBER: US/10/121,050
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-050-288

  Query Match             29.0%;  Score 377.5;  DB 6;  Length 204;
  Best Local Similarity   40.9%;  Pred. No. 5.2e-28;
  Matches   85;  Conservative   20;  Mismatches   78;  Indels   25;  Gaps    6;

Qy     19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
          |||      |  :|| |:|||||   | | ||: | :|||:|| ||||
Db      7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA------- 59

Qy     79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
               |||:||:|    |: |   |:   ||:|||| | | | | ||||||:: |:|| |
Db     60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118

Qy    138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
          |  || ||||| | |    :|||:|| |     :||        ||    |  |    :|
Db    119 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHDNPQEKRLAADD 169

Qy    198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
               |:|  |       :|:    |||
Db    170 -----PEVRVLHSIGHSAAPRL--FPLA 190


RESULT   9
US-10-121-053-288
; Sequence 288, Application US/10121053
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C23
;  CURRENT APPLICATION NUMBER: US/10/121,053
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-053-288


  Query Match             29.0%;  Score 377.5;  DB 6;  Length 204;
  Best Local Similarity   40.9%;  Pred. No. 5.2e-28;
  Matches   85;  Conservative   20;  Mismatches   78;  Indels   25;  Gaps    6;

Qy     19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
          |||      |  :|| |:|||||   | | ||: | :|||:|| ||||
Db      7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA------- 59

Qy     79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
               |||:||:|    |: |   |:   ||:|||| | | | | ||||||:: |:|| |
```

```
Db      60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118

Qy     138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
           |  || ||||| | |    :|||:|| |     :||        ||    |  |    :|
Db     119 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHDNPQEKRLAADD 169

Qy     198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
                |:|  |       :|:    |||
Db     170 -----PEVRVLHSIGHSAAPRL--FPLA 190


RESULT  10
US-10-121-043-288
; Sequence 288, Application US/10121043
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C15
;  CURRENT APPLICATION NUMBER: US/10/121,043
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-043-288


  Query Match             29.0%;  Score 377.5;  DB 6;  Length 204;
  Best Local Similarity   40.9%;  Pred. No. 5.2e-28;
  Matches   85;  Conservative   20;  Mismatches   78;  Indels   25;  Gaps    6;

Qy      19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
           |||      |  :|| |:|||||   | | ||: | :|||:|| ||||
Db       7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA------- 59

Qy      79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                |||:||:|    |: |   |:   ||:|||| | | | | ||||||:: |:|| |
Db      60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118

Qy     138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
           |  || ||||| | |    :|||:|| |     :||        ||    |  |    :|
Db     119 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHDNPQEKRLAADD 169

Qy     198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
                |:|  |       :|:    |||
Db     170 -----PEVRVLHSIGHSAAPRL--FPLA 190


RESULT  11
US-10-121-044-288
; Sequence 288, Application US/10121044
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
```

```
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C5
;  CURRENT APPLICATION NUMBER: US/10/121,044
;  CURRENT FILING DATE:  2002-04-11
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-044-288


  Query Match             29.0%;  Score 377.5;  DB 6;  Length 204;
  Best Local Similarity   40.9%;  Pred. No. 5.2e-28;
  Matches   85;  Conservative   20;  Mismatches   78;  Indels   25;  Gaps    6;

Qy      19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
           |||      |  :|| |:|||||   | | ||: | :|||:|| ||||
Db       7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA------- 59

Qy      79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                |||:||:|    |: |   |:   ||:|||| | | | | ||||||:: |:|| |
Db      60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118

Qy     138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
           |  || ||||| | |    :|||:|| |     :||        ||    |  |    :|
Db     119 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHDNPQEKRLAADD 169

Qy     198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
                |:|  |       :|:    |||
Db     170 -----PEVRVLHSIGHSAAPRL--FPLA 190


RESULT  12
US-10-121-047-288
; Sequence 288, Application US/10121047
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
```

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;  FILE REFERENCE: P3330R1C4
;  CURRENT APPLICATION NUMBER: US/10/121,047
;  CURRENT FILING DATE:  2002-04-11
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-047-288


  Query Match             29.0%;  Score 377.5;  DB 6;  Length 204;
  Best Local Similarity   40.9%;  Pred. No. 5.2e-28;
  Matches   85;  Conservative   20;  Mismatches   78;  Indels   25;  Gaps    6;

Qy      19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
           |||      |  :|| |:|||||   | | ||: | :|||:|| ||||
Db       7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA------- 59

Qy      79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                |||:||:|    |:  |   |:   ||:|||| | | | | ||||||:: |:|| |
Db      60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118

Qy     138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
           |  || ||||| | |    :|||:|| |     :||        ||    |  |    :|
Db     119 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHDNPQEKRLAADD 169

Qy     198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
                |:|  |       :|:    |||
Db     170 -----PEVRVLHSIGHSAAPRL--FPLA 190


RESULT  13
US-10-121-054-288
; Sequence 288, Application US/10121054
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C14
;  CURRENT APPLICATION NUMBER: US/10/121,054
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-054-288


  Query Match             29.0%;  Score 377.5;  DB 6;  Length 204;
  Best Local Similarity   40.9%;  Pred. No. 5.2e-28;
  Matches   85;  Conservative   20;  Mismatches   78;  Indels   25;  Gaps    6;

Qy      19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
           |||      |  :|| |:|||||   | | ||: | :|||:|| ||||
Db       7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA------- 59

Qy      79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                |||:||:|    |:  |   |:   ||:|||| | | | | ||||||:: |:|| |
Db      60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118

Qy     138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
           |  || ||||| | |    :|||:|| |     :||        ||    |  |    :|
Db     119 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHDNPQEKRLAADD 169

Qy     198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
                |:|  |       :|:    |||
Db     170 -----PEVRVLHSIGHSAAPRL--FPLA 190


RESULT  14
US-10-121-056-288
; Sequence 288, Application US/10121056
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C25
;  CURRENT APPLICATION NUMBER: US/10/121,056
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-056-288


  Query Match             29.0%;  Score 377.5;  DB 6;  Length 204;
  Best Local Similarity   40.9%;  Pred. No. 5.2e-28;
  Matches   85;  Conservative   20;  Mismatches   78;  Indels   25;  Gaps    6;

Qy      19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
           |||      |  :|| |:|||||   | | ||: | :|||:|| ||||
Db       7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA------- 59

Qy      79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                |||:||:|    |:  |   |:   ||:|||| | | | | ||||||:: |:|| |
Db      60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118

Qy     138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
           |  || ||||| | |    :|||:|| |     :||        ||    |  |    :|
Db     119 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHDNPQEKRLAADD 169

Qy     198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
                |:|  |       :|:    |||
Db     170 -----PEVRVLHSIGHSAAPRL--FPLA 190


RESULT  15
```

```
US-10-121-057-288
; Sequence 288, Application US/10121057
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C13
;  CURRENT APPLICATION NUMBER: US/10/121,057
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-057-288


  Query Match             29.0%;  Score 377.5;  DB 6;  Length 204;
  Best Local Similarity   40.9%;  Pred. No. 5.2e-28;
  Matches   85;  Conservative   20;  Mismatches   78;  Indels   25;  Gaps    6;

Qy      19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
           |||      |  :|| |:|||||   | | ||: | :|||:|| ||||
Db       7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSA------- 59

Qy      79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                |||:||:|    |: |   |:   ||:|||| | | | | ||||||:: |:|| |
Db      60 -DAAMEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 118

Qy     138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
           |  || ||||| | |    :|||:|| |     :||        ||    |  |    :|
Db     119 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHDNPQEKRLAADD 169

Qy     198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
                |:|  |       :|:    |||
Db     170 -----PEVRVLHSIGHSAAPRL--FPLA 190


Search completed: September 28, 2002, 01:45:54
Job time: 619 sec
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```
                    GenCore version 4.5
             Copyright (c) 1993 - 2000  Compugen Ltd.


OM protein - protein search, using sw model

Run on:         September 28, 2002, 00:26:55 ; Search time 49.23 Seconds
                                               (without alignments)
                                               464.539 Million cell updates/sec

Title:          US-09-904-954-2
Perfect score:  1301
Sequence:       1 MAAAPLLLLLLLVPVPLLPL..........REHLPLAVGIAFFLMTFLAS 238

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:      283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_71:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
                       %
Result                Query
   No.    Score  Match Length DB  ID                     Description
 -------------------------------------------------------------------------------
     1     1301  100.0    238  2  I38849                 LERK-3 - human
     2      437   33.6    209  2  A54984                 ELF-1 protein prec
     3      434   33.4    213  2  JE0322                 ephrin-A2 - human
     4    415.5   31.9    228  2  I58170                 LERK-7 precursor -
     5    404.5   31.1    228  2  A57084                 repulsive axon gui
     6      390   30.0    205  2  A36377                 B61 protein precur
     7    364.5   28.0    201  2  I38850                 LERK-4 - human
     8    171.5   13.2    333  2  I84743                 hepatoma transmemb
     9    171.5   13.2    336  2  I49766                 hepatoma transmemb
    10    148.5   11.4    346  2  S46993                 elk ligand - human
    11    143.5   11.0    462  2  T32645                 hypothetical prote
    12    139.5   10.7    345  2  I48780                 Stra1/Eplg2 protei
    13    132.5   10.2    345  2  I58406                 LERK-2 - rat
    14      100    7.7    356  2  T40265                 hypothetical zinc-
    15       91    7.0   2206  1  GNNY27                 genome polyprotein
    16     88.5    6.8   1024  2  E90678                 beta-D-galactosida
    17     88.5    6.8   1024  2  A85529                 beta-D-galactosida
    18       87    6.7    817  2  T21336                 hypothetical prote
    19     85.5    6.6    709  2  T28712                 hypothetical prote
    20       84    6.5   1027  2  T19173                 hypothetical prote
    21     83.5    6.4    488  2  S67744                 hypothetical prote
    22     82.5    6.3    432  2  A25483                 env polyprotein, r
    23     82.5    6.3    466  1  TWFF                   transcription fact
    24       82    6.3    237  2  T19914                 hypothetical prote
    25       82    6.3    334  2  T16772                 hypothetical prote
    26       82    6.3    376  2  B84463                 hypothetical prote
    27       82    6.3    728  2  A48830                 probable transcrip
    28       82    6.3   1144  2  A75132                 hypothetical prote
    29     81.5    6.3   1173  2  I50620                 procKr2 - chicken
```

```
    30       81    6.2    457  2  T19109                 hypothetical prote
    31       81    6.2   1613  2  S39059                 protein BRG1 - hum
    32       81    6.2   1647  2  S45252                 SNF2beta protein -
    33     79.5    6.1    434  2  B72410                 alkaline phosphata
    34       79    6.1    612  2  A54282                 reversed polarity
    35       79    6.1    859  1  VCLJMN                 env polyprotein pr
    36     78.5    6.0    202  2  T01605                 phytocyanin At2g44
    37     78.5    6.0    498  2  B84789                 probable protein w
    38     78.5    6.0   1024  1  GBEC                   beta-galactosidase
    39     78.5    6.0   1291  2  T13389                 hypothetical prote
    40       78    6.0    321  2  I38238                 transcription fact
    41       78    6.0    328  1  S05426                 chitinase (EC 3.2.
    42       78    6.0    700  2  A32392                 protein kinase C (
    43       78    6.0   2206  1  GNNY4P                 genome polyprotein
    44       78    6.0   2206  2  S03822                 genome polyprotein
    45     77.5    6.0    570  2  H90370                 thermopsin precurs


                              ALIGNMENTS


RESULT   1
I38849
LERK-3 - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C;Accession: I38849
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D
Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs en
A;Reference number: I38849; MUID:95140419
A;Accession: I38849
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-238 <RES>
A;Cross-references: EMBL:U14187; NID:g642832; PIDN:AAC50078.1; PID:g642833
C;Genetics:
A;Gene: GDB:EPLG3
A;Cross-references: GDB:438336; OMIM:601381
A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein


  Query Match             100.0%;  Score 1301;  DB 2;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-114;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180

Qy      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238


RESULT   2
A54984
ELF-1 protein precursor - mouse
N;Alternate names: Cek7 ligand
C;Species: Mus musculus (house mouse)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 29-Sep-1999
C;Accession: A54984; A55873
R;Cheng, H.J.; Flanagan, J.G.
Cell 79, 157-168, 1994
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A;Title: Identification and cloning of ELF-1, a developmentally expressed ligand for the
A;Reference number: A54984; MUID:95007776
A;Accession: A54984
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-209 <CHE>
A;Cross-references: GB:U14941; NID:g558836; PIDN:AAA53636.1; PID:g558837
R;Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.
J. Biol. Chem. 270, 3467-3470, 1995
A;Title: cDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase li
A;Reference number: A55873; MUID:95181289
A;Accession: A55873
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-209 <SHA>
A;Cross-references: GB:U14752; NID:g681886; PIDN:AAA68520.1; PID:g681887
C;Superfamily: axon guidance signal protein
C;Keywords: lipoprotein; membrane protein


  Query Match             33.6%;  Score 437;  DB 2;  Length 209;
  Best Local Similarity   50.5%;  Pred. No. 1.6e-33;
  Matches   96;  Conservative   25;  Mismatches   47;  Indels   22;  Gaps    7;

Qy        2 AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE------GYTVQV 53
            |  ||| ||||    |||| |  : |  |  :|:||||| ||   :        ||||:|
Db        4 AQRPLLPLLLL----LLPLRARNEDPARANADRYAVYWNRSNPRFQVSAVGDGGGYTVEV 59

Qy       54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
            ::|||||||||||       ||   |    |:|:||||:  |: :|:  | |||||||||
Db       60 SINDYLDIYCPHY-------GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKRWECNR 112

Qy      113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
            | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db      113 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNLVDRPCLRLKVYVRPTNET 172

Qy      171 SHSGEKPVPT 180
             :   :|: |
Db      173 LYEAPEPIFT 182

RESULT   3
JE0322
ephrin-A2 - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C;Accession: JE0322
R;Aasheim, H.; Pedeutour, F.; Grosgeorge, J.; Logtenberg, T.
Biochem. Biophys. Res. Commun. 252, 378-382, 1998
A;Title: Cloning, chromosal mapping, and tissue expression of the gene encoding the huma
A;Reference number: JE0322; MUID:99045414
A;Accession: JE0322
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-213 <AAS>
A;Cross-references: GB:AJ007292; NID:g3688367; PIDN:CAA07435.1; PID:g3688368
C;Superfamily: axon guidance signal protein


  Query Match             33.4%;  Score 434;  DB 2;  Length 213;
  Best Local Similarity   50.5%;  Pred. No. 3.2e-33;
  Matches   96;  Conservative   24;  Mismatches   52;  Indels   18;  Gaps    7;

Qy        2 AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR------EGYTVQV 53
            | |||| |||||:|:|  |    :    |  :|:||||| ||            ||||:|
Db        4 AQAPLLPLLLLLLPLPPPPFAPPEDRRRANSDRYAVYWNRSNPRFHAGAGDDGGGYTVEV 63

Qy       54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
            ::|||||||||||       ||   |    | ||||||:  |: :|:  | |||||||||
Db       64 SINDYLDIYCPHY-------GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR 116

Qy      113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
            | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
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Db      117 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNAVDRPCLRLKVYVRPTNET 176

Qy      171 SHSGEKPVPT 180
             :   :|: |
Db      177 LYEAPEPIFT 186

RESULT   4
I58170
LERK-7 precursor - human
N;Alternate names: AL-1
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: I58170; G01812
R;Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P
Neuron 14, 973-981, 1995
A;Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involv
A;Reference number: I58170; MUID:95267434
A;Accession: I58170
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-228 <RES>
A;Cross-references: GB:S77167; NID:g914184; PID:g914185
R;Kozlosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, D.P.; Carpenter, M.K.
submitted to the EMBL Data Library, May 1995
A;Reference number: G08477
A;Accession: G01812
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-228 <KOZ>
A;Cross-references: EMBL:U26403; NID:g1019430; PIDN:AAB60377.1; PID:g1019431
C;Genetics:
A;Gene: GDB:EPLG7; AF1; LERK7
A;Cross-references: GDB:568757; OMIM:601535
A;Map position: 13q33-13q33
C;Superfamily: axon guidance signal protein


  Query Match             31.9%;  Score 415.5;  DB 2;  Length 228;
  Best Local Similarity   39.5%;  Pred. No. 1.9e-31;
  Matches   98;  Conservative   37;  Mismatches   66;  Indels   47;  Gaps   11;

Qy        8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
            :| |:  |  : : :| ||  |: :|:||||||||   :|  | : | :|||||::||||
Db        6 MLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCPHY 65

Qy       67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
              |         |    |:||||||: :||  | : |:|||||||||||:|: |:|||||
Db       66 EDS--------VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK 117

Qy      126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
            || :: ||||:||  | ||:|||:    |    ||::||||     |  |    ::
Db      118 FQLFTPFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDR---- 173

Qy      181 LPQFTMGPNVKINVLEDFE-----------GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
               | :   |: | ||  :           |||  | |::        | |      : |
Db      174 --VFDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI--------PSR-----LLAI 217

Qy      229 AFFLMTFL 236
              ||:  |
Db      218 LLFLLAML 225


RESULT   5
A57084
repulsive axon guidance signal protein RAGS precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C;Accession: A57084
R;Drescher, U.; Kremoser, C.; Handweker, C.; Loeschinger, J.; Noda, M.; Bonhoeffer, F
Cell 82, 359-370, 1995
A;Title: In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa tectal pr
A;Reference number: A57084; MUID:95360980
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A;Accession: A57084
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-228 <DRE>
A;Cross-references: GB:X90377; NID:g1061113; PIDN:CAA62027.1; PID:g984118
C;Superfamily: axon guidance signal protein
C;Keywords: glycoprotein; membrane protein; phosphatidylinositol linkage
F;1-20/Domain: signal sequence #status predicted <SIG>

  Query Match             31.1%;  Score 404.5;  DB 2;  Length 228;
  Best Local Similarity   49.1%;  Pred. No. 2e-30;
  Matches   79;  Conservative   29;  Mismatches   42;  Indels   11;  Gaps    4;

Qy      8 LLLLLVPVPLLPLLAQGPG-GALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
          :||| |    : :  | ||  |: :|:||||||:|   ::  | : | :|||||::||||
Db      6 MLLLAVAALWVCVRGQEPGRKAVADRYAVYWNSTNPRFQQGDYHIDVCINDYLDVFCPHY 65

Qy     67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
            |         |    |:||||||: :|| :| : |:|||||||||||:|: |:|||||
Db     66 EDS--------VPEDKTERYVLYMVNFDGYSSCDHISKGFKRWECNRPHSPNGPLKFSEK 117

Qy    126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV 165
          || :: ||||:||  | ||:|||:    |    ||::||||
Db    118 FQLFTPFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFV 158


RESULT   6
A36377
B61 protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-Sep-1999
C;Accession: A36377
R;Holzman, L.B.; Marks, R.M.; Dixit, V.M.
Mol. Cell. Biol. 10, 5830-5838, 1990
A;Title: A novel immediate-early response gene of endothelium is induced by cytokines an
A;Reference number: A36377; MUID:91042512
A;Accession: A36377
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-205 <HOL>
A;Cross-references: GB:M57730; GB:M37476; NID:g179320; PIDN:AAA58388.1; PID:g179321
C;Superfamily: axon guidance signal protein

  Query Match             30.0%;  Score 390;  DB 2;  Length 205;
  Best Local Similarity   41.8%;  Pred. No. 4.1e-29;
  Matches   87;  Conservative   21;  Mismatches   76;  Indels   24;  Gaps    6;

Qy     19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
          |||      |  :|| |:|||||   | | ||: | :|||:|| ||||    |   |
Db      7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSVADAA--- 63

Qy     79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
               |||:||:|    |: |   |:   ||:|||| | | | | ||||||:: |:|| |
Db     64 ----MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 119

Qy    138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
          |  || ||||| | |    :|||:|| |     :||        ||  : |  |    :|
Db    120 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHVNPQEKRLAADD 170

Qy    198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
               |:|  |       :|:    |||
Db    171 -----PEVRVLHSIGHSAAPRL--FPLA 191


RESULT   7
I38850
LERK-4 - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C;Accession: I38850
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D.;
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Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs en
A;Reference number: I38849; MUID:95140419
A;Accession: I38850
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-201 <RES>
A;Cross-references: EMBL:U14188; NID:g642834; PIDN:AAC50079.1; PID:g642835
C;Genetics:
A;Gene: GDB:EPLG4
A;Cross-references: GDB:438337; OMIM:601380
A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein

  Query Match             28.0%;  Score 364.5;  DB 2;  Length 201;
  Best Local Similarity   44.5%;  Pred. No. 9.9e-27;
  Matches   77;  Conservative   16;  Mismatches   67;  Indels   13;  Gaps    3;

Qy      8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67
          || ||  |     |     |    || |||||||  | |    |:: :|||||| ||||
Db      3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62

Qy     68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEK 125
                  ||||  | | : ||||   || :| |   : :||| |:    |   ::||||
Db     63 --------GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEK 111

Qy    126 FQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 178
           ||:: ||||:||  |  ||||| ||     :|||::| |||         ||
Db    112 IQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164


RESULT   8
I84743
hepatoma transmembrane kinase ligand - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C;Accession: I84743
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matth
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine
A;Reference number: I49766; MUID:95199254
A;Accession: I84743
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-333 <RES>
A;Cross-references: GB:L38734; NID:g769675; PIDN:AAC41752.1; PID:g769676
C;Genetics:
A;Gene: GDB:EPLG5; LERK5
A;Cross-references: GDB:438338; OMIM:600527
A;Map position: 13q33-13q33

  Query Match             13.2%;  Score 171.5;  DB 2;  Length 333;
  Best Local Similarity   28.3%;  Pred. No. 2.3e-08;
  Matches   63;  Conservative   23;  Mismatches  100;  Indels   37;  Gaps    7;

Qy     35 VYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSR 93
          :|||||| : |  :|  :   : | ||| ||  :|  ||           | | :||| :
Db     33 IYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKVDSKTVGQ---------YEYYKVYMVDK 83

Qy     94 NGYRTCNASQGFKRWECNRP----HAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIST 149
          :    |   :       | |      |   |||: ||| :|    | ||    :|| |||
Db     84 DQADRCTIKKE------NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIIST 137

Qy    150 PTHNLH--------------WKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVL 195
             :|                |  | |||    :|   :  |     |:   | | : :
Db    138 SNGSLEGLDNQEGGVCQTRAMKIL-MKVGQDASSAGSTRNKDPTRRPELEAGTNGRSSTT 196

Qy    196 EDFEGENPQVPKLEKSI--SGTSPKREHLPLAVGIAFFLMTFL 236
            |   ||       |   || :     : |  |||   : |:
Db    197 SPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFI 239
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RESULT   9
I49766
hepatoma transmembrane kinase ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I49766
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kin
A;Reference number: I49766; MUID:95199254
A;Accession: I49766
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-336 <RES>
A;Cross-references: GB:L38847; NID:g769677; PIDN:AAC42052.1; PID:g769678
C;Genetics:
A;Gene: HTK


  Query Match             13.2%;  Score 171.5;  DB 2;  Length 336;
  Best Local Similarity   28.3%;  Pred. No. 2.4e-08;
  Matches   62;  Conservative   27;  Mismatches  101;  Indels   29;  Gaps    8;

Qy      35 VYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSR 93
           :|||||| : |  :|  :   : | ||| ||  :|  ||           | | :||| :
Db      36 IYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKVDSKTVGQ---------YEYYKVYMVDK 86

Qy      94 NGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTH 152
           :    |    :      | |   |   :||: ||| :|    | ||    :|| |||
Db      87 DQADRCTIKKENTPLLNCAR---PDQDVKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNG 143

Qy     153 NLH---------WKCLRMKVFVCC---ASTSHSGEKPVPT-LPQFTMGPNVKINVLEDFE 199
           :|           :   ||: :     ||:: |     ||  |:   | | : :    |
Db     144 SLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTNGRSSTTSPFV 203

Qy     200 GENPQVPKLEKSI--SGTSPKREHLPLAVGIAFFLMTFL 236
             ||       |   || :     : |  |||   : |:
Db     204 KPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFI 242


RESULT  10
S46993
elk ligand - human
C;Species: Homo sapiens (man)
C;Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 28-May-1999
C;Accession: S46993
R;Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Kozlo
EMBO J. 13, 3757-3762, 1994
A;Title: Molecular characterization of a family of ligands for eph-related tyrosine kina
A;Reference number: S46993; MUID:94349923
A;Accession: S46993
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-346 <BEC>
A;Cross-references: GB:U09304; NID:g538366; PIDN:AAA53093.1; PID:g538367


  Query Match             11.4%;  Score 148.5;  DB 2;  Length 346;
  Best Local Similarity   26.4%;  Pred. No. 3.5e-06;
  Matches   55;  Conservative   26;  Mismatches   90;  Indels   37;  Gaps    7;

Qy      31 NRHAVYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLY 89
           |   | |:| | : |  :|  :   : | ||| ||   :           |   | | ||
Db      31 NLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEA-----------GRPYEYYKLY 79

Qy      90 MVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS 148
           :|       |:          |||   |   |:|: ||| :|   :| ||   |:||  |
Db      80 LVRPEQAAACSTVLDPNVLVTCNR---PEQEIRFTIKFQEFSPNYMGLEFKKHHDYYITS 136

Qy     149 TPTHNLH---------WKCLRMKVFVCCA-----------STSHSGEKPVPTLPQFTMGP 188
           |   :|           :   ||: :              :||   ::   |:   |  |
Db     137 TSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTTSRPSKEADNTVKMATQAP 196

Qy     189 NVKINVLEDFEGENPQVPKLEKSISGTS 216
             :   | | :|::  | : |||  | |
Db     197 GSR-GSLGDSDGKHETVNQEEKSGPGAS 223

RESULT  11
T32645
hypothetical protein F56A11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32645
R;Gattung, S.; Goela, D.; Harper, M.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F56A11.
A;Reference number: Z21204
A;Accession: T32645
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-462 <GAT>
A;Cross-references: EMBL:AF038619; PIDN:AAB92075.1; GSPDB:GN00022; CESP:F56A11.3
A;Experimental source: strain Bristol N2; clone F56A11
C;Genetics:
A;Gene: CESP:F56A11.3
A;Map position: 4
A;Introns: 37/3; 69/2; 103/2; 220/1; 388/1; 412/3


  Query Match             11.0%;  Score 143.5;  DB 2;  Length 462;
  Best Local Similarity   23.1%;  Pred. No. 1.5e-05;
  Matches   54;  Conservative   30;  Mismatches   93;  Indels   57;  Gaps   10;

Qy      26 GGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQ 85
           | |  : | |||||:|   |    |::| : | :   ||  |  |   |         |
Db      86 GLAAADEHIVYWNSTNSLFRNRQPTIEVRMGDVVRFVCPD-NEEGRNDG---------EY 135

Qy      86 YVLYMVSRNGYRTC------------------------NASQGFKRWECNRPHAPHSPIK 121
            ::| |:      |                            | :| :  :   |  |
Db     136 LIVYEVTEFAMDDCALESHSREVIRCAPEGTAEKVLRTQQLSGGRREDWKKQKVP--PKN 193

Qy     122 FSEKFQRYSAFSLGYEFHAGHEYYYISTPT-------HNLHWKC------LRMKVFVCCA 168
            ::  :: :    | |:  |  |||::| |       | ::  |      | |||    |
Db     194 VAQLIRQLNPIPNGKEYQPGQTYYYMTTSTGKANGTNHRMYGLCESQNMRLSMKV---SA 250

Qy     169 STSHSGEKPVPTLPQFTMGPNVKINVL---EDFEGENPQVPKLEKSISG-TSPK 218
           |  |   :  ||  |          ::   ||  : :|     | : : | |:||
Db     251 SQPHPTRR-APTRRQEDFVTTASAELMGGQEDEDSDNDNAHLLPRDLEGSTNPK 303


RESULT  12
I48780
Stra1/Eplg2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I48780; A55507; A55062; S52670
R;Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, B.; Doll
Dev. Biol. 170, 420-433, 1995
A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryona
A;Reference number: I48780; MUID:95377533
A;Accession: I48780
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-345 <RES>
A;Cross-references: EMBL:Z48781; NID:g747858; PIDN:CAA88695.1; PID:g747859
R;Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A
Genomics 24, 127-132, 1994
A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene enc
A;Reference number: A55507; MUID:95203867
A;Accession: A55507
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <FLE>
A;Cross-references: GB:U07598
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R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.
J. Biol. Chem. 269, 26606-26609, 1994
A;Title: cDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyr
A;Reference number: A55062; MUID:95014510
A;Accession: A55062
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-89,'T',91-345 <SHA>
A;Cross-references: GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:g575929
C;Genetics:
A;Gene: EPLG2

  Query Match             10.7%;  Score 139.5;  DB 2;  Length 345;
  Best Local Similarity   24.2%;  Pred. No. 2.4e-05;
  Matches   59;  Conservative   27;  Mismatches   87;  Indels   71;  Gaps    8;

Qy      4 APLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSN-QHLRREGYTVQVNVNDYLDIY 62
          | ::| |  :  ||             |   | |:| | : |  :|  :   : | |||
Db     15 AMVVLTLCRLATPLAK-----------NLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMV------------SRNGYRTCNASQGFKRWEC 110
          ||   :           |   | | ||:|              |   |||
Db     64 CPRAEA-----------GRPYEYYKLYLVRPEQAAACSTVLDPNVLVTCN---------- 102

Qy    111 NRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLH---------WKCLRM 161
               ||  |:|: ||| :|   :| ||   |:||  ||   :|           :   |
Db    103 ----KPHQEIRFTIKFQEFSPNYMGLEFKKYHDYYITSTSNGSLEGLENREGGVCRTRTM 158

Qy    162 KVFVCCA-----------STSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEK 210
          |: :              :||   ::   |:   |  |        | :|::  | : ||
Db    159 KIVMKVGQDPNAVTPEQLTTSRPSKESDNTVKTATQAPG--RGSQGDSDGKHETVNQEEK 216

Qy    211 SISG 214
          |  |
Db    217 SGPG 220

RESULT  13
I58406
LERK-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I58406
R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollin
Oncogene 9, 3241-3248, 1994
A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conser
A;Reference number: I58406; MUID:95022634
A;Accession: I58406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-345 <RES>
A;Cross-references: EMBL:U07560; NID:g563118; PIDN:AAA53092.1; PID:g563119
C;Genetics:
A;Gene: Eplg2

  Query Match             10.2%;  Score 132.5;  DB 2;  Length 345;
  Best Local Similarity   23.8%;  Pred. No. 0.00011;
  Matches   58;  Conservative   27;  Mismatches   88;  Indels   71;  Gaps    8;

Qy      4 APLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSN-QHLRREGYTVQVNVNDYLDIY 62
          | ::| |  :  ||             |   | |:| | : |  :|  :   : | |||
Db     15 AMVVLTLCRLATPLAK-----------NLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMV------------SRNGYRTCNASQGFKRWEC 110
          ||   :           |   | | ||:|              |   |||
Db     64 CPRAEA-----------GRPYEYYKLYLVRPEQAAACSTVLDPNVLVTCN---------- 102

Qy    111 NRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLH---------WKCLRM 161
               |   |:|: ||| :|   :| ||   |:||  ||   :|           :   |
Db    103 ----KPQQEIRFTIKFQEFSPNYMGLEFKKYHDYYITSTSNGSLEGLENREGGVCRTRTM 158
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Qy    162 KVFVCCA-----------STSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEK 210
          |: :              :||   ::   |:   |  |        | :|::  | : ||
Db    159 KIVMKVGQDPNAVTPEQLTTSRPSKESDNTVKTATQAPG--RGSQGDSDGKHETVNQQEK 216

Qy    211 SISG 214
          |  |
Db    217 SGPG 220

RESULT  14
T40265
hypothetical zinc-finger protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40265
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z21868
A;Accession: T40265
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-356 <LYN>
A;Cross-references: EMBL:AL031854; PIDN:CAA21282.1; GSPDB:GN00067; SPDB:SPBC337.12
A;Experimental source: strain 972h-; cosmid c337
C;Genetics:
A;Gene: SPDB:SPBC337.12
A;Map position: 2

  Query Match             7.7%;  Score 100;  DB 2;  Length 356;
  Best Local Similarity   19.0%;  Pred. No. 0.13;
  Matches   42;  Conservative   31;  Mismatches   64;  Indels   84;  Gaps    8;

Qy     35 VYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSR- 93
          :|||: :  |::: :  :|  |    :|| :||::|:        | ||    ::  :|
Db    161 LYWNNKSYLLKKKRFLKEVG-NSPSAVYCRYYNANGI-------CGKGAACRFVHEPTRK 212

Qy     94 -----------NGYRTCN-----------ASQGFKRWECNRPHAPHSPIKFSE------K 125
                     |    ||           | : |   :|| |:  :  | :||      :
Db    213 TICPKFLNGRCNKAEDCNLSHELDPRRIPACRYFLLGKCNNPNCRYVHIHYSENAPICFE 272

Qy    126 FQRYSAFSLGYEFHAGHEYYYISTPTHNLH-WKCLRMKVFVCCASTSHSGEKPVPTLPQF 184
          | :|    ||             |   | |  :|    :|  |
Db    273 FAKYGFCELG-------------TSCKNQHILQCTDYAMFGSC----------------- 302

Qy    185 TMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLA 225
                           |||      ::|   |::   |::
Db    303 ----------------NNPQCSLYHGAVSADVPEQTEAPIS 327

RESULT  15
GNNY27
genome polyprotein - human poliovirus 3 (strain 23127)
N;Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; c
A-directed RNA polymerase (EC 2.7.7.48)
C;Species: human poliovirus 3
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Jul-1999
C;Accession: A27245
R;Hughes, P.J.; Evans, D.M.A.; Minor, P.D.; Schild, G.C.; Almond, J.W.; Stanway, G.
J. Gen. Virol. 67, 2093-2102, 1986
A;Title: The nucleotide sequence of a type 3 poliovirus isolated during a recent outb
A;Reference number: A27245; MUID:87010550
A;Accession: A27245
A;Molecule type: genomic RNA
A;Residues: 1-2206 <HUG>
A;Cross-references: GB:X04468; NID:g61112; PIDN:CAA28155.1; PID:g61113
C;Superfamily: poliovirus genome polyprotein
C;Keywords: coat protein; core protein; genome-linked protein; nucleotidyltransferase
F;1-69/Product: coat protein VP4 #status predicted <VP4>
F;70-340/Product: coat protein VP2 #status predicted <VP2>
F;341-578/Product: coat protein VP3 #status predicted <VP3>
F;579-878/Product: coat protein VP1 #status predicted <VP1>
F;879-1027/Product: core protein P2-3b #status predicted <P3B>
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F;1028-1124/Product: core protein P2-5b #status predicted <P5B>
F;1125-1453/Product: core protein P2-X #status predicted <P2X>
F;1454-1540/Product: protein P3-1b #status predicted <P1B>
F;1541-1562/Product: genome-linked protein VPg #status predicted <VPG>
F;1563-1745/Product: proteinase #status predicted <PTS>
F;1746-2206/Product: RNA-directed RNA polymerase #status predicted <RNS>
F;1543/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

  Query Match             7.0%;  Score 91;  DB 1;  Length 2206;
  Best Local Similarity   20.5%;  Pred. No. 8.1;
  Matches   52;  Conservative   29;  Mismatches  109;  Indels   64;  Gaps    9;

Qy       26 GGALGNRHAV--YWNSSNQHLRREGYTVQVN-----VNDYLDIYCPHYNSSGVGPGAGPG 78
            ||:  |   :  | :|::    :: |:   :     : | |    |  ||  |
Db       21 GGSTINYTTINYYKDSASNAASKQDYSQDPSKFTEPLKDVLIKTAPALNSPNV------- 73

Qy       79 PGGGAEQYVLYMVSRNGYRT----CNASQGFKRW-------ECNRPHAPHSPIKFSEKFQ 127
               |    || :   |   |     |:   : ||       | |    |  |   : :|
Db       74 EACGYSDRVLQLTLGNSTITTQEAANSVVAYGRWPEFIRDDEANPVDQPTEPDVATSRFY 133

Qy      128 RYSAFSLGYE-----------------FHAGHEYYYISTPTHNLHWKCLRMKVFVCCAST 170
                   | |                 |     |:|:    : :| :        | ||
Db      134 TLDTVMWGKESRGWWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQ--------CNASK 185

Qy      171 SHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQ------VPKLEKSISGTSPKREHLP- 223
             | |   |  :|:| :  :        :   ||         :  |  : ||||||  |
Db      186 FHQGSLGVFAIPEFCLAGDSDTQRYTSYANANPGEKGGKFYAQFNKDTAVTSPKREFCPV 245

Qy      224 -------LAVGIAF 230
                   : :| ||
Db      246 DYLLGCGVLIGNAF 259


Search completed: September 28, 2002, 01:38:54
Job time: 4319 sec
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                 GenCore version 4.5
      Copyright (c) 1993 - 2000  Compugen Ltd.


OM protein - protein search, using sw model

Run on:          September 28, 2002, 01:37:46 ; Search time 27.02 Seconds
                                                (without alignments)
                                                341.053 Million cell updates/sec

Title:           US-09-904-954-2
Perfect score:   1301
Sequence:        1 MAAAPLLLLLLLVPVPLLPL..........REHLPLAVGIAFFLMTFLAS 238

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:      105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SwissProt_40:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES
                  %
Result          Query
  No.   Score   Match Length DB  ID                  Description
 ----------------------------------------------------------------------------
    1    1301   100.0    238  1  EFA3_HUMAN          P52797 homo sapien
    2     963    74.0    187  1  EFA3_MOUSE          O08545 mus musculu
    3     437    33.6    209  1  EFA2_MOUSE          P52801 mus musculu
    4     437    33.6    213  1  EFA2_HUMAN          O43921 homo sapien
    5     426    32.7    195  1  EFA2_BRARE          P79727 brachydanio
    6     421    32.4    200  1  EFA2_CHICK          P52802 gallus gall
    7   415.5    31.9    228  1  EFA5_HUMAN          P52803 homo sapien
    8   414.5    31.9    228  1  EFA5_MOUSE          O08543 mus musculu
    9   414.5    31.9    228  1  EFA5_RAT            P97605 rattus norv
   10     410    31.5    206  1  EFA4_MOUSE          O08542 mus musculu
   11   404.5    31.1    228  1  EFA5_CHICK          P52804 gallus gall
   12     397    30.5    228  1  EFA5_BRARE          P79728 brachydanio
   13     390    30.0    205  1  EFA1_HUMAN          P20827 homo sapien
   14   375.5    28.9    216  1  EFA1_XENLA          P52794 xenopus lae
   15     374    28.7    205  1  EFA1_MOUSE          P52793 mus musculu
   16   364.5    28.0    201  1  EFA4_HUMAN          P52798 homo sapien
   17     362    27.8    205  1  EFA1_RAT            P97553 rattus norv
   18     179    13.8    340  1  EFB3_HUMAN          Q15768 homo sapien
   19     177    13.6    340  1  EFB3_MOUSE          O35393 mus musculu
   20   171.5    13.2    333  1  EFB2_HUMAN          P52799 homo sapien
   21   171.5    13.2    336  1  EFB2_MOUSE          P52800 mus musculu
   22   148.5    11.4    346  1  EFB1_HUMAN          P98172 homo sapien
   23     147    11.3    332  1  EFB2_BRARE          O73874 brachydanio
   24   139.5    10.7    345  1  EFB1_MOUSE          P52795 mus musculu
   25     134    10.3    327  1  EFB1_XENLA          O13097 xenopus lae
   26   132.5    10.2    345  1  EFB1_RAT            P52796 rattus norv
   27   122.5     9.4    334  1  EFB1_CHICK          O73612 gallus gall
   28      91     7.0   2206  1  POLG_POL32          P06209 poliovirus
   29    88.5     6.8    894  1  ILF3_HUMAN          Q12906 h interleuk
   30      85     6.5    400  1  CASP_MOUSE          Q9cyd3 mus musculu
   31    83.5     6.4    910  1  ILF3_RAT            Q9jil3 rattus norv
   32    82.5     6.3    432  1  ENV2_MOUSE          P11370 mus musculu
   33    82.5     6.3    466  1  KRUP_DROME          P07247 drosophila
   34      82     6.3    319  1  SOX2_MOUSE          P48432 mus musculu
   35      82     6.3    334  1  CAHX_CAEEL          Q10462 caenorhabdi
   36      81     6.2    911  1  ILF3_MOUSE          Q9z1x4 mus musculu
   37      81     6.2   1647  1  SN24_HUMAN          P51532 homo sapien
   38    79.5     6.1    391  1  ROG_HUMAN           P38159 homo sapien
   39      79     6.1    856  1  ENV_HV1MN           P05877 human immun
   40    78.5     6.0   1023  1  BGAL_ECOLI          P00722 escherichia
   41      78     6.0    284  1  HXBD_HUMAN          Q92826 homo sapien
   42      78     6.0    317  1  SOX2_HUMAN          P48431 homo sapien
   43      78     6.0    320  1  SOX2_SHEEP          P54231 ovis aries
   44      78     6.0    328  1  CHIT_SOLTU          P05315 solanum tub
   45      78     6.0    700  1  KPC2_DROME          P13677 drosophila


                                ALIGNMENTS


RESULT   1
EFA3_HUMAN
ID   EFA3_HUMAN     STANDARD;      PRT;   238 AA.
AC   P52797;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ephrin-A3 precursor (EPH-related receptor tyrosine kinase ligand 3)
DE   (LERK-3) (EHK1 ligand) (EHK1-L).
GN   EFNA3 OR EPLG3 OR LERK3 OR EFL-2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95140419; PubMed=7838529;
RA   Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,
RA   Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
RA   Cerretti D.P., Beckmann M.P.;
RT   "Ligands for the receptor tyrosine kinases hek and elk: isolation of
RT   cDNAs encoding a family of proteins.";
RL   Oncogene 10:299-306(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95063919; PubMed=7973638;
RA   Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C., Lhotak V.,
RA   Pawson T., Goldfarb M., Yancopoulos G.D.;
RT   "Ligands for EPH-related receptor tyrosine kinases that require
RT   membrane attachment or clustering for activity.";
RL   Science 266:816-819(1994).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKELETAL MUSCLE, SPLEEN,
CC       THYMUS, PROSTATE, TESTIS, OVARY, SMALL INTESTINE, AND PERIPHERAL
CC       BLOOD LEUKOCYTES.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U14187; AAC50078.1; -.
DR   EMBL; L37360; AAA52368.1; -.
DR   MIM; 601381; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    238       EPHRIN-A3.
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FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     67     67       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    100    100       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     71     74       MISSING (IN REF. 2).
SQ   SEQUENCE   238 AA;  26350 MW;  8EFD6AE8FE33FDDA CRC64;

  Query Match             100.0%;  Score 1301;  DB 1;  Length 238;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-115;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60

Qy     61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120

Qy    121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180

Qy    181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238


RESULT   2
EFA3_MOUSE
ID   EFA3_MOUSE     STANDARD;      PRT;   187 AA.
AC   O08545; O55217;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ephrin-A3 (EPH-related receptor tyrosine kinase ligand 3) (LERK-3)
DE   (EHK1 ligand) (EHK1-L) (Fragment).
GN   EFNA3 OR EPLG3 OR LERK3 OR EPL3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RX   MEDLINE=98126446; PubMed=9465306;
RA   Cerretti D.P., Nelson N.;
RT   "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
RT   mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
RT   conservation of intron/exon structure.";
RL   Genomics 47:131-135(1998).
RN   [2]
RP   SEQUENCE OF 17-78 FROM N.A.
RX   MEDLINE=97060319; PubMed=8903354;
RA   Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
RT   "Distinct and overlapping expression patterns of ligands for
RT   Eph-related receptor tyrosine kinases during mouse embryogenesis.";
RL   Dev. Biol. 179:382-401(1996).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U92885; AAC39961.1; -.
DR   EMBL; U90666; AAB50241.1; -.
DR   MGD; MGI:106644; Efna3.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor.
FT   NON_TER       1      1
FT   CARBOHYD     24     24       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     41     41       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     49     49       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     19     19       Y -> I (IN REF. 2).
FT   CONFLICT     33     34       EQ -> DR (IN REF. 2).
FT   CONFLICT     46     47       RT -> QP (IN REF. 2).
FT   CONFLICT     78     78       Y -> W (IN REF. 2).
SQ   SEQUENCE   187 AA;  21171 MW;  CCE4915751760743 CRC64;

  Query Match              74.0%;  Score 963;  DB 1;  Length 187;
  Best Local Similarity   91.3%;  Pred. No. 1.3e-83;
  Matches  178;  Conservative    3;  Mismatches    6;  Indels    8;  Gaps    1;

Qy     44 LRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ 103
          :|||||||||||||||||||||||||        ||||||||||||||: :|||||||||
Db      1 MRREGYTVQVNVNDYLDIYCPHYNSS--------GPGGGAEQYVLYMVNLSGYRTCNASQ 52

Qy    104 GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKV 163
          | ||||||| || ||||||||||||||||||||||||| |||||||||||||||||||||
Db     53 GSKRWECNRQHASHSPIKFSEKFQRYSAFSLGYEFHAGQEYYYISTPTHNLHWKCLRMKV 112

Qy    164 FVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    113 FVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 172

Qy    224 LAVGIAFFLMTFLAS 238
          ||||||||||| |||
Db    173 LAVGIAFFLMTLLAS 187


RESULT   3
EFA2_MOUSE
ID   EFA2_MOUSE     STANDARD;      PRT;   209 AA.
AC   P52801;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (ELF-1) (CEK7-ligand) (CEK7-L).
GN   EFNA2 OR EPLG6 OR LERK6 OR ELF1 OR EPL6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SWISS WEBSTER; TISSUE=Brain;
RX   MEDLINE=95007776; PubMed=7522971;
RA   Cheng H.J., Flanagan J.G.;
RT   "Identification and cloning of ELF-1, a developmentally expressed
RT   ligand for the Mek4 and Sek receptor tyrosine kinases.";
RL   Cell 79:157-168(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=95181289; PubMed=7876076;
RA   Shao H., Lou L., Pandey A., Verderame M.F., Siever D.A., Dixit V.M.;
RT   "cDNA cloning and characterization of a Cek7 receptor
RT   protein-tyrosine kinase ligand that is identical to the ligand
RT   (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases.";
RL   J. Biol. Chem. 270:3467-3470(1995).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND
CC       EPHA5.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
```

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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U14941; AAA53636.1; -.
DR   EMBL; U14752; AAA68520.1; -.
DR   MGD; MGI:102707; Efna2.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    209       EPHRIN-A2.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    184    184       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   209 AA;  23586 MW;  F1997545F25B9ABC CRC64;


  Query Match             33.6%;  Score 437;  DB 1;  Length 209;
  Best Local Similarity   50.5%;  Pred. No. 4.9e-34;
  Matches   96;  Conservative   25;  Mismatches   47;  Indels   22;  Gaps    7;

Qy        2 AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE------GYTVQV 53
            |  ||| ||||    |||| |  : |  |  :|:||||| ||   :        ||||:|
Db        4 AQRPLLPLLLL----LLPLRARNEDPARANADRYAVYWNRSNPRFQVSAVGDGGGYTVEV 59

Qy       54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
            ::|||||||||||       ||   |    |:|:||||:  |: :|:  | |||||||||
Db       60 SINDYLDIYCPHY-------GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKRWECNR 112

Qy      113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
            | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db      113 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNLVDRPCLRLKVYVRPTNET 172

Qy      171 SHSGEKPVPT 180
             :   :|: |
Db      173 LYEAPEPIFT 182


RESULT   4
EFA2_HUMAN
ID   EFA2_HUMAN     STANDARD;      PRT;   213 AA.
AC   O43921; O76020;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (HEK7-ligand) (HEK7-L).
GN   EFNA2 OR EPLG6 OR LERK6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98126446; PubMed=9465306;
RA   Cerretti D.P., Nelson N.;
RT   "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
RT   mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
RT   conservation of intron/exon structure.";
RL   Genomics 47:131-135(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA   Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA   Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,
RA   Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,
RA   Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
RA   Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
RA   Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
RA   Carrano A.V.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99045414; PubMed=9826538;
RA   Aasheim H.C., Pedeutour F., Grosgeorge J., Logtenberg T.;
RT   "Cloning, chromosal mapping, and tissue expression of the gene
RT   encoding the human Eph-family kinase ligand ephrin-A2.";
RL   Biochem. Biophys. Res. Commun. 252:378-382(1998).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND
CC       EPHA5.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U92896; AAC39577.1; -.
DR   EMBL; U92893; AAC39577.1; JOINED.
DR   EMBL; U92894; AAC39577.1; JOINED.
DR   EMBL; AC004258; AAC04896.1; -.
DR   EMBL; AJ007292; CAA07435.1; -.
DR   MIM; 602756; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    213       EPHRIN-A2.
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    188    188       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      6      6       R -> A (IN REF. 3).
FT   CONFLICT     25     26       RA -> PP (IN REF. 3).
FT   CONFLICT     29     30       AA -> RR (IN REF. 3).
SQ   SEQUENCE   213 AA;  23878 MW;  33C9FB1A8168B2D0 CRC64;


  Query Match             33.6%;  Score 437;  DB 1;  Length 213;
  Best Local Similarity   50.5%;  Pred. No. 5e-34;
  Matches   96;  Conservative   24;  Mismatches   52;  Indels   18;  Gaps    7;

Qy        2 AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR------EGYTVQV 53
            |  ||| |||||:|:|  |   |:    |  :|:||||| ||            ||||:|
Db        4 AQRPLLPLLLLLLPLPPPPFARAEDAARANSDRYAVYWNRSNPRFHAGAGDDGGGYTVEV 63

Qy       54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR 112
            ::|||||||||||       ||   |    | ||||||:  |: :|:  | |||||||||
Db       64 SINDYLDIYCPHY-------GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR 116

Qy      113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T 170
            | ||  |:||||||| :: ||||:||  |||||||| || : :   |||:||:|   : |
Db      117 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNAVDRPCLRLKVYVRPTNET 176

Qy      171 SHSGEKPVPT 180
             :   :|: |
Db      177 LYEAPEPIFT 186


RESULT   5
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EFA2_BRARE
ID   EFA2_BRARE     STANDARD;      PRT;   195 AA.
AC   P79727;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (ELF-1) (ZFEPHL3).
GN   EFNA2 OR EPLG6 OR LERK6.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97195707; PubMed=9043080;
RA   Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U.,
RA   Bonhoeffer F., Holder N.;
RT   "Two Eph receptor tyrosine kinase ligands control axon growth and may
RT   be involved in the creation of the retinotectal map in the
RT   zebrafish.";
RL   Development 124:655-664(1997).
CC   -!- FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE CREATION
CC       OF THE RETINO-TECTAL MAP.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDBRAIN OF
CC       DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT IS
CC       EXPRESSED THROUGHOUT THE MIDBRAIN INCLUDING THE REGION OF THE
CC       PRESUMPTIVE TECTUM. AT LATER STAGES IT IS EXPRESSED IN A GRADED
CC       FASHION THROUGHOUT THE TECTUM.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Y09668; CAA70863.1; -.
DR   ZFIN; ZDB-GENE-990415-66; efna2.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    195       EPHRIN-A2.
FT   CARBOHYD     32     32       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   195 AA;  22688 MW;  9EE284FEB61D0C42 CRC64;

  Query Match             32.7%;  Score 426;  DB 1;  Length 195;
  Best Local Similarity   52.3%;  Pred. No. 4.9e-33;
  Matches   81;  Conservative   24;  Mismatches   38;  Indels   12;  Gaps    4;

Qy     29 LGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVL 88
          : :||||||||||    :  ||| |::|||||:|||:| |        | |    |:|:|
Db     23 ISDRHAVYWNSSNSRFWQGEYTVAVSINDYLDVYCPYYES--------PQPHSRMERYIL 74

Qy     89 YMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYI 147
          :||: :|| || :  :|||||||||| :|  |::|||||| ::  ||||:||  |||||||
Db     75 FMVNHDGYLTCEHRMRGFKRWECNRPQSPDGPLRFSEKFQLFTPFSLGFEFRPGHEYYYI 134

Qy    148 STPTHNLHWK-CLRMKVFVCCASTSHSGEKPVPTL 181
          |:|  |   | ||::||:|    ||   | | | |
Db    135 SSPHPNHAGKPCLKLKVYV--KPTSSGYESPEPFL 167
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RESULT   6
EFA2_CHICK
ID   EFA2_CHICK     STANDARD;      PRT;   200 AA.
AC   P52802;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (ELF-1).
GN   EFNA2 OR EPLG6 OR LERK6 OR ELF1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95360981; PubMed=7634327;
RA   Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.;
RT   "Complementary gradients in expression and binding of ELF-1 and Mek4
RT   in development of the topographic retinotectal projection map.";
RL   Cell 82:371-381(1995).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND
CC       EPHA5 (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT ACROSS THE TECTUM
CC       BEING MORE STRONGLY EXPRESSED AT THE POSTERIOR POLE.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; L40932; AAC42229.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    200       EPHRIN-A2.
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    175    175       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   200 AA;  23049 MW;  8FAB1AE5E45EED96 CRC64;

  Query Match             32.4%;  Score 421;  DB 1;  Length 200;
  Best Local Similarity   47.5%;  Pred. No. 1.5e-32;
  Matches   86;  Conservative   29;  Mismatches   50;  Indels   16;  Gaps    5;

Qy      3 AAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
          || ||  :: | |      :  ||  : :|:||||| ||    |  |||:|::|||||||
Db      6 AAALLAAIVGVCV-----WSDDPGKVISDRYAVYWNRSNPRFHRGDYTVEVSINDYLDIY 60

Qy     63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK 121
          ||||          | |    |:||||||:  |: :|:  | |||||||||| :|  |:|
Db     61 CPHYEE--------PLPAERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLK 112

Qy    122 FSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP 179
          |||||| :: ||||:||  |||||||| :| : :   ||::||:|   : | :   :|:
Db    113 FSEKFQLFTPFSLGFEFRPGHEYYYISASPLNVVDRPCLKLKVYVRPTNDSLYESPEPIF 172

Qy    180 T 180
          |
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Db      173 T 173


RESULT   7
EFA5_HUMAN
ID   EFA5_HUMAN     STANDARD;      PRT;   228 AA.
AC   P52803;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
DE   (LERK-7) (AL-1).
GN   EFNA5 OR EPLG7 OR LERK7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95267434; PubMed=7748564;
RA   Winslow J.W., Moran P., Valverde J., Shih A., Yuan J.Q., Wong S.C.,
RA   Tsai S.P., Goddard A., Henzel W.J., Hefti F.;
RT   "Cloning of AL-1, a ligand for an Eph-related tyrosine kinase
RT   receptor involved in axon bundle formation.";
RL   Neuron 14:973-981(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97392664; PubMed=9245480;
RA   Kozlosky C.J., Vandenbos T., Park L.S., Cerretti D.P., Carpenter M.K.;
RT   "LERK-7: a ligand of the Eph-related kinases is developmentally
RT   regulated in the brain.";
RL   Cytokine 9:540-549(1997).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=20069483; PubMed=10601038;
RA   Davy A., Gale N.W., Murray E.W., Klinghoffer R.A., Soriano P.,
RA   Feuerstein C., Robbins S.M.;
RT   "Compartmentalized signaling by GPI-anchored ephrin-A5 requires the
RT   Fyn tyrosine kinase to regulate cellular adhesion.";
RL   Genes Dev. 13:3125-3135(1999).
CC   -!- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.
CC       INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE
CC       MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS
CC       COGNATE RECEPTOR. THIS SIGNALING EVENT REQUIRES THE ACTIVITY OF
CC       THE FYN TYROSINE KINASE.
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
CC       EPHB1.
CC   -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT
CC       IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
CC       MICRODOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U26403; AAB60377.1; -.
DR   MIM; 601535; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal;
KW   Polymorphism.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    228       EPHRIN-A5.
FT   CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      55     55       N -> K (IN DBSNP:469062).
FT                                /FTId=VAR_012035.
SQ   SEQUENCE   228 AA;  26297 MW;  6893B1CCACFF3F57 CRC64;

  Query Match             31.9%;  Score 415.5;  DB 1;  Length 228;
  Best Local Similarity   39.5%;  Pred. No. 5.7e-32;
  Matches   98;  Conservative   37;  Mismatches   66;  Indels   47;  Gaps   11;

Qy        8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
            :| |:  |  : : :| ||  |: :|:||||||||   :|  | : | :|||||::||||
Db        6 MLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCPHY 65

Qy       67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
              |         |    |:||||||: :||  | : |:|||||||||||:|: |:|||||
Db       66 EDS--------VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK 117

Qy      126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
            || :: ||||:||  | ||:|||:    |    ||::|||||     |  |    ::
Db      118 FQLFTPFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDR---- 173

Qy      181 LPQFTMGPNVKINVLEDFE-----------GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
               | :   |: | ||  :           |||  | |::        | |      : |
Db      174 --VFDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI--------PSR-----LLAI 217

Qy      229 AFFLMTFL 236
              ||:  |
Db      218 LLFLLAML 225


RESULT   8
EFA5_MOUSE
ID   EFA5_MOUSE     STANDARD;      PRT;   228 AA.
AC   O08543; O08544;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
DE   (LERK-7) (AL-1).
GN   EFNA5 OR EPLG7 OR LERK7 OR EPL7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97060319; PubMed=8903354;
RA   Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
RT   "Distinct and overlapping expression patterns of ligands for
RT   Eph-related receptor tyrosine kinases during mouse embryogenesis.";
RL   Dev. Biol. 179:382-401(1996).
CC   -!- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.
CC       INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE
CC       MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS
CC       COGNATE RECEPTOR. THIS SIGNALLING EVENT REQUIRES THE ACTIVITY OF
CC       THE FYN TYROSINE KINASE (BY SIMILARITY).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
CC       EPHB1 (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT
CC       IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
CC       MICRODOMAINS (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
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DR   EMBL; U90664; AAB50239.1; -.
DR   EMBL; U90665; AAB50240.1; -.
DR   MGD; MGI:107444; Efna5.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal;
KW   Alternative splicing.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    228       EPHRIN-A5.
FT   CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    163    189       MISSING (IN SHORT ISOFORM).
SQ   SEQUENCE   228 AA;  26339 MW;  85439F5337420022 CRC64;

  Query Match             31.9%;  Score 414.5;  DB 1;  Length 228;
  Best Local Similarity   39.5%;  Pred. No. 7.1e-32;
  Matches   98;  Conservative   36;  Mismatches   67;  Indels   47;  Gaps   11;

Qy      8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
          :| ||  |  : : :| ||   : :|:||||||||   :|  | : | :|||||::||||
Db      6 MLTLLFLVLWMCVFSQDPGSKVVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCPHY 65

Qy     67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
            |         |    |:||||||: :||  | : |:|||||||||||:|: |:|||||
Db     66 EDS--------VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK 117

Qy    126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
          || :: ||||:||  | ||:|||:    |    ||::||||     |  |    ::
Db    118 FQLFTPFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDR---- 173

Qy    181 LPQFTMGPNVKINVLEDFE-----------GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
             | :   |: |  ||  :          |||  | |::        | |      : |
Db    174 --VFDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI--------PSR-----LLAI 217

Qy    229 AFFLMTFL 236
            ||:  |
Db    218 LLFLLAML 225


RESULT   9
EFA5_RAT
ID   EFA5_RAT       STANDARD;      PRT;   228 AA.
AC   P97605;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
DE   (LERK-7) (AL-1).
GN   EFNA5 OR EPLG7 OR LERK7.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=SPRAGUE-DAWLEY;
RX   MEDLINE=95267434; PubMed=7748564;
RA   Winslow J.W., Moran P., Valverde J., Shih A., Yuan J.Q., Wong S.C.,
RA   Tsai S.P., Goddard A., Henzel W.J., Hefti F., Beck K.D., Caras I.W.;
RT   "Cloning of AL-1, a ligand for an Eph-related tyrosine kinase
RT   receptor involved in axon bundle formation.";
RL   Neuron 14:973-981(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RA   Li Y.Y., McTiernan C.F., Feldman A.M.;
RT   "rLERK7, rat ligand for Eph-related receptor tyrosine kinase.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.
CC       INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE
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CC       MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS
CC       COGNATE RECEPTOR. THIS SIGNALLING EVENT REQUIRES THE ACTIVITY OF
CC       THE FYN TYROSINE KINASE (BY SIMILARITY).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
CC       EPHB1 (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT
CC       IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
CC       MICRODOMAINS (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, PLACENTA AND LUNG.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U69279; AAC05801.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    228       EPHRIN-A5.
FT   CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   228 AA;  26358 MW;  855985532D580022 CRC64;

  Query Match             31.9%;  Score 414.5;  DB 1;  Length 228;
  Best Local Similarity   39.5%;  Pred. No. 7.1e-32;
  Matches   98;  Conservative   36;  Mismatches   67;  Indels   47;  Gaps   11;

Qy      8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
          :| ||  |  : : :| ||   : :|:||||||||   :|  | : | :|||||::||||
Db      6 MLTLLFLVLWMCVFSQDPGSKVVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCPHY 65

Qy     67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
            |         |    |:||||||: :||  | : |:|||||||||||:|: |:|||||
Db     66 EDS--------VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK 117

Qy    126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT 180
          || :: ||||:||  | ||:|||:    |    ||::||||     |  |    ::
Db    118 FQLFTPFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVRDR---- 173

Qy    181 LPQFTMGPNVKINVLEDFE-----------GEN-PQVPKLEKSISGTSPKREHLPLAVGI 228
             | :   |: |  ||  :          |||  | |::        | |      : |
Db    174 --VFDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI--------PSR-----LLAI 217

Qy    229 AFFLMTFL 236
            ||:  |
Db    218 LLFLLAML 225


RESULT  10
EFA4_MOUSE
ID   EFA4_MOUSE     STANDARD;      PRT;   206 AA.
AC   O08542; O55218;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ephrin-A4 precursor (EPH-related receptor tyrosine kinase ligand 4)
DE   (LERK-4).
GN   EFNA4 OR EPLG4 OR LERK4 OR EPL4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
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RX   MEDLINE=97060319; PubMed=8903354;
RA   Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
RT   "Distinct and overlapping expression patterns of ligands for
RT   Eph-related receptor tyrosine kinases during mouse embryogenesis.";
RL   Dev. Biol. 179:382-401(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RX   MEDLINE=98126446; PubMed=9465306;
RA   Cerretti D.P., Nelson N.;
RT   "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
RT   mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
RT   conservation of intron/exon structure.";
RL   Genomics 47:131-135(1998).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U90663; AAB50238.1; -.
DR   EMBL; U92890; AAC39962.1; -.
DR   EMBL; U92889; AAC39962.1; JOINED.
DR   MGD; MGI:106643; Efna4.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    206       EPHRIN-A4.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   SITE         41     43       CELL ATTACHMENT SITE (POTENTIAL).
FT   CONFLICT      1      4       MRLL -> MLLRLGLIYPPTRPPAPPGPLV (IN REF.
FT                                1).
SQ   SEQUENCE   206 AA;  22861 MW;  43501971DD1C6EA5 CRC64;

  Query Match             31.5%;  Score 410;  DB 1;  Length 206;
  Best Local Similarity   47.4%;  Pred. No. 1.7e-31;
  Matches   83;  Conservative   18;  Mismatches   62;  Indels   12;  Gaps    3;

Qy          8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67
              || ||  |    ||     |    || :||||||  | |    |::  ||||||:||||
Db          3 LLPLLRTVLWAALLGSRLPGCSSLRHPIYWNSSNPRLLRGDAVVELGFNDYLDIFCPHYE 62

Qy         68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNA--SQGFKRWECNRPHAPHSPIKFSEK 125
              |        |||  | | : ||||  :||  | |  :  |:|| |: | || ||::||||
Db         63 S--------PGPPEGPETFALYMVDWSGYEACTAEGANAFQRWNCSMPFAPFSPVRFSEK 114

Qy        126 FQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCC--ASTSHSGEKPV 178
               |||: | ||:||  |  ||||| ||     :|||::| |||  : :||    ||
Db        115 IQRYTPFPLGFEFLPGETYYYISVPTPESPGRCLRLQVSVCCKESGSSHESAHPV 169


RESULT 11
EFA5_CHICK
ID   EFA5_CHICK     STANDARD;      PRT;   228 AA.
AC   P52804;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
DE   (LERK-7) (RAGS protein).
GN   EFNA5 OR RAGS.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Posterior tectum;
RX   MEDLINE=95360980; PubMed=7634326;
RA   Drescher U., Kremoser C., Handwerker C., Loschinger J., Noda M.,
RA   Bonhoeffer F.;
RT   "In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa
RT   tectal protein related to ligands for Eph receptor tyrosine
RT   kinases.";
RL   Cell 82:359-370(1995).
CC   -!- FUNCTION: INDUCES GROWTH CONE COLLAPSE AND REPULSION OF RETINAL
CC       GANGLION CELL AXONS.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A GRADED FASHION ACROSS THE
CC       TECTUM BEING MORE STRONGLY EXPRESSED TOWARDS THE POSTERIOR POLE.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X90377; CAA62027.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    228       EPHRIN-A5.
FT   CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   228 AA;  26206 MW;  56D8E4FBDECF18AD CRC64;

  Query Match             31.1%;  Score 404.5;  DB 1;  Length 228;
  Best Local Similarity   49.1%;  Pred. No. 6.2e-31;
  Matches   79;  Conservative   29;  Mismatches   42;  Indels   11;  Gaps    4;

Qy          8 LLLLLVPVPLLPLLAQGPG-GALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
              :||| |    : :  | ||  |: :|:||||||:|   ::  | : | :|||||::||||
Db          6 MLLLAVAALWVCVRGQEPGRKAVADRYAVYWNSTNPRFQQGDYHIDVCINDYLDVFCPHY 65

Qy         67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                |         |    |:||||||: :|| :| : |:|||||||||||:|: |:|||||
Db         66 EDS--------VPEDKTERYVLYMVNFDGYSSCDHISKGFKRWECNRPHSPNGPLKFSEK 117

Qy        126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV 165
              || ::  ||||:||  |  ||:|||:    |    ||::||||
Db        118 FQLFTPFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFV 158


RESULT 12
EFA5_BRARE
ID   EFA5_BRARE     STANDARD;      PRT;   228 AA.
AC   P79728;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
DE   (LERK-7) (AL-1) (ZFEPHL4).
GN   EFNA5 OR EFNA5B OR AL1 OR EPLG7 OR LERK7.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97195707; PubMed=9043080;
RA   Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U.,
RA   Bonhoeffer F., Holder N.;
RT   "Two Eph receptor tyrosine kinase ligands control axon growth and may
RT   be involved in the creation of the retinotectal map in the
RT   zebrafish.";
RL   Development 124:655-664(1997).
CC   -!- FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE CREATION
CC       OF THE RETINO-TECTAL MAP.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDBRAIN OF
CC       DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT IS
CC       STRONGLY EXPRESSED IN THE MIDBRAIN CAUDAL TO THE PRESUMPTIVE
CC       TECTUM. AT LATER STAGES IT IS MAINTAINED AT THE POSTERIOR MARGIN
CC       OF THE TECTUM.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; Y09669; CAA70864.1; -.
DR   ZFIN; ZDB-GENE-980526-186; efna5b.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    228       EPHRIN-A5.
FT   CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   228 AA;  26595 MW;  74B3406C05418E6E CRC64;

  Query Match             30.5%;  Score 397;  DB 1;  Length 228;
  Best Local Similarity   47.8%;  Pred. No. 3.1e-30;
  Matches   77;  Conservative   30;  Mismatches   42;  Indels   12;  Gaps    5;

Qy          9 LLLLVPVPL-LPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY 66
              ::: | | | : : :| |    : :|:||:|| :|   :|  | : | :|||||:|||||
Db          6 MIVFVGVILWMCVFSQEPSSKVMADRYAVFWNRTNPRFQRGDYHIDVCINDYLDVYCPHY 65

Qy         67 NSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK 125
                |         |    |:||||||: :|| || : ::|||||||||||:|: |:|||||
Db         66 EDS--------VPEERTERYVLYMVNYDGYSTCDHTAKGFKRWECNRPHSPNGPLKFSEK 117

Qy        126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV 165
              || :: ||||:||  | ||||||:  |      ||::||||
Db        118 FQLFTPFSLGFEFRPGREYYYISSMITETGRRSCLKLKVFV 158


RESULT 13
EFA1_HUMAN
ID   EFA1_HUMAN     STANDARD;      PRT;   205 AA.
AC   P20827;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Ephrin-A1 precursor (EPH-related receptor tyrosine kinase ligand 1)
DE   (LERK-1) (Immediate early response protein B61) (Tumor necrosis
```

```
DE   factor, alpha-induced protein 4).
GN   EFNA1 OR EPGL1 OR LERK1 OR TNFAIP4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91042512; PubMed=2233719;
RA   Holzman L.B., Marks R.M., Dixit V.M.;
RT   "A novel immediate-early response gene of endothelium is induced by
RT   cytokines and encodes a secreted protein.";
RL   Mol. Cell. Biol. 10:5830-5838(1990).
RN   [2]
RP   GPI-ANCHOR.
RX   MEDLINE=95140419; PubMed=7838529;
RA   Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,
RA   Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
RA   Cerretti D.P., Beckmann M.P.;
RT   "Ligands for the receptor tyrosine kinases hek and elk: isolation of
RT   cDNAs encoding a family of proteins.";
RL   Oncogene 10:299-306(1995).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
CC       EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- INDUCTION: BY TNF-ALPHA AND INTERLEUKIN-1 BETA.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; M57730; AAA58388.1; -.
DR   PIR; A36377; A36377.
DR   MIM; 191164; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    205       EPHRIN-A1.
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   205 AA;  23771 MW;  4FEFC6BF4C1251A9 CRC64;


  Query Match             30.0%;  Score 390;  DB 1;  Length 205;
  Best Local Similarity   41.8%;  Pred. No. 1.3e-29;
  Matches   87;  Conservative   21;  Mismatches   76;  Indels   24;  Gaps    6;

Qy         19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
              |||      |  :|| |:|||||   |  | ||: |  :|||:|| ||||    |   |
Db          7 PLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSVADAA--- 63

Qy         79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
                   |||:||:|    |:  |   |:   ||:|||| | | | | ||||||:: |:|| |
Db         64 ----MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE 119

Qy        138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
              |  || ||||| | |    :|||:|| |     :||        ||  : |  |    :|
Db        120 FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS--------PQAHVNPQEKRLAADD 170

Qy        198 FEGENPQVPKLEKSISGTSPKREHLPLA 225
                   |:|  |       :|:    |||
Db        171 -----PEVRVLHSIGHSAAPRL--FPLA 191


RESULT 14
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```
EFA1_XENLA
ID   EFA1_XENLA     STANDARD;      PRT;   216 AA.
AC   P52794;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ephrin-A1 precursor (EPH-related receptor tyrosine kinase ligand 1)
DE   (LERK-1) (XELF).
GN   EFNA1 OR EPGL1 OR ELF.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97000306; PubMed=8843391;
RA   Weinstein D.C., Rahman S.M., Ruiz J.C., Hemmati-Brivanlou A.;
RT   "Embryonic expression of eph signalling factors in Xenopus.";
RL   Mech. Dev. 57:133-144(1996).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
CC       EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1 (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U31204; AAA74485.1; -.
DR   EMBL; U31205; AAA74486.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Alternative splicing; Signal.
FT   SIGNAL        1     28       POTENTIAL.
FT   CHAIN        29    216       EPHRIN-A1.
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    162    216       TPPPVNVHTPRSHIQSDEPEVPLPGVMKSVAGNSAAPGTPC
FT                                TLYGLLLAALLLRL -> SE (IN ISOFORM A').
SQ   SEQUENCE   216 AA;  24755 MW;  1B3A508E0A7B872E CRC64;

  Query Match             28.9%;  Score 375.5;  DB 1;  Length 216;
  Best Local Similarity   41.1%;  Pred. No. 3.1e-28;
  Matches   79;  Conservative   25;  Mismatches   63;  Indels   25;  Gaps    5;

Qy         28 ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYV 87
              | | || |:|||||    :| ||||| :|||||| ||:|    |        |   |:|
Db         26 AQGERHIVFWNSSNYRFMQEDYTVQVQLNDYLDIVCPYYEEGSVA-------GHTVERYT 78

Qy         88 LYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYY 146
              |::|    | ||   |:   |||||:| ||| | || ||||::: |:|| ||  |  |||
Db         79 LFLVDYEEYETCKPKSKDQVRWECNKPFAPHGPEKFCEKFQKFTPFTLGTEFREGRTYYY 138

Qy        147 ISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQV- 205
              || | |     |:|::| |       ||    | :   |   ::        : : |:|
Db        139 ISKPIHYHGETCMRLRVHV-------SGRTTPPPVNVHTPRSHI--------QSDEPEVP 183

Qy        206 -PKLEKSISGTS 216
               | : ||::| |
Db        184 LPGVMKSVAGNS 195

RESULT  15
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EFA1_MOUSE
ID   EFA1_MOUSE     STANDARD;      PRT;   205 AA.
AC   P52793; P97331;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A1 precursor (EPH-related receptor tyrosine kinase ligand 1)
DE   (LERK-1) (Immediate early response protein B61).
GN   EFNA1 OR EPGL1 OR LERK1 OR EPL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR;
RX   MEDLINE=95405853; PubMed=7675446;
RA   Takahashi H., Ikeda T.;
RT   "Molecular cloning and expression of rat and mouse B61 gene:
RT   implications on organogenesis.";
RL   Oncogene 11:879-883(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Morris J.C., Ciarletta A., Morris G.E., Giannotti J., Caruso A.,
RA   Hammett D.J., Finnerty H., Turner K., Wood C.R.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97060319; PubMed=8903354;
RA   Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
RT   "Distinct and overlapping expression patterns of ligands for
RT   Eph-related receptor tyrosine kinases during mouse embryogenesis.";
RL   Dev. Biol. 179:382-401(1996).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
CC       EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; D38146; BAA07344.1; -.
DR   EMBL; U26188; AAA67563.1; -.
DR   EMBL; U90662; AAB50237.1; -.
DR   MGD; MGI:103236; Efna1.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    205       EPHRIN-A1.
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     74     74       H -> Y (IN REF. 1).
FT   CONFLICT     79     79       A -> T (IN REF. 1).
FT   CONFLICT     81     81       Q -> E (IN REF. 1).
FT   CONFLICT     91     91       N -> K (IN REF. 1).
FT   CONFLICT     94     94       R -> Q (IN REF. 1).
FT   CONFLICT    112    112       T -> S (IN REF. 1).
FT   CONFLICT    115    115       I -> T (IN REF. 1).
FT   CONFLICT    138    138       S -> T (IN REF. 1).
FT   CONFLICT    154    154       N -> S (IN REF. 1).
FT   CONFLICT    156    156       Q -> H (IN REF. 1).
FT   CONFLICT    159    159       V -> A (IN REF. 1).
FT   CONFLICT    181    181       Y -> H (IN REF. 1).
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FT   CONFLICT    204    204       S -> T (IN REF. 1).
SQ   SEQUENCE   205 AA;  23802 MW;  5A8F3A6E2091E868 CRC64;


  Query Match             28.7%;  Score 374;  DB 1;  Length 205;
  Best Local Similarity   38.7%;  Pred. No. 4e-28;
  Matches   86;  Conservative   23;  Mismatches   87;  Indels   26;  Gaps    6;

Qy     19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
          |||      |  :|| |:|||||   | | ||| | :|||||| ||||    |   |
Db      7 PLLGLCCSLAAADRHIVFWNSSNPKFREEDYTVHVQLNDYLDIICPHYEDDSVADAA--- 63

Qy     79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
               |:| ||||    |  |   |:   || |||| | | | | ||||||:: | || |
Db     64 ----MERYTLYMVEHQEYVACQPQSKDQVRWNCNRPSAKHGPEKLSEKFQRFTPFILGKE 119

Qy    138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
          |  || ||||| | ::   :||::|| |       :|        : |  |   :|  |
Db    120 FKEGHSYYYISKPIYHQESQCLKLKVTV-------NG--------KITHNPQAHVNPQEK 164

Qy    198 -FEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
            : ::|:|  |       :|:    ||   :    :  | |
Db    165 RLQADDPEVQVLHSIGYSAAPRL--FPLVWAVLLLPLLLLQS 204


Search completed: September 28, 2002, 01:48:24
Job time: 638 sec
```

```
                   GenCore version 4.5
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OM protein - protein search, using sw model

Run on:          September 28, 2002, 01:36:55 ; Search time 79.86 Seconds
                                                (without alignments)
                                                515.562 Million cell updates/sec

Title:           US-09-904-954-2
Perfect score:   1301
Sequence:        1 MAAAPLLLLLLLVPVPLLPL..........REHLPLAVGIAFFLMTFLAS 238

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:      562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SPTREMBL_19:*
                1:  sp_archea:*
                2:  sp_bacteria:*
                3:  sp_fungi:*
                4:  sp_human:*
                5:  sp_invertebrate:*
                6:  sp_mammal:*
                7:  sp_mhc:*
                8:  sp_organelle:*
                9:  sp_phage:*
                10:  sp_plant:*
                11:  sp_rodent:*
                12:  sp_virus:*
                13:  sp_vertebrate:*
                14:  sp_unclassified:*
                15:  sp_rvirus:*
                16:  sp_bacteriap:*
                17:  sp_archeap:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result              Query
  No.    Score      Match Length DB  ID                            Description
-----------------------------------------------------------------------------------
    1      727      55.9    219  13  Q90YC5                        Q90yc5 brachydanio
    2      586      45.0    118  11  Q923G4                        Q923g4 rattus norv
    3    424.5      32.6    202  13  Q98TZ1                        Q98tz1 gallus gall
    4      406      31.2     88  13  Q9PTD0                        Q9ptd0 ctenophorus
    5      406      31.2    206  11  Q9CZS8                        Q9czs8 mus musculu
    6      373      28.7    229  13  O93431                        O93431 brachydanio
    7      367      28.2    205  11  Q9D7K8                        Q9d7k8 mus musculu
    8      338      26.0    102  11  Q9WUE7                        Q9wue7 rattus norv
    9    268.5      20.6     93  13  Q9PTD1                        Q9ptd1 ctenophorus
   10    247.5      19.0     80  13  O42304                        O42304 brachydanio
   11      208      16.0     42  11  Q9CRL3                        Q9crl3 mus musculu
   12      178      13.7     70  13  Q90ZG7                        Q90zg7 brachydanio
   13    166.5      12.8    331  13  Q90Z31                        Q90z31 brachydanio
   14    164.5      12.6    327  13  Q9PT69                        Q9pt69 xenopus lae
   15    162.5      12.5    333  13  Q9PUJ4                        Q9puj4 gallus gall
   16      145      11.1    652  5  Q9V4E1                        Q9v4e1 drosophila
   17    143.5      11.0    348  5  O44516                         O44516 caenorhabdi
   18    138.5      10.6    279  5  Q9U474                         Q9u474 caenorhabdi
   19      138      10.6    334  13  Q90Z32                         Q90z32 brachydanio
   20    124.5       9.6    341  13  Q90Z33                         Q90z33 brachydanio
   21      100       7.7    377  3  O74823                         O74823 schizosacch
   22       96       7.4   1199  5  Q9V9Y3                         Q9v9y3 drosophila
   23       92       7.1    855  15  Q9YKQ0                         Q9ykq0 human immun
   24     88.5       6.8    441  4  Q9NQ99                         Q9nq99 homo sapien
   25     88.5       6.8    709  4  Q9NRN2                         Q9nrn2 homo sapien
   26     88.5       6.8    894  4  Q9UMZ9                         Q9umz9 homo sapien
   27     87.5       6.7    765  11  Q91ZV1                         Q91zv1 mus musculu
   28     87.5       6.7    765  11  Q91V98                         Q91v98 mus musculu
   29     87.5       6.7    894  4  Q9BZH4                         Q9bzh4 homo sapien
   30       87       6.7    817  5  Q93560                         Q93560 caenorhabdi
   31       86       6.6    438  11  Q9R262                         Q9r262 mus musculu
   32       86       6.6    442  11  Q9Z2L7                         Q9z2l7 mus musculu
   33     85.5       6.6    709  5  O16783                         O16783 caenorhabdi
   34       84       6.5    855  15  Q9YKQ4                         Q9ykq4 human immun
   35       84       6.5   1027  5  Q17657                         Q17657 caenorhabdi
   36     83.5       6.4    457  3  Q05672                         Q05672 saccharomyc
   37     83.5       6.4    473  5  Q961A1                         Q961a1 drosophila
   38     83.5       6.4    488  3  Q07619                         Q07619 saccharomyc
   39     83.5       6.4    502  5  Q9W0V9                         Q9w0v9 drosophila
   40     83.5       6.4    561  5  Q9V9N4                         Q9v9n4 drosophila
   41     83.5       6.4    910  11  Q9JIL3                         Q9jil3 rattus norv
   42       83       6.4   1342  5  Q9GPP6                         Q9gpp6 drosophila
   43       83       6.4   2206  12  Q9DIF1                         Q9dif1 human polio
   44     82.5       6.3    304  4  Q9HBC3                         Q9hbc3 homo sapien
   45     82.5       6.3    463  4  Q13648                         Q13648 homo sapien


                              ALIGNMENTS


RESULT   1
Q90YC5
ID    Q90YC5      PRELIMINARY;      PRT;   219 AA.
AC    Q90YC5;
DT    01-DEC-2001 (TrEMBLrel. 19, Created)
DT    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT    01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE    EPHRIN-A3.
GN    EPHRIN-A3.
OS    Brachydanio rerio (Zebrafish) (Zebra danio).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC    Cypriniformes; Cyprinidae; Danio.
OX    NCBI_TaxID=7955;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=21412237; PubMed=11520665;
RA    Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
RT    "Identification of ephrin-A3 and novel genes specific to the midbrain-
RT    MHB in embryonic zebrafish by ordered differential display.";
RL    Mech. Dev. 107:83-96(2001).
DR    EMBL; AB051678; BAB55891.1; -.
SQ    SEQUENCE   219 AA;  25146 MW;  7191927E03F8EA01 CRC64;


  Query Match             55.9%;  Score 727;  DB 13;  Length 219;
  Best Local Similarity   61.9%;  Pred. No. 1.4e-67;
  Matches  140;  Conservative   25;  Mismatches   43;  Indels   18;  Gaps    3;

Qy        1 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
            ||   | | || :      |:          ||||:|||||  ||:||||:|||||||||
Db        1 MALYALCLFLLTLTCTNFALVTAA-------RHAVHWNSSNILLRKEGYTLQVNVNDYLD 53

Qy       61 IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
            |||||||||           | ||||||||||  |||||:   ||||||||||||||:||
Db       54 IYCPHYNSS---------QRGIAEQYVLYMVSYRGYRTCDPQLGFKRWECNRPHAPHAPI 104

Qy      121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
            ||||||||||||||||||| | ||||||||||:    |||::|:|||:: | | ::| ||
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Db       105 KFSEKFQRYSAFSLGYEFHVGQEYYYISTPTHHHGRSCLRLRVYVCCSTASDSDDEPQPT 164

Qy       181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAV 226
              | :|: ||:||: |:|:  :||:||||||||||:|| |: | | |
Db       165 EPDYTLRPNIKIDDLDDY--DNPEVPKLEKSISGSSPSRDRLLLTV 208


RESULT   2
Q923G4
ID   Q923G4       PRELIMINARY;      PRT;   118 AA.
AC   Q923G4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN A3 (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Munoz J.J., Alonso-C L.M., Sacedon R., Crompton T., Vicente A.,
RA   Jimenez E., Varas A., Zapata A.G.;
RT   "Expression and function of the Eph A receptors and their ligands
RT   ephrins A in the rat thymus.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY045577; AAK92219.1; -.
FT   NON_TER       1      1
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13470 MW;  FF0277F079783A46 CRC64;


  Query Match             45.0%;  Score 586;  DB 11;  Length 118;
  Best Local Similarity   72.4%;  Pred. No. 3e-53;
  Matches  110;  Conservative    3;  Mismatches    5;  Indels   34;  Gaps    2;

Qy        63 CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPIKF 122
             |||||||        ||||||||||||||: :|||||||||| ||||||| || ||||||
Db         1 CPHYNSS--------GPGGGAEQYVLYMVNLSGYRTCNASQGSKRWECNRQHASHSPIKF 52

Qy       123 SEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLP 182
             ||||||||||||||||||| |||||||||||||||||||||||||||
Db        53 SEKFQRYSAFSLGYEFHAGQEYYYISTPTHNLHWKCLRMKVFVCCAS------------ 99

Qy       183 QFTMGPNVKINVLEDFEGENPQVPKLEKSISG 214
                          :||||||||||||||||||
Db       100 -------------KDFEGENPQVPKLEKSISG 118

RESULT   3
Q98TZ1
ID   Q98TZ1       PRELIMINARY;      PRT;   202 AA.
AC   Q98TZ1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   EPHRIN-A6 (FRAGMENT).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Menzel P., Valencia F., Godement P., Dodelet V.C., Pasquale E.B.;
RT   "Ephrin-A6, a new ligand for EphA receptors in the developing visual
RT   system.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF317286; AAK00944.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
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DR   PROSITE; PS01299; EPHRIN; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   202 AA;  22624 MW;  91E2716FF91353F9 CRC64;

  Query Match             32.6%;  Score 424.5;  DB 13;  Length 202;
  Best Local Similarity   45.4%;  Pred. No. 3.8e-36;
  Matches   84;  Conservative   28;  Mismatches   56;  Indels   17;  Gaps    4;

Qy         6 LLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPH 65
             || |||       |||   |    | || |||| ||    :: |::||::||:|||||||
Db         1 LLGLLLWA-----PLLWAPPPPVRGRRHGVYWNGSNPRFLQDDYSIQVSINDHLDIYCPH 55

Qy        66 YNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQG-FKRWECNRPHAPHSPIKFSE 124
             |::          |   || : |:||   ||| |: : | |||||||:| ||  |::|||
Db        56 YSA----------PTPWAESFTLFMVDEEGYRGCSETPGAFKRWECNKPFAPFVPVRFSE 105

Qy       125 KFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVP-TLPQ 183
             | ||:: ||||:||  |  |||||  ||     :||:::| ||| :::      || : |:
Db       106 KIQRFTPFSLGFEFRPGETYYYISVPTPGSAGRCLKLRVSVCCRASTPEPLTEVPNSQPR 165

Qy       184 FTMGP 188
                ||
Db       166 GRGGP 170


RESULT   4
Q9PTD0
ID   Q9PTD0       PRELIMINARY;      PRT;    88 AA.
AC   Q9PTD0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   EPHRIN A3 (FRAGMENT).
OS   Ctenophorus ornatus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
OC   Ctenophorus.
OX   NCBI_TaxID=95347;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Chen P.B., Rodger J., Dunlop S.A., Beazley L.D.;
RT   "Ephrin homologs are expressed in the adult lizard visual system.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Scarborough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.;
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF209777; AAF19444.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
FT   NON_TER       1      1
FT   NON_TER      88     88
SQ   SEQUENCE   88 AA;  10636 MW;  C56FCD8B13F219E7 CRC64;


  Query Match             31.2%;  Score 406;  DB 13;  Length 88;
  Best Local Similarity   75.0%;  Pred. No. 1.1e-34;
  Matches   72;  Conservative    7;  Mismatches    9;  Indels    8;  Gaps    1;

Qy        35 VYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRN 94
             |:|| || |||||||||||:|||||||||||||:|         | |  |||:||||:
Db         1 VFWNRSNPHLRREGYTVQVSVNDYLDIYCPHYNAS--------VPEGRVEQYILYMVNYE 52

Qy        95 GYRTCNASQGFKRWECNRPHAPHSPIKFSEKFQRYS 130
             |||||| |||||||||||||||||||||||||||::
Db        53 GYRTCNISQGFKRWECNRPHAPHSPIKFSEKFQRFT 88


RESULT   5
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Q9CZS8
ID   Q9CZS8      PRELIMINARY;      PRT;   206 AA.
AC   Q9CZS8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   10 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE   CLONE:2610529M21, FULL INSERT SEQUENCE.
GN   EFNA4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK012195; BAB28092.1; -.
DR   MGD; MGI:106643; Efna4.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
SQ   SEQUENCE   206 AA;  22859 MW;  675E32971D1C6EBC CRC64;

  Query Match             31.2%;  Score 406;  DB 11;  Length 206;
  Best Local Similarity   46.9%;  Pred. No. 3.3e-34;
  Matches   82;  Conservative   19;  Mismatches   62;  Indels   12;  Gaps    3;

Qy        8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67
            || ||  |    ||     |    || :||||||  | |    |::  ||||||:||||
Db        3 LLPLLRTVLWAALLGSRLPGCSSLRHPIYWNSSNPRLLRGDAVVELGFNDYLDIFCPHYE 62

Qy       68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNA--SQGFKRWECNRPHAPHSPIKFSEK 125
            |        |||  | | : ||:|  :||  | |  :  |:|| |: | || ||::||||
Db       63 S--------PGPPEGPETFALYIVDWSGYEACTAEGANSFQRWNCSMPFAPFSPVRFSEK 114

Qy      126 FQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCC--ASTSHSGEKPV 178
             |||: | ||:||  |  ||||| ||     :|||::| |||  : :||    ||
Db      115 IQRYTPFPLGFEFLPGETYYYISVPTPESPGRCLRLQVSVCCKESGSSHESAHPV 169

RESULT   6
O93431
ID   O93431      PRELIMINARY;      PRT;   229 AA.
AC   O93431;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN A-L1.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Durbin L., Brennan C.H., Shiomi K., Cooke J.;
RT   "Eph signalling is required for segmentation and differentiation of
RT   the somites.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ006838; CAA07264.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   229 AA;  26115 MW;  8684462F67AF6F5C CRC64;

  Query Match             28.7%;  Score 373;  DB 13;  Length 229;
  Best Local Similarity   40.0%;  Pred. No. 1e-30;
  Matches   84;  Conservative   25;  Mismatches   59;  Indels   42;  Gaps    6;

Qy       28 ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYV 87
            |   ||:|||||:| :   : ||| | :|||||| ||||         |      ||:||
Db       18 ASAERHSVYWNSTNANFLWDDYTVDVRINDYLDIICPHY-------AHGEIASQEAERYV 70

Qy       88 LYMVSRNGYRTCNA-SQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYY 146
            ||||    |  |   |    ||||:|| |||:| ||||||||:: |:|| ||  |  |||
Db       71 LYMVELEDYENCKPHSFDQLRWECSRPFAPHAPEKFSEKFQRFTPFTLGKEFRQGESYYY 130

Qy      147 ISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGE----- 201
            || | |:   :|||:|| |     | : :|               :  :|: ||:
Db      131 ISKPLHHHGQECLRLKVDVVGPHGSKNKKK--------------MVEKVEEIEGKMAAGG 176

Qy      202 --NP-----------QVPKLEKSI--SGTS 216
              ||            :| :::|:  || |
Db      177 VHNPSNRLPADDPIAMIPVVQRSVGSSGVS 206

RESULT   7
Q9D7K8
ID   Q9D7K8      PRELIMINARY;      PRT;   205 AA.
AC   Q9D7K8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ADULT MALE TONGUE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE   CLONE:2310004J15, FULL INSERT SEQUENCE.
GN   EFNA1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TONGUE;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
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RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK009144; BAB26102.1; -.
DR   MGD; MGI:103236; Efna1.
DR   InterPro; IPR001799; Ephrin.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
SQ   SEQUENCE   205 AA;  23772 MW;  E37E55767459A4EC CRC64;


  Query Match             28.2%;  Score 367;  DB 11;  Length 205;
  Best Local Similarity   38.3%;  Pred. No. 3.7e-30;
  Matches   85;  Conservative   23;  Mismatches   88;  Indels   26;  Gaps    6;

Qy     19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG 78
          |||      |  :|| |:|||||   | | ||| | :|||||| ||||    |   |
Db      7 PLLGLCCSLAAADRHIVFWNSSNPKFREEDYTVHVQLNDYLDIICPHYEDDSVADAA--- 63

Qy     79 PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE 137
               |:| ||||    |  |   |:  || |||| | | | | | ||||:: | || |
Db     64 ----MERYTLYMVEHQEYVACQPQSKDQVRWNCNRPSAKHGPEKLSVKFQRFTPFILGKE 119
.
Qy    138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED 197
          |  || ||||| | ::   :||::|| |       :|        : |  |   :| .|
Db    120 FKEGHSYYYISKPIYHQESQCLKLKVTV-------NG--------KITHNPQAHVNPQEK 164

Qy    198 -FEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
            : ::|:|  |       :|:    ||   :    :  | |
Db    165 RLQADDPEVQVLHSIGYSAAPRL--FPLVWAVLLLPLLLLQS 204


RESULT   8
Q9WUE7
ID   Q9WUE7      PRELIMINARY;      PRT;   102 AA.
AC   Q9WUE7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN A-2 (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Matsunaga T., Davis J.G., Greene M.I.;
RT   "Cellular and subcellular compartmentalization of adult peripheral
RT   vestibular system by distinctive and overlapping expression of Eph
RT   receptors and ephrins.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF131912; AAD33515.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
FT   NON_TER       1      1
FT   NON_TER     102    102
SQ   SEQUENCE   102 AA;  11838 MW;  A497302F7FD7364B CRC64;


  Query Match             26.0%;  Score 338;  DB 11;  Length 102;
  Best Local Similarity   58.9%;  Pred. No. 1.6e-27;
  Matches   63;  Conservative   13;  Mismatches   23;  Indels    8;  Gaps    2;

Qy     49 YTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKR 107
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          |||:|::|||||||||||       ||   |    |:|:||||:  |: :|:  | ||||
Db      1 YTVEVSINDYLDIYCPHY-------GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKR 53

Qy    108 WECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNL 154
          |||||| ||  |:||||||| :: ||||:||  ||||||||    ||
Db     54 WECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNL 100


RESULT   9
Q9PTD1
ID   Q9PTD1      PRELIMINARY;      PRT;    93 AA.
AC   Q9PTD1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   EPHRIN A2 (FRAGMENT).
OS   Ctenophorus ornatus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
OC   Ctenophorus.
OX   NCBI_TaxID=95347;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Scarborough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.;
RT   "Ephrin homologs are expressed in the adult lizard visual system.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF209776; AAF19443.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
FT   NON_TER       1      1
FT   NON_TER      93     93
SQ   SEQUENCE   93 AA;  11323 MW;  BD561F18D34C0F28 CRC64;


  Query Match             20.6%;  Score 268.5;  DB 13;  Length 93;
  Best Local Similarity   49.5%;  Pred. No. 2.4e-20;
  Matches   48;  Conservative   18;  Mismatches   22;  Indels    9;  Gaps    2;

Qy     35 VYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRN 94
          |: | ||    :  ||| |::|||||:|||:| |        | |    |:|:|:||: :
Db      1 VFCNRSNPRFWQGEYTVAVSINDYLDVYCPYYES--------PQPHSRMERYILFMVNHD 52

Qy     95 GYRTC-NASQGFKRWECNRPHAPHSPIKFSEKFQRYS 130
          || || :  :|||||||||| :|  |::|||||||::
Db     53 GYLTCEHRMRGFKRWECNRPQSPDGPLRFSEKFQRFT 89


RESULT  10
O42304
ID   O42304      PRELIMINARY;      PRT;    80 AA.
AC   O42304;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN-A5 (FRAGMENT).
GN   EFNA5A.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   MacDonald R., Scholes J., Strahle U., Brennan C., Holder N., Brand M.,
RA   Wilson S.;
RT   "The Pax protein Noi protein is required for commissural axon pathway
RT   formation in the rostral forebrain.";
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Y12928; CAA73391.1; -.
DR   ZFIN; ZDB-GENE-001128-1; efna5a.
DR   InterPro; IPR001799; Ephrin.
```

```
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
FT   NON_TER       1      1
FT   NON_TER      80     80
SQ   SEQUENCE   80 AA;  9674 MW;  712DDC6058214993 CRC64;

  Query Match             19.0%;  Score 247.5;  DB 13;  Length 80;
  Best Local Similarity   51.2%;  Pred. No. 3.1e-18;
  Matches   44;  Conservative   16;  Mismatches   17;  Indels    9;  Gaps    2;

Qy     46 REGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQG 104
          |  | : | :|||||:|||||  :         |    |:||||||: :|| :| : ::|
Db      3 RGDYHIDVCINDYLDVYCPHYMDT--------VPEERTERYVLYMVNYDGYSSCDHTAKG 54

Qy    105 FKRWECNRPHAPHSPIKFSEKFQRYS 130
          ||||||||||:|: |:||||||| ::
Db     55 FKRWECNRPHSPNGPLKFSEKFQLFT 80


RESULT 11
Q9CRL3
ID   Q9CRL3      PRELIMINARY;      PRT;    42 AA.
AC   Q9CRL3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   12 DAYS EMBRYO EMBRYONIC BODY BETWEEN DIAPHRAGM REGION AND NECK CDNA,
DE   RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:9430025D14, FULL INSERT
DE   SEQUENCE (FRAGMENT).
GN   EFNA3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RC   TISSUE=EMBRYONIC BODY BETWEEN DIAPHRAGM REGION, AND NECK;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK020438; BAB32100.1; -.
DR   MGD; MGI:106644; Efna3.
FT   NON_TER       1      1
SQ   SEQUENCE   42 AA;  4569 MW;  55DB95E5E0B1B0E2 CRC64;

  Query Match             16.0%;  Score 208;  DB 11;  Length 42;
  Best Local Similarity   97.6%;  Pred. No. 1.7e-14;
  Matches   41;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    197 DFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
          |||||||||||||||||||||||||||||||||||||| |||
Db      1 DFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTLLAS 42
```

```
RESULT 12
Q90ZG7
ID   Q90ZG7      PRELIMINARY;      PRT;    70 AA.
AC   Q90ZG7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   D160 PROTEIN (FRAGMENT).
GN   D160.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
RT   "A systematic search for the downstream target genes of the midbrain-
RT   MHB reciprocal inductive signaling by ordered differential display
RT   revealed the expression of ephrin-A3 in the posterior tectum of
RT   zebrafish embryos.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB055674; BAB62805.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   70 AA;  7621 MW;  91F2BE4E657E10FD CRC64;

  Query Match             13.7%;  Score 178;  DB 13;  Length 70;
  Best Local Similarity   54.1%;  Pred. No. 4.4e-11;
  Matches   33;  Conservative   14;  Mismatches   12;  Indels    2;  Gaps    1;

Qy    166 CCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLA 225
          ||:: | | ::| || | :|: ||:||: |:|:  :||:||||||||||:|| |: | |
Db      1 CCSTASDSDDEPQPTEPDYTLRPNIKIDDLDDY--DNPEVPKLEKSISGSSPSRDRLLLT 58

Qy    226 V 226
          |
Db     59 V 59


RESULT 13
Q90Z31
ID   Q90Z31      PRELIMINARY;      PRT;   331 AA.
AC   Q90Z31;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN B3.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21290827; PubMed=11397014;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
RL   Dev. Biol. 234:470-482(2001).
DR   EMBL; AF375227; AAK64277.1; -.
SQ   SEQUENCE   331 AA;  35638 MW;  6A5EACD509A09818 CRC64;

  Query Match             12.8%;  Score 166.5;  DB 13;  Length 331;
  Best Local Similarity   26.8%;  Pred. No. 5e-09;
  Matches   70;  Conservative   28;  Mismatches   88;  Indels   75;  Gaps   12;

Qy      9 LLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67
          :||:  | || : |        |   :|||| |:    : || :   : | ||: ||  :
```

```
Db     12 ILLIFLVDLLGITAT-------NMEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSD 64

Qy     68 SSGVGPGAGPGPGGGA--EQYVLYMVSR-------------NGYRTCNASQGFKRWECNR 112
                   |||   |  | | ||:||              |   ||:
Db     65 P--------PGPRAPADYEYYKLYLVSSREQADRCEVTGAPNLLLTCD----------- 104

Qy    113 PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSH 172
             |:| ::|: ||| ||    |:||   |:|: |:| :         |:  ||
Db    105 --KPNSDMRFTIKFQEYSPNLWGHEFKTNHDYFIIAT-SDGTRQGLESMRGGVCAT---- 157

Qy    173 SGEKPVPTLPQFTMGPNVK---------INVLEDFEGE--NPQVPKLEKSISGTSPKREH 221
           | | |  : |   |   |         ||      |   :||:|       |:  :
Db    158 QGMKVVLKVGQSPYGLPAKSPKPDSAGRINNPNPGTGNSTHPQIPP-----RGSGGENGP 212

Qy    222 LP---------LAVGIAFFLM 233
          ||          | | || |:
Db    213 LPASNIAVIAGAAGGSAFLLL 233


RESULT 14
Q9PT69
ID   Q9PT69      PRELIMINARY;      PRT;   327 AA.
AC   Q9PT69;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN-B3 PRECURSOR.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYO;
RX   MEDLINE=20099673; PubMed=10633856;
RA   Helbling P.M., Saulnier D.M.E., Robinson V., Christiansen J.H.,
RA   Wilkinson D.G., Brandli A.W.;
RT   "Comparative analysis of embryonic gene expression defines potential
RT   interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";
RL   Dev. Dyn. 216:361-373(1999).
DR   EMBL; AJ236866; CAB65511.1; -.
DR   InterPro; IPR002086; Aldehyde_dehydr.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Signal.
FT   SIGNAL        1     24       POTENTIAL.
SQ   SEQUENCE   327 AA;  35913 MW;  4BB0FA39D4C22DCD CRC64;

  Query Match             12.6%;  Score 164.5;  DB 13;  Length 327;
  Best Local Similarity   26.6%;  Pred. No. 8e-09;
  Matches   63;  Conservative   31;  Mismatches   78;  Indels   65;  Gaps   13;

Qy     35 VYWNSSNQHLR-REGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMV-- 91
          :||||||:     ||| :   : | ||: ||           ||      | | ||:|
Db     30 IYWNSSNKRFEDTEGYVLYPQIGDRLDLLCPRSEPQ------GPFSSSPYEYYKLYLVGT 83

Qy     92 -----SRNGYRTCNASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYY 146
               | :  || |         |:|   |   ::|: ||| :|    |:|| :  :||
Db     84 KEEMSSCSILRTPNL-----LLTCDR---PSQDLRFTIKFQEFSPNLWGHEFQSQRDYYI 135

Qy    147 ISTPTHNL-----------HWKCLRMKVFVCCASTSHSGEKPVPTLPQFT-----MGPNV 190
          |:|    :             | ::: : |     | :|  | |  |        : |:|
Db    136 IATSDGTMDGIETLQGGVCETKGMKVTLKV---GQSPNGATP-PRRPSSAGKDSGISPSV 191

Qy    191 KINVLEDFEGENPQVPKLEKSISGTSPKR--------EHLPL----AVGIAFFLMTF 235
                     || :| : :: || : |          |:||    | | |  |: |
Db    192 ----------PNPDIPNVGET-SGNATKTGENGPLPISHVPLVAGAAGGAALLLLVF 237
```

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RESULT 15
Q9PUJ4
ID   Q9PUJ4      PRELIMINARY;      PRT;   333 AA.
AC   Q9PUJ4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   EPHRIN-B2 PRECURSOR.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Menzel P., Pasquale E.B.;
RT   "Coding sequence of chicken ephrin-B2.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF180729; AAD53948.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Signal.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    333       EPHRIN-B2.
SQ   SEQUENCE   333 AA;  36761 MW;  4C28E8CB211B7783 CRC64;

  Query Match             12.5%;  Score 162.5;  DB 13;  Length 333;
  Best Local Similarity   27.1%;  Pred. No. 1.3e-08;
  Matches   61;  Conservative   29;  Mismatches   92;  Indels   43;  Gaps    9;

Qy     35 VYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSR 93
          :|||||| : |  :|  :   : | ||| ||  :|  ||           | | :||| :
Db     35 IYWNSSNPKFLPGQGLVLYPQIGDKLDIICPKVDSKTVGQ---------YEYYKVYMVDK 85

Qy     94 NGYRTCNASQGFKRWECNRP----HAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIST 149
          :   :|   :       | |      |   :||: ||| :|    | ||    :|| |||
Db     86 DQADSCAIRKD------NTPLLNCAKPDQDVKFTIKFQEFSPNLWGLEFQKNKDYYVIST 139

Qy    150 PTHNLH---------WKCLRMKVFVCCASTSHSGEKPVPT----LPQFTMGPNVKINV-- 194
             :|           :   ||: :      :|   |  |     |:   | | | :
Db    140 SNGSLEGLNNQEGGVCQTKTMKILMKVGQDPNSAGLPRSTDPTKRPEQEAGTNGKSSTTS 199

Qy    195 --LEDFEGENPQVPKL-EKSISGTSPKREHLPLAVGIAFFLMTFL 236
            ::|  | :    |    || |:      : |  |||   : |:
Db    200 PFVKDHSGSSTDGSKAGHSSILGS-----EVALFAGIASGCIIFI 239


Search completed: September 28, 2002, 01:47:36
Job time: 641 sec
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                GenCore version 4.5
        Copyright (c) 1993 - 2000  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         September 27, 2002, 22:47:01 ; Search time 2277.04 Seconds
                                                (without alignments)
                                                5844.991 Million cell updates/sec

Title:          US-09-904-954-3
Perfect score:  636
Sequence:       1 GCCAGACCAAACCGGACCTC..........TTCTGCGAATTCTGTGAGCC 636

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters:      3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      GenEmbl:*
               1:  gb_ba:*
               2:  gb_htg:*
               3:  gb_in:*
               4:  gb_om:*
               5:  gb_ov:*
               6:  gb_pat:*
               7:  gb_ph:*
               8:  gb_pl:*
               9:  gb_pr:*
               10:  gb_ro:*
               11:  gb_sts:*
               12:  gb_sy:*
               13:  gb_un:*
               14:  gb_vi:*
               15:  em_ba:*
               16:  em_fun:*
               17:  em_hum:*
               18:  em_in:*
               19:  em_mu:*
               20:  em_om:*
               21:  em_or:*
               22:  em_ov:*
               23:  em_pat:*
               24:  em_ph:*
               25:  em_pl:*
               26:  em_ro:*
               27:  em_sts:*
               28:  em_un:*
               29:  em_vi:*
               30:  em_htg_hum:*
               31:  em_htg_inv:*
               32:  em_htg_other:*
               33:  em_htgo_inv:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                 SUMMARIES

                 %
Result           Query
  No.   Score    Match Length DB  ID                        Description
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      1     636  100.0     636  6  AR001065                 AR001065 Sequence
      2     636  100.0     636  6  AR080872                 AR080872 Sequence
      3     636  100.0     636  6  AR164470                 AR164470 Sequence
      4     636  100.0     636  6  I20810                   I20810 Sequence 3
      5     636  100.0     636  9  HSU14188                 U14188 Human recep
      6     636  100.0    1181  9  HSA6352                  AJ006352 Homo sapi
      7     497   78.1    1036  9  HSA6353                  AJ006353 Homo sapi
      8   419.2   65.9     813 10   MMU90663                 U90663 Mus musculu
      9   288.6   45.4  175826  2  AC021890                 AC021890 Homo sapi
     10   204.8   32.2   95907  2  AC098750                 AC098750 Rattus no
     11   203.2   31.9    3226 10   MM4LK02                  U92890 Mus musculu
c    12   203.2   31.9  289579  2  AC104632                 AC104632 Mus muscu
c    13   203.2   31.9  326750  2  AC104327                 AC104327 Mus muscu
     14   149.8   23.6     981  5  AF317286                 AF317286 Gallus ga
     15   121.6   19.1     783  6  AR023765                 AR023765 Sequence
     16   120.6   19.0     665  5  CHKELF1LIG               L40932 Gallus gall
     17   117.2   18.4     650 10   MM4LK01                  U92889 Mus musculu
     18   117.2   18.4  289579  2  AC104632                 AC104632 Mus muscu
     19   115.4   18.1     758  9  HUMEFL2                  L37360 Homo sapien
     20   115.4   18.1    1070  6  AR004292                 AR004292 Sequence
c    21   114.6   18.0   95907  2  AC098750                 AC098750 Rattus no
     22   112.6   17.7     799  5  GDRNARAGS                X90377 G.domesticu
     23   103.4   16.3     987  9  HSU14187                 U14187 Human recep
     24   103.4   16.3    1037  6  AR001064                 AR001064 Sequence
     25   103.4   16.3    1037  6  AR080871                 AR080871 Sequence
     26   103.4   16.3    1037  6  AR164469                 AR164469 Sequence
     27   103.4   16.3    1037  6  I20809                   I20809 Sequence 1
     28   103.4   16.3    1769  9  BC017722                 BC017722 Homo sapi
     29   101.8   16.0    1480  6  AR048795                 AR048795 Sequence
     30   101.8   16.0    1480  6  AR103236                 AR103236 Sequence
     31   101.8   16.0    1480  6  I56902                   I56902 Sequence 11
     32   101.8   16.0    1480  6  I88172                   I88172 Sequence 11
     33   101.8   16.0    1480  9  HUMB61                   M57730 Human B61 m
     34   101.8   16.0    1496  6  AX055732                 AX055732 Sequence
     35   101.8   16.0    1496  6  AX201360                 AX201360 Sequence
     36   101.8   16.0    1498  6  I34756                   I34756 Sequence 1
     37   101.8   16.0    1498  6  I74360                   I74360 Sequence 1
     38   100.4   15.8     958 10   MMU26188                 U26188 Mus musculu
     39   100.4   15.8    1466 10   BC002046                 BC002046 Mus muscu
     40   100.2   15.8     741 10   MMU90662                 U90662 Mus musculu
     41   100.2   15.8    1925  9  AK057845                 AK057845 Homo sapi
     42     100   15.7    2272  5  DRTKLELF1                Y09668 D.rerio mRN
     43      99   15.6    1650  5  DRTKRAL1                 Y09669 D.rerio mRN
     44    98.6   15.5     649 10   MUSMB61B                 D38146 Mouse B61 m
     45    97.2   15.3     439  6  AX210445                 AX210445 Sequence


                             ALIGNMENTS


RESULT   1
AR001065
LOCUS       AR001065                 636 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5738844.
ACCESSION   AR001065
VERSION     AR001065.1  GI:3963132
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 636)
  AUTHORS   Beckmann,M.Patricia. and Cerretti,D.P.
  TITLE     Cytokines that bind the cell surface receptor hek
  JOURNAL   Patent: US 5738844-A 3 14-APR-1998;
FEATURES             Location/Qualifiers
     source          1..636
                     /organism="unknown"
BASE COUNT      102 a    202 c    186 g    146 t
ORIGIN


  Query Match             100.0%;  Score 636;  DB 6;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 2e-125;
```

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  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60

Qy       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
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Db       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120

Qy      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
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Db      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180

Qy      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
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Db      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240

Qy      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
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Db      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300

Qy      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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Db      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360

Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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Db      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420

Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
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Db      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480

Qy      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
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Db      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540

Qy      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
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Db      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600

Qy      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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Db      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636


RESULT   2
AR080872
LOCUS       AR080872                 636 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 3 from patent US 5969110.
ACCESSION   AR080872
VERSION     AR080872.1  GI:10007601
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 636)
  AUTHORS   Beckmann,M.Patricia. and Cerretti,D.P.
  TITLE     Antibodies that bind hek ligands
  JOURNAL   Patent: US 5969110-A 3 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1..636
                     /organism="unknown"
BASE COUNT      102 a    202 c    186 g    146 t
ORIGIN


  Query Match             100.0%;  Score 636;  DB 6;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 2e-125;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Qy       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
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Db       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120

Qy      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
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Db      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180

Qy      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
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Qy      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
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Db      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300

Qy      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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Db      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360

Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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Db      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420

Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
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Db      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480

Qy      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
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Db      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540

Qy      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
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Db      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600

Qy      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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Db      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636


RESULT   3
AR164470
LOCUS       AR164470                 636 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 3 from patent US 6274117.
ACCESSION   AR164470
VERSION     AR164470.1  GI:16237510
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 636)
  AUTHORS   Beckmann,M.Patricia and Cerretti,D.P.
  TITLE     Cytokines that bind the cell surface receptor Hek
  JOURNAL   Patent: US 6274117-A 3 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1..636
                     /organism="unknown"
BASE COUNT      102 a    202 c    186 g    146 t
ORIGIN


  Query Match             100.0%;  Score 636;  DB 6;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 2e-125;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Qy       61 TGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
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Db       61 TGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120

Qy      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
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Db      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180

Qy      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240

Qy      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300

Qy      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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Db      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360

Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420

Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
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Db      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480

Qy      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
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Db      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540

Qy      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
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Db      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600

Qy      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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Db      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636


RESULT    4
I20810
LOCUS       I20810                   636 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 3 from patent US 5516658.
ACCESSION   I20810
VERSION     I20810.1  GI:1601165
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 636)
  AUTHORS   Beckmann,M.Patricia. and Cerretti,D.P.
  TITLE     DNA encoding cytokines that bind the cell surface receptor hek
  JOURNAL   Patent: US 5516658-A 3 14-MAY-1996;
FEATURES             Location/Qualifiers
     source          1..636
                     /organism="unknown"
BASE COUNT      102 a    202 c    186 g    146 t
ORIGIN


  Query Match             100.0%;  Score 636;  DB 6;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 2e-125;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60

Qy       61 TGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
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Qy      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
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Db      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180

Qy      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240

Qy      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
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Db      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300

Qy      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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Db      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360

Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420

Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
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Db      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480

Qy      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
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Db      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540

Qy      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
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Db      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600

Qy      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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Db      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636


RESULT    5
HSU14188
LOCUS       HSU14188                 636 bp    mRNA    linear   PRI 04-FEB-1995
DEFINITION  Human receptor tyrosine kinase LERK-4 (EPLG4) mRNA, complete cds.
ACCESSION   U14188
VERSION     U14188.1  GI:642834
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 636)
  AUTHORS   Kozlosky,C.J., Maraskovsky,E., McGrew,J.T., VandenBos,T., Teepe,M.,
            Lyman,S.D., Srinivasan,S., Fletcher,F.A., Gayle,R.B. III,
            Cerretti,D.P. and Beckmann,M.P.
  TITLE     Ligands for the receptor tyrosine kinases hek and elk: isolation of
            cDNAs encoding a family of proteins
  JOURNAL   Oncogene 10 (2), 299-306 (1995)
  MEDLINE   95140419
REFERENCE   2  (bases 1 to 636)
  AUTHORS   Cerretti,D.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1994) Immunex Corp., 51 University St., Seattle,
            WA 98101, USA
FEATURES             Location/Qualifiers
     source          1..636
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                     /db_xref="taxon:9606"
     gene            1..636
                     /gene="EPLG4"
     CDS             28..633
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                     /note="membrane-bound protein;
                     glycosyl-phosphatidylinositol (GPI) anchored"
                     /codon_start=1
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                     /product="LERK-4"
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                     VVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLP
                     FGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSES
                     AHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLILRLLRIL"
     sig_peptide     28..93
                     /gene="EPLG4"
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     mat_peptide     94..630
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BASE COUNT      102 a    202 c    186 g    146 t
ORIGIN

  Query Match            100.0%;  Score 636;  DB 9;  Length 636;
  Best Local Similarity  100.0%;  Pred. No. 2e-125;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db          1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60

Qy         61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120

Qy        121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180

Qy        181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240

Qy        241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
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Db        241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300

Qy        301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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Db        301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360

Qy        361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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Db        361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420

Qy        421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
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Db        421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480

Qy        481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
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Db        481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540

Qy        541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
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Db        541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600

Qy        601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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Db        601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636


RESULT 6
HSA6352
LOCUS       HSA6352                 1181 bp    mRNA    linear   PRI 02-NOV-1998
DEFINITION  Homo sapiens mRNA for ephrin-A4 protein, membrane bound form.
ACCESSION   AJ006352
VERSION     AJ006352.1  GI:3821234
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KEYWORDS    ephrin-A4 gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1181)
  AUTHORS   Aasheim,H.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAY-1998) Aasheim H.C., Department of Immunology, The
            Norwegian Radium Hospital, Montebello, 0310 n-Oslo, NORWAY
REFERENCE   2  (bases 1 to 1181)
  AUTHORS   Aasheim,H.C., Munthe,E., Funderud,S., Smeland,E., Beiske,K. and
            Logtenberg,T.
  TITLE     Identification and characterization of a putative secreted splice
            variants of the ephrin-A4 (Lerk-4) ligand for Eph receptor tyrosine
            kinases expressed in cells of the B cell lineage
  JOURNAL   Unpublished
FEATURES             Location/Qualifiers
     source          1..1181
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                     /tissue_lib="Reh cDNA library"
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     gene            28..633
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     CDS             28..633
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                     /function="ephrin-A4 protein, membrane bound form"
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                     /evidence=experimental
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BASE COUNT      234 a    353 c    331 g    263 t
ORIGIN


  Query Match            100.0%;  Score 636;  DB 9;  Length 1181;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-125;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60

Qy         61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120

Qy        121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
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Db        121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180

Qy        181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
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Db        181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240

Qy        241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
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Db        241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300

Qy        301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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Db        301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360

Qy        361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420

Qy     421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
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Db     421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480

Qy     481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
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Qy     541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
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Qy     601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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Db     601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636


RESULT   7
HSA6353
LOCUS       HSA6353                 1036 bp    mRNA    linear   PRI 02-NOV-1998
DEFINITION  Homo sapiens mRNA for ephrin-A4 protein, soluble form.
ACCESSION   AJ006353
VERSION     AJ006353.1  GI:3821236
KEYWORDS    ephrin-A4 gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1036)
  AUTHORS   Aasheim,H.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAY-1998) Aasheim H.C., Department of Immunology, The
            Norwegian Radium Hospital, Montebello, 0310 n-Oslo, NORWAY
REFERENCE   2  (bases 1 to 1036)
  AUTHORS   Aasheim,H.C., Munthe,E., Funderud,S., Smeland,E., Beiske,K. and
            Logtenberg,T.
  TITLE     Identification and characterization of a putative secreted splice
            variants of the ephrin-A4 (Lerk-4) ligand for Eph receptor tyrosine
            kinases expressed in cells of the B cell lineage
  JOURNAL   Unpublished
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                     /note="leukemia"
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     CDS             28. .609
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                     /function="ephrin-A4 protein, soluble form"
                     /codon_start=1
                     /evidence=experimental
                     /protein_id="CAA06993.1"
                     /db_xref="GI:3821237"
                     /translation="MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDA
                     VVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLP
                     FGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERNLPS
                     HPKEPESSQDPLEEEGSLLPALGVPIQTDKMEH"
BASE COUNT      210 a    312 c    289 g    225 t
ORIGIN


  Query Match             78.1%;  Score 497;  DB 9;  Length 1036;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-96;
  Matches  497;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db       1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60

Qy      61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120

Qy     121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180

Qy     181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240

Qy     241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
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Db     241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300

Qy     301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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Qy     361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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Qy     421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
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Db     421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480

Qy     481 TGCTGCAAGGAGAGGAA 497
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Db     481 TGCTGCAAGGAGAGGAA 497


RESULT  .8
MMU90663
LOCUS       MMU90663                 813 bp    mRNA    linear   ROD 25-MAR-1997
DEFINITION  Mus musculus ligand LERK-4 mRNA, complete cds.
ACCESSION   U90663
VERSION     U90663.1  GI:1906016
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 813)
  AUTHORS   Flenniken,A.M., Gale,N.W., Yancopoulos,G.D. and Wilkinson,D.G.
  TITLE     Distinct and overlapping expression patterns of ligands for
            Eph-related receptor tyrosine kinases during mouse embryogenesis
  JOURNAL   Dev. Biol. 179 (2), 382-401 (1996)
  MEDLINE   97060319
REFERENCE   2  (bases 1 to 813)
  AUTHORS   Flenniken,A.M. and Wilkinson,D.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-1997) Developmental Neurobiology, National
            Institute for Medical Research, The Ridgeway, London NW7 1AA,
            England
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
     CDS             25. .699
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                     /codon_start=1
                     /product="ligand LERK-4"
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                     /db_xref="GI:1906017"
                     /translation="MLLRLGLIYPPTRPPAPPGPLVPLLRTVLWAALLGSRLPGCSSL
                     RHPIYWNSSNPRLLRGDAVVELGFNDYLDIFCPHYESPGPPEGPETFALYMVDWSGYE
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                SPGRCLRLQVSVCCKESGSSHESAHPVGSPGESGTSGWRGGHAPSPLCLLLLLLLPIL
                RLLRVL"
BASE COUNT      151 a    262 c    225 g    175 t
ORIGIN


  Query Match            65.9%;  Score 419.2;  DB 10;  Length 813;
  Best Local Similarity  81.9%;  Pred. No. 2.7e-79;
  Matches  513;  Conservative    0;  Mismatches   98;  Indels   15;  Gaps    2;

Qy     26 CGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCTCGGCTCCCCTC 85
          ||   | |||| | ||||||||||||||||| |||||||||||| | |||||||| |  |
Db     77 CGGGCCCGCTGGTTCCCCTGCTGCGGACTGTGCTCTGGGCCGCGCTGCTCGGCTCGCGCC 136

Qy     86 TGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAACCCCAGGTTGC 145
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Db    137 TGCCGGGGTGCTCCAGCCTCCGCCACCCAATCTACTGGAACTCCTCTAACCCCAGGTTGC 196

Qy    146 TTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCC 205
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Db    197 TCCGAGGAGATGCCGTGGTGGAGCTGGGCTTCAACGATTACCTAGACATCTTCTGCCCAC 256

Qy    206 ACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACT 265
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Db    257 ATTATGAAAGCCCAGGGCCCCCAGAAGGCCCGGAAACCTTTGCATTATACATGGTGGACT 316

Qy    266 GGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCT 325
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Db    317 GGTCAGGCTACGAGGCCTGCACGGCAGAGGGGGCAAATGCCTTCCAGCGCTGGAATTGCT 376

Qy    326 CCCTGCCCTTTG---------GCCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACAC 376
          |  |||| ||||         ||| ||||| ||||||||| ||||||||||||| |||||
Db    377 CGATGCCTTTTGCCCCTTTCAGCCCTGTTCGATTCTCAGAAAAGATTCAGCGCTACACAC 436

Qy    377 CTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGTGCCCA 436
          | ||| | || |||||||||||||| |||||||||||||||||||||||||||||||| |
Db    437 CCTTCCCGCTGGGCTTTGAGTTCTTGCCTGGAGAGACTTACTACTACATCTCGGTGCCGA 496

Qy    437 CTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGGAGAGGA 496
          |||| |||||| |||||| |||| |||| |||||||||||||||||||||||||||||
Db    497 CTCCGGAGAGTCCTGGCCGGTGCCTGAGACTCCAGGTGTCTGTCTGCTGCAAGGAGAGCG 556

Qy    497 AGTC------TGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGCACATCAGGGT 550
           |||      ||||||||| |||||||||||||| |||||||| || || || || ||||
Db    557 GGTCATCACATGAGTCAGCTCATCCTGTTGGGAGTCCTGGAGAAAGCGGTACGTCCGGGT 616

Qy    551 GGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTGCTTCTGATTC 610
          |||| || ||  || | ||||||||||| |||||||||||  | |||||||| |  || |
Db    617 GGCGGGGAGGACACGCGCCCAGCCCCCTGTGTCTCTTGCTGCTGCTGCTGCTCCCAATCC 676

Qy    611 TTCGTCTTCTGCGAATTCTGTGAGCC 636
          | ||||| ||| || |||||||||||
Db    677 TCCGTCTCCTGAGAGTTCTGTGAGCC 702


RESULT   9
AC021890
LOCUS       AC021890             175826 bp    DNA     linear   HTG 10-NOV-2000
DEFINITION  Homo sapiens chromosome 3 clone RP11-498A2, WORKING DRAFT SEQUENCE,
            22 unordered pieces.
ACCESSION   AC021890
VERSION     AC021890.12  GI:11128300
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 175826)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
            Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
            Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
            Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
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            Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
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            Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
            Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
            Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
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            Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
            Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
            and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 175826)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JAN-2000) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 9, 2000 this sequence version replaced gi:9719697.
            ------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            ------------- Project Information
                Center project name: HMZE
                Center clone name: RP11-498A2
            ------------- Summary Statistics
                Sequencing vector: M13; L08821
                Chemistry: Dye-terminator Big Dye: 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 144734 bases at least Q40
                Consensus quality: 162873 bases at least Q30
                Consensus quality: 169424 bases at least Q20
                Estimated insert size: 170770; sum-of-contigs estimation
                Quality coverage: 0x in Q20 bases; agarose-fp estimation
                Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation
            -------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 22 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1   21031: contig of 21031 bp in length
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        *     21132     40475: contig of 19344 bp in length
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        *     40576     57617: contig of 17042 bp in length
        *     57618     57717: gap of unknown length
        *     57718     75708: contig of 17991 bp in length
        *     75709     75808: gap of unknown length
        *     75809     89018: contig of 13210 bp in length
        *     89019     89118: gap of unknown length
        *     89119    100348: contig of 11230 bp in length
        *    100349    100448: gap of unknown length
        *    100449    110704: contig of 10256 bp in length
        *    110705    110804: gap of unknown length
        *    110805    123156: contig of 12352 bp in length
        *    123157    123256: gap of unknown length
        *    123257    132467: contig of 9211 bp in length
        *    132468    132567: gap of unknown length
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        *    169968    171580: contig of 1613 bp in length
        *    171581    171680: gap of unknown length
        *    171681    172882: contig of 1202 bp in length
        *    172883    172982: gap of unknown length
        *    172983    174431: contig of 1449 bp in length
        *    174432    174531: gap of unknown length
        *    174532    175826: contig of 1295 bp in length.
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                     /db_xref="taxon:9606"
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                     /clone="RP11-498A2"
BASE COUNT    39638 a  46653 c  47059 g  40343 t   2133 others
ORIGIN


  Query Match             45.4%;  Score 288.6;  DB 2;  Length 175826;
  Best Local Similarity   98.6%;  Pred. No. 6.1e-52;
  Matches  291;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      138 CAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGT 197
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Qy      198 CTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACAT 257
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Qy      258 GGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTG 317
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Db   115530 GGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTG 115589

Qy      318 GGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACC 377
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Qy      378 TTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGTG 432
             |||||||||||||||||||||||||||||||||||||||||||||||||  | |
Db   115650 CTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTGTGAG 115704


RESULT 10
AC098750
LOCUS       AC098750               95907 bp    DNA     linear   HTG 21-DEC-2001
DEFINITION  Rattus norvegicus clone CH230-54E23, *** SEQUENCING IN PROGRESS
            ***, 50 unordered pieces.
ACCESSION   AC098750
VERSION     AC098750.2  GI:17975664
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 95907)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
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            Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 95907)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Dec 21, 2001 this sequence version replaced gi:16572779.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GGKA
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    Center clone name: CH230-54E23
-------------- Summary Statistics
    Assembly program: Phrap; version 0.990329First call to
findPhrapList
    Consensus quality: 73847 bases at least Q40
    Consensus quality: 80027 bases at least Q30
    Consensus quality: 84314 bases at least Q20
    Estimated insert size: 73738; sum-of-contigs estimation
    Quality coverage: 0x in Q20 bases; agarose-fp estimation
    Quality coverage: 0.8x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
*   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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ORIGIN


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Qy    246 TGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGC 305
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Qy    306 CTACAAGCGCTGGGTGTGCTCCCT---------GCCCTTTGGCCATGTTCAATTCTCAGA 356
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Qy    417 CTACTACATCTCGGTG 432
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DEFINITION  Mus musculus LERK-4 (Epl4) gene, exons 2, 3, 4, and complete cds.
ACCESSION   U92890
VERSION     U92890.1  GI:2843101
KEYWORDS    .
SEGMENT     2 of 2
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3226)
  AUTHORS   Cerretti,D.P. and Nelson,N.
  TITLE     Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
            mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
            conservation of intron/exon structure
  JOURNAL   Genomics 47 (1), 131-135 (1998)
  MEDLINE   98126446
REFERENCE   2  (bases 1 to 3226)
  AUTHORS   Cerretti,D.P. and Nelson,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-MAR-1997) Molecular Biology, Immunex Corp., 51
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BASE COUNT      768 a    793 c    921 g    744 t
ORIGIN


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  Best Local Similarity   80.4%;  Pred. No. 2e-33;
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Db   1306 CCCTTGTGCCCACAGGTTGCTCCGAGGAGATGCCGTGGTGGAGCTGGGCTTCAACGATTA 1365

Qy    186 CCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTT 245
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Qy    246 TGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGC 305
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          || | ||||||||   |||||  |||| ||||         ||| ||||| |||||||||
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Qy    417 CTACTACATCTCGGTG 432
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RESULT  12
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LOCUS       AC104632              289579 bp    DNA     linear   HTG 29-DEC-2001
DEFINITION  Mus musculus clone rp23-368d24 strain C57BL/6J, WORKING DRAFT
            SEQUENCE, 72 unordered pieces.
ACCESSION   AC104632
VERSION     AC104632.2  GI:17998594
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 289579)
  AUTHORS   Hua,A. and Roe,B.A.
  TITLE     Mus musculus BAC Clone rp23-368d24
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 289579)
  AUTHORS   Hua,A. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-DEC-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT     On Dec 29, 2001 this sequence version replaced gi:17861055.
            ------------- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            ----------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 72 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
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      *    38833     40937: contig of 2105 bp in length
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      *    62046     65116: contig of 3071 bp in length
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      *    65217     67626: contig of 2410 bp in length
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             *   192069    192168: gap of unknown length
             *   192169    198394: contig of 6226 bp in length
             *   198395    198494: gap of unknown length
             *   198495    203084: contig of 4590 bp in length
             *   203085    203184: gap of unknown length
             *   203185    208688: contig of 5504 bp in length
             *   208689    208788: gap of unknown length
             *   208789    214457: contig of 5669 bp in length
             *   214458    214557: gap of unknown length
             *   214558    219456: contig of 4899 bp in length
             *   219457    219556: gap of unknown length
             *   219557    226019: contig of 6463 bp in length
             *   226020    226119: gap of unknown length
             *   226120    234001: contig of 7882 bp in length
             *   234002    234101: gap of unknown length
             *   234102    241499: contig of 7398 bp in length
             *   241500    241599: gap of unknown length
             *   241600    249134: contig of 7535 bp in length
             *   249135    249234: gap of unknown length
             *   249235    259781: contig of 10547 bp in length
             *   259782    259881: gap of unknown length
             *   259882    267444: contig of 7563 bp in length
             *   267445    267544: gap of unknown length
             *   267545    279432: contig of 11888 bp in length
             *   279433    279532: gap of unknown length
             *   279533    289579: contig of 10047 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="rp23-368d24"
                     /clone_lib="RPCI mouse BAC library 23"
BASE COUNT    70974 a  71815 c  70765 g  68626 t   7399 others
ORIGIN

  Query Match            31.9%;  Score 203.2;  DB 2;  Length 289579;
  Best Local Similarity   80.4%;  Pred. No. 8.4e-34;
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  Matches  254;  Conservative    0;  Mismatches   53;  Indels    9;  Gaps    1;

Qy     126 CTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTA 185
           | |  ||  || ||||||||| |||||||| |||||||||||||||||| ||||||||||
Db  216942 CCCTTGTGCCCACAGGTTGCTCCGAGGAGATGCCGTGGTGGAGCTGGGCTTCAACGATTA 216883

Qy     186 CCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTT 245
           |||||||||  ||||||| || || ||| ||||||||||||| || ||||| ||  | ||
Db  216882 CCTAGACATCTTCTGCCCACATTATGAAAGCCCAGGGCCCCCAGAAGGCCCGGAAACCTT 216823

Qy     246 TGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGC 305
           ||| || ||||||||||||||| ||||||| ||| |||||  |||||||||  |    ||
Db  216822 TGCATTATACATGGTGGACTGGTCAGGCTACGAGGCCTGCACGGCAGAGGGGGCAAATGC 216763

Qy     306 CTACAAGCGCTGGGTGTGCTCCCTGCCCTTTG---------GCCATGTTCAATTCTCAGA 356
           || | ||||||||   |||||  |||| ||||         ||| ||||| |||||||||
Db  216762 CTTCCAGCGCTGGAATTGCTCGATGCCTTTTGCCCCTTTCAGCCCTGTTCGATTCTCAGA 216703

Qy     357 GAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTA 416
            ||||||||||||| |||||| ||| | || |||||||||||||| ||||||||||||||
Db  216702 AAAGATTCAGCGCTACACACCCTTCCCGCTGGGCTTTGAGTTCTTGCCTGGAGAGACTTA 216643

Qy     417 CTACTACATCTCGGTG 432
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Db  216642 CTACTACATCTGTGAG 216627


RESULT 13
AC104327/c
LOCUS       AC104327               326750 bp    DNA     linear   HTG 24-DEC-2001
DEFINITION  Mus musculus clone rp23-295a4 strain C57BL/6J, WORKING DRAFT
            SEQUENCE, 66 unordered pieces.
ACCESSION   AC104327
VERSION     AC104327.2  GI:17978117
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 326750)
  AUTHORS   Hua,A. and Roe,B.A.
  TITLE     Mus musculus BAC Clone rp23-295a4
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 326750)
  AUTHORS   Hua,A. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT     On Dec 24, 2001 this sequence version replaced gi:17439220.
            ------------- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            ----------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 66 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2180: contig of 2180 bp in length
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            *     2281     4455: contig of 2175 bp in length
            *     4456     4555: gap of unknown length
            *     4556     7347: contig of 2792 bp in length
            *     7348     7447: gap of unknown length
            *     7448    10057: contig of 2610 bp in length
            *    10058    10157: gap of unknown length
            *    10158    12254: contig of 2097 bp in length
            *    12255    12354: gap of unknown length
            *    12355    14417: contig of 2063 bp in length
            *    14418    14517: gap of unknown length
            *    14518    18079: contig of 3562 bp in length
            *    18080    18179: gap of unknown length
            *    18180    20239: contig of 2060 bp in length
            *    20240    20339: gap of unknown length
            *    20340    22342: contig of 2003 bp in length
            *    22343    22442: gap of unknown length
            *    22443    24502: contig of 2060 bp in length
            *    24503    24602: gap of unknown length
            *    24603    26620: contig of 2018 bp in length
            *    26621    26720: gap of unknown length
            *    26721    30776: contig of 4056 bp in length
            *    30777    30876: gap of unknown length
            *    30877    33188: contig of 2312 bp in length
            *    33189    33288: gap of unknown length
            *    33289    36016: contig of 2728 bp in length
            *    36017    36116: gap of unknown length
            *    36117    38176: contig of 2060 bp in length
            *    38177    38276: gap of unknown length
            *    38277    40782: contig of 2506 bp in length
            *    40783    40882: gap of unknown length
            *    40883    43672: contig of 2790 bp in length
            *    43673    43772: gap of unknown length
            *    43773    46580: contig of 2808 bp in length
            *    46581    46680: gap of unknown length
            *    46681    49679: contig of 2999 bp in length
            *    49680    49779: gap of unknown length
            *    49780    52528: contig of 2749 bp in length
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            *    52629    56785: contig of 4157 bp in length
            *    56786    56885: gap of unknown length
            *    56886    59118: contig of 2233 bp in length
            *    59119    59218: gap of unknown length
            *    59219    62964: contig of 3746 bp in length
            *    62965    63064: gap of unknown length
            *    63065    65910: contig of 2846 bp in length
            *    65911    66010: gap of unknown length
            *    66011    69396: contig of 3386 bp in length
            *    69397    69496: gap of unknown length
            *    69497    72554: contig of 3058 bp in length
            *    72555    72654: gap of unknown length
            *    72655    75720: contig of 3066 bp in length
            *    75721    75820: gap of unknown length
            *    75821    79364: contig of 3544 bp in length
            *    79365    79464: gap of unknown length
            *    79465    82599: contig of 3135 bp in length
            *    82600    82699: gap of unknown length
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            *    85398    89123: contig of 3726 bp in length
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            *    89224    92441: contig of 3218 bp in length
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            *    92542    95856: contig of 3315 bp in length
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            *   103890   109457: contig of 5568 bp in length
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            *   109558   114011: contig of 4454 bp in length
            *   114012   114111: gap of unknown length
            *   114112   118651: contig of 4540 bp in length
            *   118652   118751: gap of unknown length
            *   118752   123608: contig of 4857 bp in length
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            *   123709   127713: contig of 4005 bp in length
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            *     155420     159447: contig of 4028 bp in length
            *     159448     159547: gap of unknown length
            *     159548     163961: contig of 4414 bp in length
            *     163962     164061: gap of unknown length
            *     164062     169232: contig of 5171 bp in length
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            *     169333     173172: contig of 3840 bp in length
            *     173173     173272: gap of unknown length
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            *     179081     188181: contig of 9101 bp in length
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            *     188282     192848: contig of 4567 bp in length
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            *     210383     218415: contig of 8033 bp in length
            *     218416     218515: gap of unknown length
            *     218516     226120: contig of 7605 bp in length
            *     226121     226220: gap of unknown length
            *     226221     236580: contig of 10360 bp in length
            *     236581     236680: gap of unknown length
            *     236681     245273: contig of 8593 bp in length
            *     245274     245373: gap of unknown length
            *     245374     256115: contig of 10742 bp in length
            *     256116     256215: gap of unknown length
            *     256216     264078: contig of 7863 bp in length
            *     264079     264178: gap of unknown length
            *     264179     273637: contig of 9459 bp in length
            *     273638     273737: gap of unknown length
            *     273738     295230: contig of 21493 bp in length
            *     295231     295330: gap of unknown length
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                     /strain="C57BL/6J"
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                     /clone="rp23-295a4"
                     /clone_lib="RPCI mouse BAC library 23"
BASE COUNT    79344 a  80488 c  78974 g  81219 t   6725 others
ORIGIN


  Query Match             31.9%;  Score 203.2;  DB 2;  Length 326750;
  Best Local Similarity   80.4%;  Pred. No. 8.2e-34;
  Matches  254;  Conservative    0;  Mismatches   53;  Indels    9;  Gaps    1;

Qy    126 CTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTA 185
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Qy    186 CCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTT 245
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Db  38898 CCTAGACATCTTCTGCCCACATTATGAAAGCCCAGGGCCCCCAGAAGGCCCGGAAACCTT 38839

Qy    246 TGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGC 305
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Db  38838 TGCATTATACATGGTGGACTGGTCAGGCTACGAGGCCTGCACGGCAGAGGGGGCAAATGC 38779

Qy    306 CTACAAGCGCTGGGTGTGCTCCCTGCCCTTTG---------GCCATGTTCAATTCTCAGA 356
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Db  38778 CTTCCAGCGCTGGAATTGCTCGATGCCTTTTGCCCCTTTCAGCCCTGTTCGATTCTCAGA 38719

Qy    357 GAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTA 416
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Db  38718 AAAGATTCAGCGCTACACACCCTTCCCGCTGGGCTTTGAGTTCTTGCCTGGAGAGACTTA 38659

Qy    417 CTACTACATCTCGGTG 432
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Db  38658 CTACTACATCTGTGAG 38643


RESULT  14
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LOCUS       AF317286                 981 bp    mRNA    linear   VRT 02-FEB-2001
DEFINITION  Gallus gallus ephrin-A6 mRNA, partial cds.
ACCESSION   AF317286
VERSION     AF317286.1  GI:12656587
KEYWORDS    .
SOURCE      chicken.
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 981)
  AUTHORS   Menzel,P., Valencia,F., Godement,P., Dodelet,V.C. and Pasquale,E.B.
  TITLE     Ephrin-A6, a new ligand for EphA receptors in the developing visual
            system
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 981)
  AUTHORS   Pasquale,E.B. and Menzel,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-OCT-2000) The Burnham Institute, 10901 N. Torrey
            Pines Rd., La Jolla, CA 92037, USA
FEATURES             Location/Qualifiers
     source          1. .981
                     /organism="Gallus gallus"
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     CDS             <1. .609
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                     FSEKIQRFTPFSLGFEFRPGETYYYISVPTPGSAGRCLKLRVSVCCRASTPEPLTEVP
                     NSQPRGRGGPEGDAGSPRDAAPIPQRSRTRLVALAVVAVLWV"
BASE COUNT      141 a    366 c    297 g    177 t
ORIGIN


  Query Match             23.6%;  Score 149.8;  DB 5;  Length 981;
  Best Local Similarity   63.0%;  Pred. No. 5.9e-22;
  Matches  289;  Conservative    0;  Mismatches  152;  Indels   18;  Gaps    3;

Qy     43 CTGCTGCGGACTGTCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGC 102
          |||||  ||    | || |||||  || | ||  |  | || | ||    ||    | ||
Db      1 CTGCTCGGGCTGCTGCTTTGGGCTCCGCTGCTTTGGGCTCCGCCGCCGCCGGTGCGCGGC 60

Qy    103 CTCCGCCACGTAGTCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTG 162
          | ||||||||  ||||||||||||   || ||||||||||| || |  |  ||   |
Db     61 CGCCGCCACGGCGTCTACTGGAACGGGAGCAACCCCAGGTTCCTGCAGGACGATTACTCC 120

Qy    163 GTGGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGG 222
           |  |  ||  | |||| ||  |||| || |||  ||||||||| |||   | |||   |
Db    121 ATCCAAGTGTCCATCAATGACCACCTGGATATTTACTGCCCCCATTACTCCGCCCCCACG 180

Qy    223 CCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCC 282
          ||      | |  | ||||  ||  |  ||| |||||||||   |   |||||   |  |
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Db    181 CC------GTGGGCTGAGAGCTTCACGCTGTTCATGGTGGATGAGGAGGGCTACCGGGGC 234

Qy    283 TGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTG---------CTCCCTGCCC 333
          |||    | |||  |||| | ||||  || ||||||| |||         || |   ||
Db    235 TGC---TCGGAGACCCCCGGCGCCTTTAAACGCTGGGAGTGTAATAAACCCTTCGCTCCG 291

Qy    334 TTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTT 393
          || | ||  ||||  ||||| |||||||| || |||||||| || |||||  | |||||
Db    292 TTCGTCCCCGTTCGGTTCTCCGAGAAGATCCAACGCTTCACCCCCTTCTCGTTGGGCTTC 351

Qy    394 GAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGC 453
          ||||||  ||| || ||||| || || || || || |||||||| || | |||  | ||
Db    352 GAGTTCAGACCCGGGGAGACGTATTATTATATATCCGTGCCCACCCCCGGGAGCGCCGGG 411

Qy    454 CAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGGAG 492
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Db    412 CGCTGCCTGAAGCTGCGCGTCTCCGTTTGCTGCAGAGCG 450


RESULT  15
AR023765
LOCUS       AR023765                 783 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 3 from patent US 5795734.
ACCESSION   AR023765
VERSION     AR023765.1  GI:3977059
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 783)
  AUTHORS   Flanagan,J.G. and Cheng,H.-J.
  TITLE     EPH receptor ligands, and uses related thereto
  JOURNAL   Patent: US 5795734-A 3 18-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .783
                     /organism="unknown"
BASE COUNT      140 a    270 c    232 g    141 t
ORIGIN


  Query Match             19.1%;  Score 121.6;  DB 6;  Length 783;
  Best Local Similarity   62.0%;  Pred. No. 6.2e-16;
  Matches  212;  Conservative    0;  Mismatches  124;  Indels    6;  Gaps    1;

Qy    105 CCGCCACGTAGTCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGT 164
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Db    172 CCGCTACGCCGTCTATTGGAACCGCAGCAACCCCAGGTTCCACCGCGGGGATTACACCGT 231

Qy    165 GGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCC 224
          |||| || || |||| || ||||| |||||   |||||| |||||||| |  ||   |||
Db    232 GGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCTCACTACGAGGAGCCGCTGCC 291

Qy    225 CCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTG 284
          | | ||| ||   |||   |  |   | ||||||||  |||     ||| | | ||||||
Db    292 CGCCGAGCGCATGGAGCGCTACGTCCTCTACATGGTCAACTACGAGGGCCACGCGTCCTG 351

Qy    285 ------CCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGG 338
                || |    |||||  |      |   || ||     |  |  |   |||   ||
Db    352 CGACCACCGGCAGAAGGGCTTCAAACGTTGGGAGTGCAACCGGCCCGACTCCCCCAGCGG 411

Qy    339 CCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTT 398
           |   |  | |||||||||||| | |||| |||||| || |||||  | ||||| |||||
Db    412 ACCCCTCAAGTTCTCAGAGAAGTTCCAGCTCTTCACCCCCTTCTCTTTGGGCTTCGAGTT 471

Qy    399 CTTACCTGGAGAGACTTACTACTACATCTCGGTGCCCACTCC 440
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Job time: 9186 sec
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                    GenCore version 4.5
             Copyright (c) 1993 - 2000  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          September 28, 2002, 00:26:44 ; Search time 239.05 Seconds
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Title:           US-09-904-954-3
Perfect score:   636
Sequence:        1 GCCAGACCAAACCGGACCTC..........TTCTGCGAATTCTGTGAGCC 636

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters:      3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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Result               Query
  No.    Score    Match Length DB  ID                        Description
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     1      636   100.0     636  16  AAQ85888                   Human hek-L protei
     2      134    21.1   17138  22  AAS14757                   Human protease gen
     3    121.6    19.1     783  17  AAT15009                   Chicken elf-1 cDNA
     4    121.6    19.1     783  19  AAV42927                   cDNA encoding an a
     5    115.4    18.1    1070  16  AAT03883                   Eph transmembrane
     6    103.4    16.3    1037  16  AAQ85887                   Human hek-L protei
     7    101.8    16.0    1438  13  AAQ24595                   B61 cDNA sequence.
     8    101.8    16.0    1480  15  AAQ63770                   B61 gene.  Homo sa
     9    101.8    16.0    1496  22  AAS21387                   Human cDNA sequenc
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      10    101.8    16.0    1496  22  AAC90574                   Human PRO202 cDNA.
      11    101.8    16.0    1496  22  AAC91576                   Human PRO202 cDNA.
      12    101.8    16.0    1527  21  AAC98823                   Human pancreatic c
      13     97.2    15.3     439  22  AAH81578                   Human differential
      14     94.8    14.9    1574  23  AAS92779                   DNA encoding novel
      15     94.8    14.9    1728  17  AAT34292                   HEK4 binding prote
      16     94.8    14.9    1839  17  AAT18897                   Human AL-1 cDNA.
      17       94    14.8    1809  17  AAT15008                   Mouse Elf-1 cDNA.
      18       94    14.8    1809  19  AAV42926                   cDNA encoding a ma
      19     93.4    14.7    1176  23  AAS92024                   DNA encoding novel
      20       92    14.5     687  17  AAT32699                   Lerk-7 coding sequ
      21     91.6    14.4     642  20  AAX32767                   Human LERK-6 polyp
      22     86.2    13.6     555  17  AAT32700                   Lerk-6 coding sequ
      23     86.2    13.6     555  17  AAT14009                   LERK-6 coding sequ
      24     86.2    13.6     555  20  AAX32761                   Murine LERK-6 poly
      25     82.2    12.9     314  17  AAT14010                   LERK-6 exon.  Homo
      26     82.2    12.9     314  20  AAX32766                   Exon sequence of h
 c    27     47.6     7.5    3066  23  AAS75651                   DNA encoding novel
      28       44     6.9     911  21  AAA76267                   Maize glutathione-
      29     41.4     6.5    1142  20  AAX27314                   Human secreted pro
 c    30     40.2     6.3    6093  20  AAX25775                   S.erythraea oleand
 c    31     40.2     6.3   50937  21  AAA09469                   Streptococcus olea
      32     39.8     6.3     424  22  AAK77253                   Human immune/haema
      33       39     6.1    1613  21  AAC48024                   Zea mays DNA fragm
      34     38.4     6.0    2271  23  AAS78101                   DNA encoding novel
 c    35     37.8     5.9 4403765   22  AAI99683                   Mycobacterium tube
      36     36.8     5.8    1618  16  AAQ75423                   Human 4-1BB-L poly
      37     36.8     5.8    1618  18  AAT91025                   Human 4-1BB ligand
      38     36.8     5.8    1619  19  AAV39013                   Nucleotide sequenc
 c    39     36.8     5.8    1877  21  AAA96493                   cDNA encoding a hu
      40     36.8     5.8    1972  21  AAD01353                   Wheat sphingolipid
 c    41     36.8     5.8    2252  22  ABA09094                   Human secreted pro
      42     36.6     5.8     957  22  AAH31653                   Human olfactory re
      43     36.6     5.8    1044  22  AAS42286                   Human cDNA encodin
 c    44     36.4     5.7     633  11  AAQ03322                   Genomic Eimeria te
      45     36.4     5.7    1462  21  AAC93431                   Human secreted pro

                                   ALIGNMENTS


RESULT   1
AAQ85888
ID   AAQ85888 standard; cDNA to mRNA; 636 BP.
XX
AC   AAQ85888;
XX
DT   03-OCT-1995  (first entry)
XX
DE   Human hek-L protein cDNA clone C6.
XX
KW   Ligand; cell surface; tyrosine kinase receptor; tumorigenesis;
KW   immunogen; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  a
FT   sig_peptide     28..93
FT                   /*tag=  b
FT   mat_peptide     94..630
FT                   /*tag=  c
XX
PN   WO9506065-A.
XX
PD   02-MAR-1995.
XX
PF   17-AUG-1994;   94WO-US09282.
XX
PR   20-AUG-1993;   93US-0109745.
PR   30-AUG-1993;   93US-0114426.
PR   03-DEC-1993;   93US-0161132.
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PR   09-MAY-1994;   94US-0240124.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Beckmann MP,  Cerretti DP;
XX
DR   WPI; 1995-106811/14.
DR   P-PSDB; AAR71482.
XX
PT   New isolated DNA encoding hek-L protein or its fusion products  -
PT   useful as assay reagent or for carrying therapeutic and
PT   diagnostic compounds to leukaemia cells.
XX
PS   Claim 3; Page 37; 45pp; English.
XX
CC   The sequence is that of a clone encoding hek-L protein, a protein
CC   that can bind hek (a cell surface receptor tyrosine kinase).  Hek-L
CC   is the first known ligand for hek and can be used to study cellular
CC   processes regulated by hek (which may be involved in tumorigenesis).
CC   It is also an immunogen for antibody production, as a reagent for
CC   detecting hek or hek-L in in vitro assays, to determine binding of
CC   hek proteins, to purify hek proteins, and to carry diagnostic or
CC   cytotoxic agents to particular leukaemia cells that express the hek
CC   antigen.  Hek-L also binds the elk tyrosine kinase receptors.
CC   See also AAQ85887.
XX
SQ   Sequence 636 BP; 102 A; 202 C; 186 G; 146 T; 0 other;


  Query Match             100.0%;  Score 636;  DB 16;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-154;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db        1 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctc 60

Qy       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 tgggccgcgttcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 120

Qy      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 tggaactccagtaaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaac 180

Qy      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 gattacctagacattgtctgcccccactacgaaggcccagggccccctgagggccccgag 240

Qy      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 acgtttgctttgtacatggtggactggccaggctatgagtcctgccaggcagagggcccc 300

Qy      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 cgggcctacaagcgctgggtgtgctccctgccctttggccatgttcaattctcagagaag 360

Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 attcagcgcttcacacctttctccctcggctttgagttcttacctggagagacttactac 420

Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 tacatctcggtgcccactccagagagttctggccagtgcttgaggctccaggtgtctgtc 480

Qy      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 tgctgcaaggagaggaagtctgagtcagcccatcctgttgggagccctggagagagtggc 540

Qy      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 acatcagggtggcgagggggggacactcccagccccctctgtctcttgctattactgctg 600

Qy      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
            ||||||||||||||||||||||||||||||||||||
Db      601 cttctgattcttcgtcttctgcgaattctgtgagcc 636


RESULT   2
AAS14757
ID   AAS14757 standard; DNA; 17138 BP.
XX
AC   AAS14757;
XX
DT   16-JAN-2002  (first entry)
XX
DE   Human protease genomic DNA.
XX
KW   Human; protease; drug development; cell proliferation; placenta; kidney;
KW   cell differentiation; cell signalling; thyroid gland; leucocyte; ovary;
KW   lung; colon; prostate; eye; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             2076..9794
FT                   /*tag= a
FT                   /product= "Human protease #2"
FT   exon            2076..2154
FT                   /*tag= b
FT                   /number= "Exon 1"
FT   intron          2155..3308
FT                   /*tag= c
FT                   /number= "Intron 1"
FT   exon            3309..3466
FT                   /*tag= d
FT                   /number= "Exon 2"
FT   intron          3467..4104
FT                   /*tag= e
FT                   /number= "Intron 2"
FT   exon            4105..4181
FT                   /*tag= f
FT                   /number= "Exon 3"
FT   intron          4182..4206
FT                   /*tag= g
FT                   /number= "Intron 3"
FT   exon            4207..4250
FT                   /*tag= h
FT                   /number= "Exon 4"
FT   intron          4251..4436
FT                   /*tag= i
FT                   /number= "Intron 4"
FT   exon            4437..4607
FT                   /*tag= j
FT                   /number= "Exon 5"
FT   intron          4608..5048
FT                   /*tag= k
FT                   /number= "Intron 5"
FT   exon            5049..5052
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FT                   /number= "Exon 6"
FT   intron          5053..6007
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FT                   /number= "Intron 6"
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FT                   /*tag= n
FT                   /number= "Exon 7"
FT   intron          6146..6528
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FT                   /number= "Intron 7"
FT   exon            6529..6589
FT                   /*tag= p
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FT   intron          6590..6668
FT                   /*tag= q
FT                   /number= "Intron 8"
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FT                   /*tag=  r
FT                   /number= "Exon 9"
FT   intron          6738..6816
FT                   /*tag=  s
FT                   /number= "Intron 9"
FT   exon            6817..6986
FT                   /*tag=  t
FT                   /number= "Exon 10"
FT   intron          6987..7122
FT                   /*tag=  u
FT                   /number= "Intron 10"
FT   exon            7123..7207
FT                   /*tag=  v
FT                   /number= "Exon 11"
FT   intron          7208..7689
FT                   /*tag=  w
FT                   /number= "Intron 11"
FT   exon            7690..7838
FT                   /*tag=  x
FT                   /number= "Exon 12"
FT   intron          7839..7943
FT                   /*tag=  y
FT                   /number= "Intron 12"
FT   exon            7944..8118
FT                   /*tag=  z
FT                   /number= "Exon 13"
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FT                   /number= "Intron 13"
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FT                   /number= "Exon 14"
FT   intron          8486..8606
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FT                   /number= "Intron 14"
FT   exon            8607..8911
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FT                   /number= "Exon 15"
FT   intron          8912..9248
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FT                   /*tag=  af
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XX
PN   US6294368-B1.
XX
PD   25-SEP-2001.
XX
PF   22-MAR-2001; 2001US-0813819.
XX
PR   22-MAR-2001; 2001US-0813819.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Merkulov GV,  Ye J,  Di Francesco V,  Beasley EM;
XX
DR   WPI; 2001-638014/73.
DR   P-PSDB; AAU08749.
XX
PT   New nucleic acids encoding human protease proteins, useful as a major
PT   target for drug action and development, as well as in biological assays
PT   for detecting changes in protease nucleic acid expression  -
XX
PS   Claim 1; Fig 3; 57pp; English.
XX
CC   The invention relates to human protease polypeptides and polynucleotides
CC   which are expressed in the placenta, lung, ovary, colon, kidney, thyroid
CC   gland, prostate, eye and leucocyte. These sequences can be used as models
CC   for the development of human therapeutic targets, in the identification
CC   of therapeutic proteins and serve as targets for the development of drugs
CC   that modulate protease activity in cells and tissues expressing protease.
CC   The nucleic acid molecules are also useful in biological assays for
CC   detecting changes in protease nucleic acid expression and for producing
CC   proteases, which are important for regulating cell proliferation,
CC   differentiation, and signalling processes. This sequence represents
CC   genomic DNA encoding a human protease polypeptide.
XX
SQ   Sequence 17138 BP; 2315 A; 3492 C; 3363 G; 2751 T; 5217 other;


  Query Match            21.1%;  Score 134;  DB 22;  Length 17138;
  Best Local Similarity  80.5%;  Pred. No. 1.4e-24;
  Matches  169;  Conservative    0;  Mismatches   40;  Indels    1;  Gaps    1;

Qy      1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16167 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtccta 16226

Qy     61 TGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16227 tggccgcg-tcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 16285

Qy    121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
          |||||||||||||||||||||| ||   |  ||  ||     | | |        ||  |
Db  16286 tggaactccagtaaccccaggtagccgggccgaaccgggcgagcgcacagccaagtctgc 16345

Qy    181 GATTACCTAGACATTGTCTGCCCCCACTAC 210
          |    ||  | | |||   || ||| | ||
Db  16346 gcgctcccgggctttgcgcgcgcccgccac 16375


RESULT   3
AAT15009
ID   AAT15009 standard; cDNA; 783 BP.
XX
AC   AAT15009;
XX
DT   02-JUL-1996  (first entry)
XX
DE   Chicken elf-1 cDNA.
XX
KW   Elf-1; EPH receptor ligand; dementia; tachycardia; gene therapy;
KW   diagnosis; transgenic animal; ss; ds.
XX
OS   Gallus sp.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..85
FT                   /*tag=  a
FT   CDS             86..688
FT                   /*tag=  b
FT   sig_peptide     86..148
FT                   /*tag=  c
FT   mat_peptide     149..685
FT                   /*tag=  d
FT   3'UTR           686..783
FT                   /*tag=  e
FT   polyA_signal    1471..1476
FT                   /*tag=  f
XX
PN   WO9609384-A1.
XX
PD   28-MAR-1996.
XX
PF   19-SEP-1995;    95WO-US11869.
XX
PR   27-FEB-1995;    95US-0393462.
PR   19-SEP-1994;    94US-0308814.
```

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XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1996-188446/19.
DR   P-PSDB; AAR94767.
XX
PT   Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis
PT   and treatment of disorders associated with the Elf-1 gene, e.g.
PT   dementia, tachycardia , etc.
XX
PS   Claim 36; Page 87-88; 107pp; English.
XX
CC   A chicken cDNA clone (AAT15009) codes for a novel EPH receptor ligand,
CC   Elf-1 (AAR94766), involved in the formation and maintenance of
CC   ordered spatial arrangements of differentiated tissue.  It was
CC   obtd. from a day-3 chick embryo cDNA library using mouse Elf-1
CC   cDNA (see AAT15008) as probe.  The cDNA can be used for the prodn.
CC   of recombinant Elf-1, in the breeding of transgenic animals,
CC   for the design of diagnostic probes, and for gene (or antisense)
CC   therapy of cellular and tissue disorders.
XX
SQ   Sequence 783 BP; 140 A; 270 C; 232 G; 141 T; 0 other;

  Query Match             19.1%;  Score 121.6;  DB 17;  Length 783;
  Best Local Similarity   62.0%;  Pred. No. 9e-22;
  Matches  212;  Conservative    0;  Mismatches  124;  Indels    6;  Gaps    1;

Qy    105 CCGCCACGTAGTCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGT 164
          |||| |||  ||||| ||||||  ||| ||||||||||| |  || || ||   |   ||
Db    172 ccgctacgccgtctattggaaccgcagcaaccccaggttccaccgcggggattacaccgt 231

Qy    165 GGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCC 224
          |||| || || |||| || ||||| |||||   |||||| |||||||| |  ||   |||
Db    232 ggaggtgagcatcaatgactacctggacatctactgccctcactacgaggagccgctgcc 291

Qy    225 CCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTG 284
          | | ||| ||   |||   |  |   | ||||||||  |||     ||| | | ||||||
Db    292 cgccgagcgcatggagcgctacgtcctctacatggtcaactacgagggccacgcgtcctg 351

Qy    285 ------CCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGG 338
                || |    |||||  |      |   || ||     |  |  |   |||   ||
Db    352 cgaccaccggcagaagggcttcaaacgttgggagtgcaaccggcccgactcccccagcgg 411

Qy    339 CCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTT 398
           |   |  | |||||||||||| | |||| |||||| || |||||  | ||||| |||||
Db    412 acccctcaagttctcagagaagttccagctcttcacccccttctctttgggcttcgagtt 471

Qy    399 CTTACCTGGAGAGACTTACTACTACATCTCGGTGCCCACTCC 440
          |   || ||  |    || ||||||||||| | | |  | ||
Db    472 ccgtcccggccacgagtattactacatctctgcgtctccccc 513

RESULT   4
AAV42927
ID   AAV42927 standard; cDNA; 783 BP.
XX
AC   AAV42927;
XX
DT   20-OCT-1998  (first entry)
XX
DE   cDNA encoding an avian Elf-1 protein.
XX
KW   Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP;
KW   tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation;
KW   intracellular signalling; increased; survival; neuronal cell;
KW   neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour;
KW   artificial liver; cartilage; bone formation; ss.
XX
OS   Gallus sp.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..85
FT                   /*tag= a
FT   CDS             86..688
FT                   /*tag= b
FT                   /product= Elf-1
FT   sig_peptide     86..148
FT                   /*tag= c
FT   3'UTR           686..783
FT                   /*tag= d
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PN   US5795734-A.
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PD   18-AUG-1998.
XX
PF   31-MAY-1995;   95US-0455001.
XX
PR   31-MAY-1995;   95US-0455001.
PR   19-SEP-1994;   94US-0308814.
PR   27-FEB-1995;   95US-0393462.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1998-466665/40.
DR   P-PSDB; AAW71007.
XX
PT   Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor
PT   - for production of Elf-1 protein, useful for regulating
PT   proliferation, differentiation, and survival of cells
XX
PS   Claim 12; Columns 73-76; 53pp; English.
XX
CC   The present sequence encodes an avian EPH receptor ligand designated
CC   Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a
CC   tyrosine kinase ligand, which is linked to the membrane through a
CC   phosphatidylinositol linkage. It shares some homology to 2 other EPH
CC   receptor ligands, B61 and LERK-2. The Elf-1 protein modulates
CC   proliferation, differentiation and survival of EPH receptor-expressing
CC   cells by stimulating or antagonising intracellular signalling mediated
CC   by the EPH receptor. Typical of many potential applications are
CC   increasing survival of neuronal cells in culture (e.g. where intended for
CC   transplantation), also therapeutically in increase neuron survival
CC   (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent
CC   nervous system and lymphatic tumours, to induce differentiation of
CC   hepatocytes to form an artificial liver, to induce cartilage and bone
CC   formation.
XX
SQ   Sequence 783 BP; 140 A; 270 C; 232 G; 141 T; 0 other;

  Query Match             19.1%;  Score 121.6;  DB 19;  Length 783;
  Best Local Similarity   62.0%;  Pred. No. 9e-22;
  Matches  212;  Conservative    0;  Mismatches  124;  Indels    6;  Gaps    1;

Qy    105 CCGCCACGTAGTCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGT 164
          |||| |||  ||||| ||||||  ||| ||||||||||| |  || || ||   |   ||
Db    172 ccgctacgccgtctattggaaccgcagcaaccccaggttccaccgcggggattacaccgt 231

Qy    165 GGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCC 224
          |||| || || |||| || ||||| |||||   |||||| |||||||| |  ||   |||
Db    232 ggaggtgagcatcaatgactacctggacatctactgccctcactacgaggagccgctgcc 291

Qy    225 CCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTG 284
          | | ||| ||   |||   |  |   | ||||||||  |||     ||| | | ||||||
Db    292 cgccgagcgcatggagcgctacgtcctctacatggtcaactacgagggccacgcgtcctg 351

Qy    285 ------CCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGG 338
                || |    |||||  |      |   || ||     |  |  |   |||   ||
Db    352 cgaccaccggcagaagggcttcaaacgttgggagtgcaaccggcccgactcccccagcgg 411

Qy    339 CCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTT 398
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           |   |  | |||||||||||| | |||| |||||| || |||||  | ||||| |||||
Db    412 acccctcaagttctcagagaagttccagctcttcacccccttctctttgggcttcgagtt 471

Qy    399 CTTACCTGGAGAGACTTACTACTACATCTCGGTGCCCACTCC 440
          |   || ||  |    || ||||||||||| | | |  | ||
Db    472 ccgtcccggccacgagtattactacatctctgcgtctccccc 513


RESULT   5
AAT03883
ID   AAT03883 standard; DNA; 1070 BP.
XX
AC   AAT03883;
XX
DT   16-MAY-1996  (first entry)
XX
DE   Eph transmembrane tyrosine kinase family ligand, Efl-2 encoding DNA.
XX
KW   Efl-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand;
KW   neurological disorder; identification; diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             46..750
FT                   /*tag=  a
FT                   /product= Efl-2
XX
PN   WO9527060-A2.
XX
PD   12-OCT-1995.
XX
PF   04-APR-1995;   95WO-US04208.
XX
PR   21-OCT-1994;   94US-0327423.
PR   04-APR-1994;   94US-0222075.
PR   12-APR-1994;   94US-0229402.
PR   01-SEP-1994;   94US-0299567.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Aldrich TH,  Davis S,  Gale N,  Goldfarb M,  Maisonpierre PC;
PI   Yancopoulos GD;
XX
DR   WPI; 1995-358635/46.
DR   P-PSDB; AAR82605.
XX
PT   Ligands which bind Eph family receptors - used in the diagnosis of
PT   neurological disorders
XX
PS   Disclosure; Fig 3; 58pp; English.
XX
CC   The DNA encodes an Eph transmembrane tyrosine kinase family ligand
CC   designated Efl-2. Efl-2 is useful for identifying other ligands for
CC   Ehk-1, -2, -3, Eck and Elk receptors.   The ligands are useful in
CC   promoting a differential function and/or influencing the phenotye,
CC   such as growth and/or proliferation, of receptor bearing cells. They
CC   may be used in the diagnosis, and treatment of neurological disorders.
XX
SQ   Sequence 1070 BP; 196 A; 341 C; 334 G; 189 T; 10 other;


  Query Match             18.1%;  Score 115.4;  DB 16;  Length 1070;
  Best Local Similarity   55.6%;  Pred. No. 3.9e-20;
  Matches  271;  Conservative    0;  Mismatches  201;  Indels   15;  Gaps    2;

Qy     15 GACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
          | |  |||   || ||| ||||||||  |||||   | | || |    |    || | ||
Db     48 ggcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgct 107

Qy     75 CGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
           | |      |   | ||||      |   ||| || |  || |||||||||  |   ||
Db    108 ggcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaa 167
```

```
Qy    135 CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
          ||      |||  ||||  | |  |   ||| || ||  | | ||||| || || || ||
Db    168 ccagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatat 227

Qy    195 TGTCTGCCCCCACTAC------------GAAGGCCCAGGGCCCCCTGAGGGCCCCGAGAC 242
          |  |||||| ||||||            |  || || ||||||   |  ||  | |||
Db    228 ttactgcccgcactacaacagctcgggggcgggaccggggcccggaggcggggcagagca 287

Qy    243 GTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC---AGAGGGCCC 299
          ||  |   |||||||||||  | |    |||||     ||||| | ||     |||||
Db    288 gtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgccagccagggctt 347

Qy    300 CCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAA 359
          |  |  ||   || ||     |     |   ||     |||   |  | ||||| |||||
Db    348 caagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaagttctcggagaa 407

Qy    360 GATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTA 419
          | | ||||||| ||   | ||||| || ||||  ||||||    | ||  |    |||||
Db    408 gttccagcgctacagcgccttctctctgggctacgagttccacgccggccacgagtacta 467

Qy    420 CTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGT 479
          |||||||||   ||||||||   |        |  ||||  ||||| |  ||||||  ||
Db    468 ctacatctccacgcccactcacaacctgcactggaagtgtctgaggatgaaggtgttcgt 527

Qy    480 CTGCTGC 486
          |||||||
Db    528 ctgctgc 534


RESULT   6
AAQ85887
ID   AAQ85887 standard; cDNA to mRNA; 1037 BP.
XX
AC   AAQ85887;
XX
DT   03-OCT-1995  (first entry)
XX
DE   Human hek-L protein cDNA clone A2.
XX
KW   Ligand; cell surface; tyrosine kinase receptor; tumorigenesis;
KW   immunogen; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             83..799
FT                   /*tag=  a
FT   sig_peptide     83..139
FT                   /*tag=  b
FT   mat_peptide     140..796
FT                   /*tag=  c
XX
PN   WO9506065-A.
XX
PD   02-MAR-1995.
XX
PF   17-AUG-1994;   94WO-US09282.
XX
PR   20-AUG-1993;   93US-0109745.
PR   30-AUG-1993;   93US-0114426.
PR   03-DEC-1993;   93US-0161132.
PR   09-MAY-1994;   94US-0240124.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Beckmann MP,  Cerretti DP;
XX
DR   WPI; 1995-106811/14.
DR   P-PSDB; AAR71481.
XX
PT   New isolated DNA encoding hek-L protein or its fusion products  -
PT   useful as assay reagent or for carrying therapeutic and
```

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PT   diagnostic compounds to leukaemia cells.
XX
PS   Claim 1; Page 34; 45pp; English.
XX
CC   The sequence is that of a clone encoding hek-L protein, a protein
CC   that can bind hek (a cell surface receptor tyrosine kinase).  Hek-L
CC   is the first known ligand for hek and can be used to study cellular
CC   processes regulated by hek (which may be involved in tumorigenesis).
CC   It is also an immunogen for antibody production, as a reagent for
CC   detecting hek or hek-L in in vitro assays, to determine binding of
CC   hek proteins, to purify hek proteins, and to carry diagnostic or
CC   cytotoxic agents to particular leukaemia cells that express the hek
CC   antigen.  Hek-L also binds the elk tyrosine kinase receptors.
CC   See also AAQ85888.
XX
SQ   Sequence 1037 BP; 187 A; 343 C; 337 G; 170 T; 0 other;

  Query Match             16.3%;  Score 103.4;  DB 16;  Length 1037;
  Best Local Similarity   54.3%;  Pred. No. 4.7e-17;
  Matches  271;  Conservative    0;  Mismatches  201;  Indels   27;  Gaps    2;

Qy       15 GACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
            | |  |||   || ||| ||||||||  |||||   | | || |    |    || | ||
Db       85 ggcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgct 144

Qy       75 CGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
             | |      |   | ||||      |   ||| || |  || |||||||||  |   ||
Db      145 ggcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaa 204

Qy      135 CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
            ||      |||  ||||  | |  |   ||| || ||  | | ||||| || || || ||
Db      205 ccagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatat 264

Qy      195 TGTCTGCCCCCACTACGAAGGC------------------------CCAGGGCCCCCTGA 230
            |  |||||| |||||| |  ||                        || ||||||   |
Db      265 ttactgcccgcactacaacagctcgggggtgggccccggggcgggaccggggcccggagg 324

Qy      231 GGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC 290
             ||  | |||  ||  |   |||||||||||  | |    |||||     ||||| | ||
Db      325 cggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgc 384

Qy      291 ---AGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCA 347
                 |||||  |  |  ||   || ||     |     |   ||     |||   |  |
Db      385 cagccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaa 444

Qy      348 ATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407
             ||||| |||||| | ||||||| ||   | ||||| || ||||  ||||||    | ||
Db      445 gttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgccgg 504

Qy      408 AGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCT 467
              |    ||||||||||||||   ||||||||   |        |  ||||  ||||| |
Db      505 ccacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggat 564

Qy      468 CCAGGTGTCTGTCTGCTGC 486
              ||||||  |||||||||
Db      565 gaaggtgttcgtctgctgc 583

RESULT   7
AAQ24595
ID   AAQ24595 standard; cDNA to mRNA; 1438 BP.
XX
AC   AAQ24595;
XX
DT   06-NOV-1992  (first entry)
XX
DE   B61 cDNA sequence.
XX
KW   Early inflammatory response; marker; antibody; therapy; induction;
KW   lipopolysaccharides; cytokines; Interleukin-2; IL-2; TNF; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..691
FT                   /*tag= a
FT   sig_peptide     74..128
FT                   /*tag= b
FT   polyA_signal    1458..1463
FT                   /*tag= c
XX
PN   WO9207094-A.
XX
PD   30-APR-1992.
XX
PF   15-OCT-1991;   91WO-US07704.
XX
PR   16-OCT-1990;   90US-0607741.
XX
PA   (UNMI ) UNIV MICHIGAN.
XX
PI   Dixit VM;
XX
DR   WPI; 1992-167172/20.
DR   P-PSDB; AAR23895.
XX
PT   Gene prod. used as marker to detect inflammatory response - by
PT   detecting the B61 gene in biological fluids or by using
PT   hybridisation probes
XX
PS   Claim 1; Fig 3; 39pp; English.
XX
CC   Poly(A)+ mRNA isolated from human umbilical vein endothelial cells
CC   (HUVE) was treated with TNF cyclohexamide and used to construct a
CC   lambda gt11 cDNA library.  The library was screened using
CC   radiolabelled cDNA fragments derived from the 5' end of B61 DNA.
CC   Hybridising cDNA inserts were isolated and subcloned into pGEM 7zf
CC   (+) for sequencing.  Clone B61.1 contained the entire OFR encoding a
CC   protein of 205 residues (24 kD).  The B61 gene is involved in early
CC   inflammatory response and serves as a marker.  It may be detected by
CC   probes or by antibody-based immunoassay of biological fluids such as
CC   plasma, CSF or urine.  These assays make it possible to predict a
CC   worsening in a disease process and allow the quantitative
CC   assessment of the magnitude of the inflammatory response.  This
CC   information will allow the earlier admin. of appropriate therapy,
CC   thereby shortening the disease process and limiting the patient's
CC   exposure to anti-inflammatory/immunosuppressive therapy.  B61
CC   induction is rapid and profound, hence it is easily detectable.
CC   The B61 response is highly specific to proinflammatory stimuli,
CC   being only made by cells exposed to lipopolysaccharides or cytokines
CC   such as IL-2 and TNF and not growth factors or interferon.
XX
SQ   Sequence 1438 BP; 358 A; 412 C; 373 G; 295 T; 0 other;

  Query Match             16.0%;  Score 101.8;  DB 13;  Length 1438;
  Best Local Similarity   56.9%;  Pred. No. 1.3e-16;
  Matches  253;  Conservative    0;  Mismatches  177;  Indels   15;  Gaps    3;

Qy       56 TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAG 115
            ||||||||||| |  || | ||           |   || | |       ||||||   |
Db       81 tcctctgggcccctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccg 140

Qy      116 TCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCC 175
            ||| |||||||      || |||| ||| |     |  |||  |    |  |  ||   |
Db      141 tcttctggaacagttcaaatcccaagttccggaatgaggactacaccatacatgtgcagc 200

Qy      176 TCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGG---CCCAGGGCCCCCTGAGG 232
            | || || ||| | |||||  |||| || ||||| ||||    | | | | |    |  |
Db      201 tgaatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgctg 260

Qy      233 GCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAG 292
             |   |||  ||      ||||| |||||||       |  ||  ||   |||||| |
Db      261 ccatggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagcccc 320
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Qy     293 AGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT---------TGGCCATG 343
           ||    ||  || | |    ||||||  ||||  || ||||           |||||  |
Db     321 ag---tccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcatggcccgg 377

Qy     344 TTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTAC 403
              |  | || |||||| | |||||||||||||||||| |||| |||   ||||||  |
Db     378 agaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggagttcaaag 437

Qy     404 CTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGA 463
             ||| | |  ||||||||||||||    ||||  |   ||  |   | ||  |||||||
Db     438 aaggacacagctactactacatctccaaacccatccaccagcatgaagaccgctgcttga 497

Qy     464 GGCTCCAGGTGTCTGTCTGCTGCAA 488
           || |  ||||| ||||| |  ||||
Db     498 ggttgaaggtgactgtcagtggcaa 522


RESULT   8
AAQ63770
ID   AAQ63770 standard; DNA; 1480 BP.
XX
AC   AAQ63770;
XX
DT   10-JAN-1995  (first entry)
XX
DE   B61 gene.
XX
KW   eck receptor; eck receptor binding protein; EBP; B61;
KW   cancer; inflammation; wound; cytokine; protein tyrosine kinase;
KW   PTK; phosphorylation; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..691
FT                   /*tag=  a
XX
PN   EP597503-A.
XX
PD   18-MAY-1994.
XX
PF   15-NOV-1993;   93EP-0118469.
XX
PR   13-NOV-1992;   92US-0977708.
PR   09-NOV-1993;   93US-0145616.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Bartley TD,  Boyle WJ,  Fox GM,  Parker VP,  Welcher AA;
XX
DR   WPI; 1994-160538/20.
DR   P-PSDB; AAR53634.
XX
PT   New eck receptor binding proteins - useful for treating cancer,
PT   inflammation, wounds, etc.
XX
PS   Disclosure; Page 27-28; 41pp; English.
XX
CC   The N-terminal sequence of EBP isolated from the conditioned medium
CC   of the SK-BR-3 cell line was identical to the N-terminal amino acid
CC   sequence predicted from the expression of the B61 gene (Holzman et al.,
CC   Mol. Cell Biol. 10, 5830 (1990); WO9207094).
CC   cDNA encoding EBP having the N-terminal
CC   NH2-DRHTVFW(N)SSNPKFRNEDYTIHVQ was cloned
CC   and sequenced and, as expected, found to be identical to the B61 gene.
CC   The EBP gene expressed in CHO cells resulted in at least two
CC   polypeptides having different mol. wts. C-terminal sequencing
CC   revealed only the sequence KRLAA-COOH which indicated a polypeptide
CC   of 150 amino acids (EBP1-150).
XX
SQ   Sequence 1480 BP; 359 A; 421 C; 393 G; 307 T; 0 other;
```

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  Query Match             16.0%;  Score 101.8;  DB 15;  Length 1480;
  Best Local Similarity   56.9%;  Pred. No. 1.3e-16;
  Matches  253;  Conservative    0;  Mismatches  177;  Indels   15;  Gaps    3;

Qy      56 TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAG 115
           ||||||||||| |  || | ||           |   || | |       ||||||   |
Db      81 tcctctgggcccctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccg 140

Qy     116 TCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCC 175
           ||| |||||||      || |||| ||| |     |  |||  |    |  |  ||   |
Db     141 tcttctggaacagttcaaatcccaagttccggaatgaggactacaccatacatgtgcagc 200

Qy     176 TCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGG---CCCAGGGCCCCCTGAGG 232
           | || || ||| | |||||  |||| || ||||| ||||    | | | | |    |  |
Db     201 tgaatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgctg 260

Qy     233 GCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAG 292
            |   |||  ||      ||||| |||||||       |  ||  ||   |||||| |
Db     261 ccatggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagcccc 320

Qy     293 AGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT---------TGGCCATG 343
           ||    ||  || | |    ||||||  ||||  || ||||           |||||  |
Db     321 ag---tccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcatggcccgg 377

Qy     344 TTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTAC 403
              |  | || |||||| | |||||||||||||||||| |||| |||   ||||||  |
Db     378 agaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggagttcaaag 437

Qy     404 CTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGA 463
             ||| | |  ||||||||||||||    ||||  |   ||  |   | ||  |||||||
Db     438 aaggacacagctactactacatctccaaacccatccaccagcatgaagaccgctgcttga 497

Qy     464 GGCTCCAGGTGTCTGTCTGCTGCAA 488
           || |  ||||| ||||| |  ||||
Db     498 ggttgaaggtgactgtcagtggcaa 522


RESULT   9
AAS21387
ID   AAS21387 standard; cDNA; 1496 BP.
XX
AC   AAS21387;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human cDNA sequence encoding for PRO202 polypeptide.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW   breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW   cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW   adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US32678.
XX
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   09-DEC-1999;   99US-0170262.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30911.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31243.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
```

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PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US04914.
PR   24-FEB-2000; 2000WO-US05004.
PR   01-MAR-2000; 2000WO-US05601.
PR   20-MAR-2000; 2000WO-US07377.
PR   21-MAR-2000; 2000WO-US07532.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   10-NOV-2000; 2000WO-US30873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   P-PSDB; AAU12315.
XX
PT   Isolated, secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing
PT   PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT   lung, breast, prostate, cervical  -
XX
PS   Claim 3; Fig 287; 813pp; English.
XX
CC   AAS21244-AAS21518 encode for novel human secretory and transmembrane
CC   PRO polypeptides. The PRO polypeptides are useful to detect other
CC   PRO polypeptides, to link bioactive molecules to cells expressing
CC   PRO polypeptides, to modulate biological activities of cells expressing
CC   PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample.
CC   Some of the 275 sequences are also useful to stimulate the release of
CC   tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC   proliferation or differentiation of chondrocytes, the proliferation or
CC   gene expression in pericyte cells, the release of proteoglycans from
CC   cartilage, the proliferation of inner ear utricular supporting cells or
CC   of T-lymphocytes, the release of a cytokine from peripheral blood
CC   monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC   the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC   skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC   to factor VIIA. The PRO polypeptides can be used in assays to identify
CC   molecules involved in binding interactions. The polynucleotides encoding
CC   PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy.
XX
SQ   Sequence 1496 BP; 362 A; 427 C; 398 G; 309 T; 0 other;


  Query Match             16.0%;  Score 101.8;  DB 22;  Length 1496;
  Best Local Similarity   56.9%;  Pred. No. 1.3e-16;
  Matches  253;  Conservative    0;  Mismatches  177;  Indels   15;  Gaps    3;

Qy     56 TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAG 115
          ||||||||||| |  || | ||           |   || | |       ||||||   |
Db     97 tcctctgggcccctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccg 156

Qy    116 TCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCC 175
          ||| |||||||      || |||| ||| |     |  |||  |    |  |  ||   |
Db    157 tcttctggaacagttcaaatcccaagttccggaatgaggactacaccatacatgtgcagc 216

Qy    176 TCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGG---CCCAGGGCCCCCTGAGG 232
          | || || ||| | |||||  |||| || ||||| ||||    | | | | |    |  |
Db    217 tgaatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgctg 276

Qy    233 GCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAG 292
           |   |||  ||      ||||| |||||||       |  ||  ||   |||||| |
Db    277 ccatggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagcccc 336

Qy    293 AGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT---------TGGCCATG 343
          ||    ||  || | |    ||||||  ||||  || ||||           |||||  |
Db    337 ag---tccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcatggcccgg 393

Qy    344 TTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTAC 403
             |  | || |||||| | |||||||||||||||||| |||| |||   ||||||  |
Db    394 agaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggagttcaaag 453

Qy    404 CTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGA 463
            ||| | |  ||||||||||||||    ||||  |   ||  |   | ||  |||||||
Db    454 aaggacacagctactactacatctccaaacccatccaccagcatgaagaccgctgcttga 513

Qy    464 GGCTCCAGGTGTCTGTCTGCTGCAA 488
          || |  ||||| ||||| |  ||||
Db    514 ggttgaaggtgactgtcagtggcaa 538


RESULT  10
AAC90574
ID   AAC90574 standard; cDNA; 1496 BP.
XX
AC   AAC90574;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO202 cDNA.
XX
KW   Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;
KW   vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;
KW   vulnerary; antianginal; gene therapy; cardiovascular disease;
KW   endothelial disorder; angiogenic disorder; cancer; periodontal disease;
KW   wound healing; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073445-A2.
XX
PD   07-DEC-2000.
XX
PF   17-MAY-2000; 2000WO-US13705.
XX
PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   28-JUL-1999;   99US-0146222.
PR   01-SEP-1999;   99WO-US20111.
PR   30-NOV-1999;   99WO-US28313.
PR   30-NOV-1999;   99WO-US28409.
PR   02-DEC-1999;   99WO-US28565.
PR   16-DEC-1999;   99WO-US30095.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   24-FEB-2000; 2000WO-US05004.
PR   02-MAR-2000; 2000WO-US05841.
PR   10-MAR-2000; 2000WO-US06319.
PR   15-MAR-2000; 2000WO-US06884.
PR   21-MAR-2000; 2000WO-US07532.
PR   30-MAR-2000; 2000WO-US08439.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Gurney AL,  Kuo SS,  Mark MR,  Marsters SA;
PI   Paoni NF,  Pitti RM,  Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2001-025251/03.
DR   P-PSDB; AAB50962.
XX
PT   Seventeen nucleic acids encoding PRO polypeptides which are useful in
```

```
PT   diagnosis and treatment of cardiovascular, endothelial or angiogenic
PT   disorders in a mammal -
XX
PS   Claim 60; Fig 23; 182pp; English.
XX
CC   The present sequence is one of seventeen nucleic acids encoding PRO
CC   polypeptides. The PRO nucleic acids, polypeptides, agonists and
CC   antagonists are useful for treating cardiovascular, endothelial or
CC   angiogenic disorders in a mammal. Examples of these disorders include
CC   cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC   atherosclerosis, hypertension, arterial restenosis, Reynaud's disease,
CC   rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis
CC   and lymphangitis. The PRO polypeptides and antagonists are also used to
CC   prevent tumour angiogenesis and for treating periodontal diseases. They
CC   are also used to stimulate wound healing and tissue regeneration.
CC   The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful
CC   for diagnosing a cardiovascular, endothelial or angiogenic disorder.
XX
SQ   Sequence 1496 BP; 362 A; 427 C; 398 G; 309 T; 0 other;


  Query Match             16.0%;  Score 101.8;  DB 22;  Length 1496;
  Best Local Similarity   56.9%;  Pred. No. 1.3e-16;
  Matches  253;  Conservative    0;  Mismatches  177;  Indels   15;  Gaps    3;

Qy     56 TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAG 115
          ||||||||||| |  || | ||           |   || | |       ||||||   |
Db     97 tcctctgggcccctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccg 156

Qy    116 TCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCC 175
          ||| |||||||      || |||| ||| |     |  |||  |    |  |  ||   |
Db    157 tcttctggaacagttcaaatcccaagttccggaatgaggactacaccatacatgtgcagc 216

Qy    176 TCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGG---CCCAGGGCCCCCTGAGG 232
          | || || ||| | |||||  |||| || ||||| ||||    | | | | |    |  |
Db    217 tgaatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgctg 276

Qy    233 GCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAG 292
           |   |||  ||      ||||| |||||||       |  ||  ||   |||||| |
Db    277 ccatggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagcccc 336

Qy    293 AGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT---------TGGCCATG 343
          ||    ||  || | |    ||||||  ||||  || ||||           |||||  |
Db    337 ag---tccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcatggcccgg 393

Qy    344 TTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTAC 403
             |  | || |||||| | |||||||||||||||||| |||| |||   ||||||  |
Db    394 agaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggagttcaaag 453

Qy    404 CTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGA 463
            ||| | |  ||||||||||||||    ||||  |   ||  |   | ||  |||||||
Db    454 aaggacacagctactactacatctccaaacccatccaccagcatgaagaccgctgcttga 513

Qy    464 GGCTCCAGGTGTCTGTCTGCTGCAA 488
          || |  ||||| ||||| |  ||||
Db    514 ggttgaaggtgactgtcagtggcaa 538


RESULT 11
AAC91576
ID   AAC91576 standard; cDNA; 1496 BP.
XX
AC   AAC91576;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO202 cDNA.
XX
KW   Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
KW   antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW   PRO agonist; cancer; inflammatory disorder; immunological disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073348-A2.
XX
PD   07-DEC-2000.
XX
PF   30-MAY-2000; 2000WO-US14941.
XX
PR   02-JUN-1999;   99WO-US12252.
PR   22-JUN-1999;   99US-0140650.
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   29-OCT-1999;   99US-0162506.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30999.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   02-MAR-2000; 2000WO-US05841.
PR   03-MAR-2000; 2000US-0187202.
PR   10-MAR-2000; 2000WO-US06319.
PR   15-MAR-2000; 2000WO-US06884.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W,  Kabakoff RC;
PI   Shelton DL,  Smith V,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-016509/02.
DR   P-PSDB; AAB50974.
XX
PT   Twenty eight nucleic acids encoding PRO polypeptides which are useful
PT   for treating various tumors, e.g. breast cancer, and other
PT   inflammatory, angiogenic and immunological disorders -
XX
PS   Claim 20; Fig 47; 188pp; English.
XX
CC   The present sequence is one of twenty eight nucleic acids encoding PRO
CC   polypeptides. The PRO polypeptides and their agonists, including
CC   antibodies, peptides, and small molecule agonists, may be used to treat
CC   various tumours, e.g., cancers such as breast cancer, ovarian cancer,
CC   renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung
CC   cancer, bladder cancer, central nervous system cancer, melanoma or
CC   leukaemia. They are also useful for treating other disorders
CC   such as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC   macrophagal, epithelial, stromal and blastocoelic disorders, and
CC   inflammatory, angiogenic and immunological disorders.
XX
SQ   Sequence 1496 BP; 362 A; 427 C; 398 G; 309 T; 0 other;


  Query Match             16.0%;  Score 101.8;  DB 22;  Length 1496;
  Best Local Similarity   56.9%;  Pred. No. 1.3e-16;
  Matches  253;  Conservative    0;  Mismatches  177;  Indels   15;  Gaps    3;

Qy     56 TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAG 115
          ||||||||||| |  || | ||           |   || | |       ||||||   |
Db     97 tcctctgggcccctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccg 156

Qy    116 TCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCC 175
          ||| |||||||      || |||| ||| |     |  |||  |    |  |  ||   |
Db    157 tcttctggaacagttcaaatcccaagttccggaatgaggactacaccatacatgtgcagc 216

Qy    176 TCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGG---CCCAGGGCCCCCTGAGG 232
          | || || ||| | |||||  |||| || ||||| ||||    | | | | |    |  |
Db    217 tgaatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgctg 276
```

```
Qy     233 GCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAG 292
            |   |||  ||      ||||| |||||||       |  ||  ||   |||||| |
Db     277 ccatggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagcccc 336

Qy     293 AGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT---------TGGCCATG 343
           ||    ||  || | |    ||||||  ||||  || ||||           |||||  |
Db     337 ag---tccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcatggcccgg 393

Qy     344 TTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTAC 403
              |  | || |||||| | |||||||||||||||||| |||| |||   ||||||  |
Db     394 agaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggagttcaaag 453

Qy     404 CTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGA 463
             ||| | |  ||||||||||||||    ||||  |   ||  |   | ||  |||||||
Db     454 aaggacacagctactactacatctccaaacccatccaccagcatgaagaccgctgcttga 513

Qy     464 GGCTCCAGGTGTCTGTCTGCTGCAA 488
           || |  ||||| ||||| |  ||||
Db     514 ggttgaaggtgactgtcagtggcaa 538

RESULT  12
AAC98823
ID   AAC98823 standard; cDNA; 1527 BP.
XX
AC   AAC98823;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:51.
XX
KW   Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
KW   detection; diagnosis; identification; cytostatic; neuroprotective;
KW   nootropic; immunomodulatory; relaxant; contraceptive; gynaecological;
KW   antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW   linkage analysis; tissue identification; tissue typing; forensic;
KW   neural; immune system; muscular; reproductive; gastrointestinal;
KW   pulmonary; cardiovascular; renal; proliferative; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055320-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05989.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-579444/54.
DR   P-PSDB; AAB54058.
XX
PT   New nucleic acid that is a pancreatic cancer antigen for preventing,
PT   treating, or ameliorating a medical condition, particular pancreatic
PT   cancer, or for use in assays for diagnosing a pathological condition -
XX
PS   Claim 1; Page 531-532; 1379pp; English.
XX
CC   AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC   proteins, called pancreatic cancer antigens, given in AAB54008 to
CC   AAB54466. The human pancreatic cancer antigens have cytostatic,
CC   neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
CC   gynaecological, cardiant and antiinflammatory activities, and can be used
CC   in gene therapy. The polynucleotide and proteins can be used for
CC   preventing, treating, or ameliorating a medical condition or in assays
CC   for diagnosing a pathological condition or a susceptibility to one in a
CC   subject. Binding partners to the proteins and the activity of the
CC   proteins can be identified. The pancreatic cancer antigens can be used to
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CC   detect, treat or prevent pancreatic disorders, especially cancer.
CC   Agonists and antagonists to the antigens can be screened for. The
CC   pancreatic cancer antigen polynucleotides can be used to design nucleic
CC   acid hybridisation probes that can be used in chromosome mapping, linkage
CC   analysis, tissue identification and/or typing and a variety of forensic
CC   and diagnostic methods. The proteins can be used to generate antibodies
CC   which are used to purify, detect and target the polypeptides, including
CC   both in vivo and in vitro diagnostic and therapeutic methods. The
CC   proteins can be used to treat or prevent neural, immune system, muscular,
CC   reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC   proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC   sequences used in the exemplification of the present invention.
XX
SQ   Sequence 1527 BP; 397 A; 426 C; 394 G; 308 T; 2 other;

  Query Match              16.0%;  Score 101.8;  DB 21;  Length 1527;
  Best Local Similarity   56.9%;  Pred. No. 1.3e-16;
  Matches  253;  Conservative    0;  Mismatches  177;  Indels   15;  Gaps    3;

Qy      56 TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAG 115
           ||||||||||| |  || | ||           |   || | |       ||||||   |
Db      98 tcctctgggcccctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccg 157

Qy     116 TCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCC 175
           ||| |||||||      || |||| ||| |     |  |||  |    |  |  ||   |
Db     158 tcttctggaacagttcaaatcccaagttccggaatgaggactacaccatacatgtgcagc 217

Qy     176 TCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGG---CCCAGGGCCCCCTGAGG 232
           | || || ||| | |||||  |||| || ||||| ||||    | | | | |    |  |
Db     218 tgaatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgctg 277

Qy     233 GCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAG 292
            |   |||  ||      ||||| |||||||       |  ||  ||   |||||| |
Db     278 ccatggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagcccc 337

Qy     293 AGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT---------TGGCCATG 343
           ||    ||  || | |    ||||||  ||||  || ||||           |||||  |
Db     338 ag---tccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcatggcccgg 394

Qy     344 TTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTAC 403
              |  | || |||||| | |||||||||||||||||| |||| |||   ||||||  |
Db     395 agaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggagttcaaag 454

Qy     404 CTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGA 463
             ||| | |  ||||||||||||||    ||||  |   ||  |   | ||  |||||||
Db     455 aaggacacagctactactacatctccaaacccatccaccagcatgaagaccgctgcttga 514

Qy     464 GGCTCCAGGTGTCTGTCTGCTGCAA 488
           || |  ||||| ||||| |  ||||
Db     515 ggttgaaggtgactgtcagtggcaa 539

RESULT  13
AAH81578
ID   AAH81578 standard; DNA; 439 BP.
XX
AC   AAH81578;
XX
DT   21-SEP-2001  (first entry)
XX
DE   Human differential transcription-associated cDNA SEQ ID 87.
XX
KW   Differential transcription; human; rat; tumour cell; cytostatic;
KW   Ras modulator; Class II tumour suppressor gene; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157058-A2.
XX
PD   09-AUG-2001.
XX
PF   31-JAN-2001; 2001WO-EP01003.
```

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XX
PR   31-JAN-2000; 2000DE-1004102.
XX
PA   (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI   Rosenthal A,  Hinzmann B,  Schaefer R,  Zuber J,  Tchernitsa O;
PI   Grips M,  Hellriegel M,  Schmitz A,  Sers C;
XX
DR   WPI; 2001-483415/52.
XX
PT   Nucleic acids differentially expressed between tumor and normal cells,
PT   useful for diagnosis or therapy of tumors and for screening active
PT   agents  -
XX
PS   Disclosure; Page 354-355; 579pp; German.
XX
CC   This invention describes a nucleic acid (I) with differential expression
CC   between tumour and normal cells and which has cytostatic activity. (I)
CC   work as modulators of Ras activity by inducing expression of tumour
CC   suppressor genes. (I), and polypeptides encoded by them, are useful as
CC   targets for diagnosis or therapy and in screening to determine the
CC   effects of an active compound (potential pharmaceutical) on a cell line,
CC   particularly for diagnosis and treatment of tumors, especially by
CC   modulating expression of (I) (by gene therapy, antisense RNA or ribozyme
CC   methods) or by modulating the amount and/or location of (I)-encoded
CC   polypeptides (by administration of the polypeptide or its activator,
CC   antibody (optionally as a conjugate) or inhibitor). The method allows
CC   identification of many Class II tumour suppressor genes (i.e. genes that
CC   are not primary targets for tumour-initiating mutations).
CC   AAH81492-AAH82376 represent the human and rat derived nucleic acid
CC   fragments described in the method of the invention.
XX
SQ   Sequence 439 BP; 106 A; 130 C; 113 G; 90 T; 0 other;

  Query Match             15.3%;  Score 97.2;  DB 22;  Length 439;
  Best Local Similarity   56.3%;  Pred. No. 1.5e-15;
  Matches  249;  Conservative    0;  Mismatches  178;  Indels   15;  Gaps    3;

Qy         58 CTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTC 117
              ||||||||| |  || | ||           |   || | |       ||||||   |||
Db          1 ctctgggcccctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccgtc 60

Qy        118 TACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTC 177
              | |||||||      || |||| ||| |     |  |||  |    |  |  ||   ||
Db         61 ttctggaacagttcaaatcccaagttccggaatgaggactacaccatacatgtgcagctg 120

Qy        178 AACGATTACCTAGACATTGTCTGCCCCCACTACGAAGGCC---CAGGGCCCCCTGAGGGC 234
              || || ||| | |||||  |||| || ||||| ||||  |   | | | |    |  | |
Db        121 aatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgctgcc 180

Qy        235 CCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAG 294
                 |||  ||      ||||| |||||||       |  ||  ||   |||||| |  ||
Db        181 atggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagccccag 240

Qy        295 GGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT---------TGGCCATGTT 345
                  ||  || | |    ||||||  ||||  || ||||           |||||  |
Db        241 t---ccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcatggcccggag 297

Qy        346 CAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCT 405
               |  | || |||||| | |||||||||||||||||| |||| |||   ||||||  |
Db        298 aagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggagttcaaagaa 357

Qy        406 GGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGG 465
              ||| | |  ||||||||||||||    ||||  |   ||  |   | ||  |||||||||
Db        358 ggacacagctactactacatctccaaacccatccaccagcatgaagaccgctgcttgagg 417

Qy        466 CTCCAGGTGTCTGTCTGCTGCA 487
               |  ||||  ||||| |  |||
Db        418 ttgaaggtaactgtcagtggca 439


RESULT  14
AAS92779
ID   AAS92779 standard; cDNA; 1574 BP.
XX
AC   AAS92779;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #28583.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG28592.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 28583; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1574 BP; 344 A; 446 C; 346 G; 438 T; 0 other;

  Query Match             14.9%;  Score 94.8;  DB 23;  Length 1574;
  Best Local Similarity   51.9%;  Pred. No. 8.5e-15;
  Matches  241;  Conservative    0;  Mismatches  217;  Indels    6;  Gaps    1;

Qy          3 CAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTG 62
              | | |||  |  ||  | |   | |  |  | ||  ||   || | | |    ||
Db        270 ctggccaggcgtgatgttgcacgtggagatgttgacgctggtgtttctggtgctctggat 329

Qy         63 GGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTG 122
              |   | ||||  |     |||      |  || |  |  |  |||| |||  ||||||||
Db        330 gtgtgtgttcagccaggacccgggctccaaggccgtcgccgaccgctacgctgtctactg 389
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Qy    123 GAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGA 182
          ||||  ||| |||||||| || |   | || |||  |    | ||  |  |  |||| ||
Db    390 gaacagcagcaaccccagattccagaggggtgactaccatattgatgtctgtatcaatga 449

Qy    183 TTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGAC 242
           ||||| ||  || ||||||| ||||| || | | | |  ||    ||     | |||
Db    450 ctacctggatgttttctgccctcactatgaggactccgtcccagaagataagactgagcg 509

Qy    243 GTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCA------GGCAGAGGG 296
           | ||   | ||||||||| |||     |||||     ||||| |        |  | ||
Db    510 ctatgtcctctacatggtgaactttgatggctacagtgcctgcgaccacacttccaaagg 569

Qy    297 CCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGA 356
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Db    570 gttcaagagatgggaatgtaaccggcctcactctccaaatggaccgctgaagttctctga 629

Qy    357 GAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTA 416
           ||  | |||| |||||| || || || || || ||||| |||   || ||       ||
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Qy    417 CTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCT 460
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Db    690 tttctacatctcctctgcaatcccagataatggaagaaggtcct 733

RESULT  15
AAT34292
ID   AAT34292 standard; cDNA; 1728 BP.
XX
AC   AAT34292;
XX
DT   24-OCT-1996  (first entry)
XX
DE   HEK4 binding protein cDNA.
XX
KW   HEK4 binding protein; HEK4 receptor; EPH-like receptor;
KW   protein tyrosine kinase; ligand; growth; differentiation; cancer;
KW   nervous system disorder; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             175..861
FT                   /*tag=  a
FT   sig_peptide     175..231
FT                   /*tag=  b
FT   mat_peptide     232..858
FT                   /*tag=  c
XX
PN   WO9623000-A1.
XX
PD   01-AUG-1996.
XX
PF   16-JAN-1996;   96WO-US01079.
XX
PR   27-JAN-1995;   95US-0379802.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Bartley TD,  Fox GM;
XX
DR   WPI; 1996-362633/36.
DR   P-PSDB; AAW00035.
XX
PT   Ligand for EPH-like receptors, partic. the HEK4 receptor - useful to
PT   modulate growth and differentiation of, e.g. liver and kidney cells,
PT   and to treat cancer and nervous system disorders
XX
PS   Claim 15; Page 38-39; 65pp; English.
XX
CC   A cDNA clone (AAT34292) codes for human HEK4 binding protein (HEK4 BP)
CC   (AAW00035), a protein that binds to and activates HEK4 and ECK
```

```
CC   receptors.  It was isolated from a human placenta cDNA library using
CC   primers (see also AAT34295-96) based on isolated peptides (AAW00036-38)
CC   of HEK4 BP.  The cDNA can be used for recombinant prodn. of HEK4 BP,
CC   useful for modulating the growth and/or differentiation of EPH sub-
CC   family receptor-bearing cells.  It can also be used to detect or
CC   quantitate HEK4 BP nucleic acids, to detect abnormalities in the
CC   HEK4 BP gene, or to control expression levels of HEK4 BP.
XX
SQ   Sequence 1728 BP; 402 A; 495 C; 401 G; 430 T; 0 other;

  Query Match             14.9%;  Score 94.8;  DB 17;  Length 1728;
  Best Local Similarity   51.9%;  Pred. No. 8.8e-15;
  Matches  241;  Conservative    0;  Mismatches  217;  Indels    6;  Gaps    1;

Qy      3 CAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTG 62
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Db    162 ctggccaggcgtgatgttgcacgtggagatgttgacgctggtgtttctggtgctctggat 221

Qy     63 GGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTG 122
          |   | ||||  |     |||      |  || |  |  |  |||| |||  ||||||||
Db    222 gtgtgtgttcagccaggacccgggctccaaggccgtcgccgaccgctacgctgtctactg 281

Qy    123 GAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGA 182
          ||||  ||| |||||||| || |   | || |||  |    | ||  |  |  |||| ||
Db    282 gaacagcagcaaccccagattccagaggggtgactaccatattgatgtctgtatcaatga 341

Qy    183 TTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGAC 242
           ||||| ||  || ||||||| ||||| || | | | |  ||    ||     | |||
Db    342 ctacctggatgttttctgccctcactatgaggactccgtcccagaagataagactgagcg 401

Qy    243 GTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCA------GGCAGAGGG 296
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Db    402 ctatgtcctctacatggtgaactttgatggctacagtgcctgcgaccacacttccaaagg 461

Qy    297 CCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGA 356
             |  |   |   |  |      |     |   ||   ||| |   |  | ||||| ||
Db    462 gttcaagagatgggaatgtaaccggcctcactctccaaatggaccgctgaagttctctga 521

Qy    357 GAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTA 416
           ||  | |||| |||||| || || || || || ||||| |||   || ||       ||
Db    522 aaaattccagctcttcactcccttttctctaggatttgaattcaggccaggccgagaata 581

Qy    417 CTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCT 460
           | |||||||||     | |  ||||| | |    |   || ||
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Search completed: September 28, 2002, 00:26:53
Job time: 11248 sec
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                    GenCore version 4.5
            Copyright (c) 1993 - 2000  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          September 27, 2002, 22:42:54 ; Search time 65.52 Seconds
                                               (without alignments)
                                               2384.355 Million cell updates/sec

Title:           US-09-904-954-3
Perfect score:   636
Sequence:        1 GCCAGACCAAACCGGACCTC.........TTCTGCGAATTCTGTGAGCC 636

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters:      767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                1:  /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                2:  /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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                6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                 %
Result          Query
  No.   Score   Match Length DB  ID                          Description
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    1     636   100.0    636  1  US-08-240-124-3              Sequence 3, Appli
    2     636   100.0    636  1  US-08-453-943-3              Sequence 3, Appli
    3     636   100.0    636  2  US-09-057-121-3              Sequence 3, Appli
    4     636   100.0    636  4  US-09-358-734-3              Sequence 3, Appli
    5     134    21.1  17138  4  US-09-813-819-3              Sequence 3, Appli
    6     134    21.1  17138  4  US-09-920-048-3              Sequence 3, Appli
    7   121.6    19.1    783  1  US-08-455-001-3              Sequence 3, Appli
    8   121.6    19.1    783  5  PCT-US95-11869-3             Sequence 3, Appli
    9   115.4    18.1   1070  1  US-08-299-567-8              Sequence 8, Appli
   10   103.4    16.3   1037  1  US-08-240-124-1              Sequence 1, Appli
   11   103.4    16.3   1037  1  US-08-453-943-1              Sequence 1, Appli
   12   103.4    16.3   1037  2  US-09-057-121-1              Sequence 1, Appli
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   14   101.8    16.0   1480  1  US-08-448-736-11             Sequence 11, Appl
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   18   101.8    16.0   1498  1  US-08-321-162-1              Sequence 1, Appli
   19   101.8    16.0   1498  1  US-08-441-216-1              Sequence 1, Appli
   20    94.8    14.9   1728  3  US-08-379-802-1              Sequence 1, Appli
   21    94.8    14.9   1728  3  US-09-048-129-1              Sequence 1, Appli
   22    94.8    14.9   1728  4  US-09-048-079-1              Sequence 1, Appli
   23    94.8    14.9   1839  1  US-08-442-248-3              Sequence 3, Appli
   24    94.8    14.9   1839  1  US-08-440-815-3              Sequence 3, Appli
   25    94.8    14.9   1839  4  US-08-486-449-3              Sequence 3, Appli
   26      94    14.8   1615  4  US-08-308-814-1              Sequence 1, Appli
   27      94    14.8   1809  1  US-08-455-001-1              Sequence 1, Appli
   28      94    14.8   1809  5  PCT-US95-11869-1             Sequence 1, Appli
   29      92    14.5    687  5  PCT-US95-15781-4             Sequence 4, Appli
   30    91.6    14.4    642  1  US-09-609-324A-9             Sequence 9, Appli
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   32    91.6    14.4    642  4  US-09-173-492-9              Sequence 9, Appli
   33    91.6    14.4    642  4  US-09-173-133-9              Sequence 9, Appli
   34    86.2    13.6    555  1  US-09-609-324A-1             Sequence 1, Appli
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   44    82.2    12.9    314  4  US-09-173-133-7              Sequence 7, Appli
   45    82.2    12.9    314  4  US-09-165-533-7              Sequence 7, Appli


                              ALIGNMENTS


RESULT   1
US-08-240-124-3
; Sequence 3, Application US/08240124
; Patent No. 5516658
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/240,124
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  636 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
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;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  hek-L C6
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  94..630
;    FEATURE:
;      NAME/KEY:  CDS
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;    FEATURE:
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;      LOCATION:  28..93
US-08-240-124-3

  Query Match             100.0%;  Score 636;  DB 1;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-162;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60

Qy       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
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Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
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Db      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540

Qy      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
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Db      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600

Qy      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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Db      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636


RESULT   2
US-08-453-943-3
; Sequence 3, Application US/08453943
; Patent No. 5738844
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,943
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/240,124
;      FILING DATE:  09-MAY-1994
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  636 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  hek-L C6
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  94..630
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  28..633
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  28..93
US-08-453-943-3

  Query Match             100.0%;  Score 636;  DB 1;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-162;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Qy       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
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Db    121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180

Qy    181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
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Qy    241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
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Qy    361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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RESULT   3
US-09-057-121-3
; Sequence 3, Application US/09057121
; Patent No. 5969110
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,121
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,124
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  636 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  hek-L C6
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  94..630
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  28..633
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  28..93
US-09-057-121-3

  Query Match             100.0%;  Score 636;  DB 2;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-162;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db      1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60

Qy     61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120

Qy    121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180

Qy    181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240

Qy    241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300

Qy    301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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Db    301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360

Qy    361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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Db    361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420

Qy    421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480

Qy    481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540

Qy    541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
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Db     541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600

Qy     601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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Db     601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636


RESULT   4
US-09-358-734-3
; Sequence 3, Application US/09358734
; Patent No. 6274117
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/358,734
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,124
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  636 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  hek-L C6
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  94..630
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  28..633
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  28..93
US-09-358-734-3
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  Query Match             100.0%;  Score 636;  DB 4;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-162;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60

Qy      61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120

Qy     121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180

Qy     181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240

Qy     241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
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Db     241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300

Qy     301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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Qy     361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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Db     361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420

Qy     421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
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Db     421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480

Qy     481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
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Db     481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540

Qy     541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600

Qy     601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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RESULT   5
US-09-813-819-3
; Sequence 3, Application US/09813819
; Patent No. 6294368
; GENERAL INFORMATION:
;  APPLICANT: MERKULOV, Gennady et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001177
;  CURRENT APPLICATION NUMBER: US/09/813,819
;  CURRENT FILING DATE:  2001-03-22
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 17138
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(17138)
;   OTHER INFORMATION: n = A,T,C or G
US-09-813-819-3
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  Query Match             21.1%;  Score 134;  DB 4;  Length 17138;
  Best Local Similarity   80.5%;  Pred. No. 8.9e-27;
  Matches  169;  Conservative    0;  Mismatches   40;  Indels    1;  Gaps    1;

Qy      1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db  16167 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtccta 16226

Qy     61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16227 tgggccgcg-tcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 16285

Qy    121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
          |||||||||||||||||||||| ||   |  ||  ||     | | |        ||  |
Db  16286 tggaactccagtaaccccaggtagccgggccgaaccgggcgagcgcacagccaagtctgc 16345

Qy    181 GATTACCTAGACATTGTCTGCCCCCACTAC 210
          |    ||  | | |||   || ||| | ||
Db  16346 gcgctcccgggctttgcgcgcgcccgccac 16375


RESULT   6
US-09-920-048-3
; Sequence 3, Application US/09920048
; Patent No. 6344352
; GENERAL INFORMATION:
;  APPLICANT: MERKULOV, Gennady et al
;  TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001177DIV
;  CURRENT APPLICATION NUMBER: US/09/920,048
;  CURRENT FILING DATE:  2001-08-02
;  PRIOR APPLICATION NUMBER: 09/813,819
;  PRIOR FILING DATE: 2001-03-22
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 17138
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(17138)
;   OTHER INFORMATION: n = A,T,C or G
US-09-920-048-3

  Query Match             21.1%;  Score 134;  DB 4;  Length 17138;
  Best Local Similarity   80.5%;  Pred. No. 8.9e-27;
  Matches  169;  Conservative    0;  Mismatches   40;  Indels    1;  Gaps    1;

Qy      1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db  16167 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtccta 16226

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          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16227 tgggccgcg-tcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 16285

Qy    121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
          |||||||||||||||||||||| ||   |  ||  ||     | | |        ||  |
Db  16286 tggaactccagtaaccccaggtagccgggccgaaccgggcgagcgcacagccaagtctgc 16345

Qy    181 GATTACCTAGACATTGTCTGCCCCCACTAC 210
          |    ||  | | |||   || ||| | ||
Db  16346 gcgctcccgggctttgcgcgcgcccgccac 16375


RESULT   7
US-08-455-001-3
; Sequence 3, Application US/08455001
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; Patent No. 5795734
;  GENERAL INFORMATION:
;    APPLICANT:  Flanagan, John G.
;    APPLICANT:  Cheng, Hwai-Jong
;    TITLE OF INVENTION:  EPH Receptor Ligands, and Uses Related
;    TITLE OF INVENTION:  Thereto
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/455,001
;      FILING DATE:  31 MAY 1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMI-011CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  783 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  86..685
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..85
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  686..783
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  86..148
US-08-455-001-3

  Query Match             19.1%;  Score 121.6;  DB 1;  Length 783;
  Best Local Similarity   62.0%;  Pred. No. 7.2e-24;
  Matches  212;  Conservative    0;  Mismatches  124;  Indels    6;  Gaps    1;

Qy    105 CCGCCACGTAGTCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGT 164
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Db    172 CCGCTACGCCGTCTATTGGAACCGCAGCAACCCCAGGTTCCACCGCGGGGATTACACCGT 231

Qy    165 GGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCC 224
          |||| || || |||| || ||||| |||||   |||||| |||||||| |  ||   |||
Db    232 GGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCTCACTACGAGGAGCCGCTGCC 291

Qy    225 CCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTG 284
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Db    292 CGCCGAGCGCATGGAGCGCTACGTCCTCTACATGGTCAACTACGAGGGCCACGCGTCCTG 351

Qy    285 ------CCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGG 338
                || |    |||||  |      |   || ||     |  |  |   |||   ||
Db    352 CGACCACCGGCAGAAGGGCTTCAAACGTTGGGAGTGCAACCGGCCCGACTCCCCCAGCGG 411

Qy    339 CCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTT 398
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Db    412 ACCCCTCAAGTTCTCAGAGAAGTTCCAGCTCTTCACCCCCTTCTCTTTGGGCTTCGAGTT 471

Qy    399 CTTACCTGGAGAGACTTACTACTACATCTCGGTGCCCACTCC 440
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Db    472 CCGTCCCGGCCACGAGTATTACTACATCTCTGCGTCTCCCCC 513


RESULT   8
PCT-US95-11869-3
; Sequence 3, Application PC/TUS9511869
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  EPH Receptor Ligands, and Uses Related
;    TITLE OF INVENTION:  Thereto
;    NUMBER OF SEQUENCES:  5
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11869
;      FILING DATE:  19-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Vincent, Matthew P.
;      REGISTRATION NUMBER:  36,709
;      REFERENCE/DOCKET NUMBER:  HMI-011CPPC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  783 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  86..685
;    FEATURE:
;      NAME/KEY:  5'UTR
;      LOCATION:  1..85
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  686..783
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  86..148
PCT-US95-11869-3

  Query Match             19.1%;  Score 121.6;  DB 5;  Length 783;
  Best Local Similarity   62.0%;  Pred. No. 7.2e-24;
  Matches  212;  Conservative    0;  Mismatches  124;  Indels    6;  Gaps    1;

Qy    105 CCGCCACGTAGTCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGT 164
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Qy    165 GGAGCTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCC 224
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Db    232 GGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCTCACTACGAGGAGCCGCTGCC 291

Qy    225 CCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTG 284
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Qy    285 ------CCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGG 338
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Db    352 CGACCACCGGCAGAAGGGCTTCAAACGTTGGGAGTGCAACCGGCCCGACTCCCCCAGCGG 411
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Qy    339 CCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTT 398
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Db    412 ACCCCTCAAGTTCTCAGAGAAGTTCCAGCTCTTCACCCCCTTCTCTTTGGGCTTCGAGTT 471

Qy    399 CTTACCTGGAGAGACTTACTACTACATCTCGGTGCCCACTCC 440
          |   || ||  |    || ||||||||||| | | |  | ||
Db    472 CCGTCCCGGCCACGAGTATTACTACATCTCTGCGTCTCCCCC 513


RESULT   9
US-08-299-567-8
; Sequence 8, Application US/08299567
; Patent No. 5747033
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, et al.
;    TITLE OF INVENTION:  METHOD OF ENHANCING THE BIOLOGICAL
;    TITLE OF INVENTION:  ACTIVITY OF EPH FAMILY LIGANDS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Regeneron Pharmaceuticals, Inc.
;      STREET:  777 Old Saw Mill River Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10591-6707
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/299,567
;      FILING DATE:  01-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kempler, Gail M.
;      REGISTRATION NUMBER:  32,143
;      REFERENCE/DOCKET NUMBER:  REG 290
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  914-345-7400
;      TELEFAX:  914-345-7721
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1070 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-299-567-8

  Query Match             18.1%;  Score 115.4;  DB 1;  Length 1070;
  Best Local Similarity   55.6%;  Pred. No. 3.7e-22;
  Matches  271;  Conservative    0;  Mismatches  201;  Indels   15;  Gaps    2;

Qy     15 GACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
          | |  |||   || ||| ||||||||  |||||   | | || |    |    || | ||
Db     48 GGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCT 107

Qy     75 CGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
           | |      |   | ||||      |   ||| || |  || |||||||||  |   ||
Db    108 GGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAA 167

Qy    135 CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
          ||      |||  ||||  | |  |   ||| || ||  | | ||||| || || || ||
Db    168 CCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 227

Qy    195 TGTCTGCCCCCACTAC------------GAAGGCCCAGGGCCCCCTGAGGGCCCCGAGAC 242
          |  |||||| ||||||            |  || || ||||||   |  ||  | |||
Db    228 TTACTGCCCGCACTACAACAGCTCGGGGGCGGGACCGGGGCCCGGAGGCGGGGCAGAGCA 287

Qy    243 GTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC---AGAGGGCCC 299
          ||  |   |||||||||||  | |    |||||     ||||| | ||     |||||
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Db    288 GTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGCCAGCCAGGGCTT 347

Qy    300 CCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAA 359
          |  |  ||   || ||     |     |   ||     |||   |  | ||||| |||||
Db    348 CAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAAGTTCTCGGAGAA 407

Qy    360 GATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTA 419
          | | ||||||| ||   | ||||| || ||||  ||||||    | ||  |    |||||
Db    408 GTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGGCCACGAGTACTA 467

Qy    420 CTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGT 479
          |||||||||   ||||||||   |        |  ||||  ||||| |  ||||||  ||
Db    468 CTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGATGAAGGTGTTCGT 527

Qy    480 CTGCTGC 486
          |||||||
Db    528 CTGCTGC 534

RESULT  10
US-08-240-124-1
; Sequence 1, Application US/08240124
; Patent No. 5516658
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/240,124
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1037 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  hek-L A2
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  83..799
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  83..139
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  140..796
US-08-240-124-1

  Query Match             16.3%;  Score 103.4;  DB 1;  Length 1037;
  Best Local Similarity   54.3%;  Pred. No. 6.2e-19;
  Matches  271;  Conservative    0;  Mismatches  201;  Indels   27;  Gaps    2;

Qy     15 GACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
          | |  |||   || ||| ||||||||  |||||   | | || |    |    || | ||
Db     85 GGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCT 144

Qy     75 CGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
           | |      |   | ||||      |   ||| || |  || |||||||||  |   ||
Db    145 GGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAA 204

Qy    135 CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
          ||      |||  ||||  | |  |   ||| || ||  | | ||||| || || || ||
Db    205 CCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 264

Qy    195 TGTCTGCCCCCACTACGAAGGC------------------------CCAGGGCCCCCTGA 230
          |  |||||| |||||| |  ||                        || ||||||   |
Db    265 TTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGG 324

Qy    231 GGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC 290
           ||  | |||  ||  |   |||||||||||  | |    |||||     ||||| | ||
Db    325 CGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGC 384

Qy    291 ---AGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCA 347
               |||||  |  |  ||   || ||     |     |   ||     |||   |  |
Db    385 CAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAA 444

Qy    348 ATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407
           ||||| |||||| | ||||||| ||   | ||||| || ||||  ||||||    | ||
Db    445 GTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGG 504

Qy    408 AGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCT 467
            |    ||||||||||||||   ||||||||   |        |  ||||  ||||| |
Db    505 CCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGAT 564

Qy    468 CCAGGTGTCTGTCTGCTGC 486
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Db    565 GAAGGTGTTCGTCTGCTGC 583

RESULT  11
US-08-453-943-1
; Sequence 1, Application US/08453943
; Patent No. 5738844
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
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;       OPERATING SYSTEM:  Apple System 7.1
;       SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/453,943
;       FILING DATE:  30-MAY-1995
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/240,124
;       FILING DATE:  09-MAY-1994
;       APPLICATION NUMBER:  US 08/161,132
;       FILING DATE:  03-DEC-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/114,426
;       FILING DATE:  30-AUG-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/109,745
;       FILING DATE:  20-AUG-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SEESE, KATHRYN A.
;       REGISTRATION NUMBER:  32,172
;       REFERENCE/DOCKET NUMBER:  2814-C
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 587-0430
;       TELEFAX:  (206) 233-0644
;       TELEX:  756822
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1037 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     IMMEDIATE SOURCE:
;       CLONE:  hek-L A2
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  83..799
;     FEATURE:
;       NAME/KEY:  sig_peptide
;       LOCATION:  83..139
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  140..796
US-08-453-943-1


  Query Match             16.3%;  Score 103.4;  DB 1;  Length 1037;
  Best Local Similarity   54.3%;  Pred. No. 6.2e-19;
  Matches  271;  Conservative    0;  Mismatches  201;  Indels   27;  Gaps    2;

Qy       15 GACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
            | |  |||   || ||| ||||||||  |||||   | | || |    |    || | ||
Db       85 GGCGGCGGCTCCGCTGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCT 144

Qy       75 CGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
             | |      |   | ||||      |   ||| || |  || |||||||||  |   ||
Db      145 GGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAA 204

Qy      135 CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
            ||      |||  ||||  | |  |   ||| || ||  | | ||||| || || || ||
Db      205 CCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 264

Qy      195 TGTCTGCCCCCACTACGAAGGC------------------------CCAGGGCCCCCTGA 230
            |  |||||| |||||| |  ||                        || ||||||   | 
Db      265 TTACTGCCCGCACTACAACAGCTCGGGGGTGGGCCCCGGGGCGGGACCGGGGCCCGGAGG 324

Qy      231 GGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC 290
             ||  | |||  ||  |   |||||||||||  | |    |||||     ||||| | ||
Db      325 CGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGC 384

Qy      291 ---AGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCA 347
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Db      385 CAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAA 444

Qy      348 ATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407
             ||||| |||||| | ||||||| ||   |  ||||| || ||||  ||||||    | ||
Db      445 GTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGG 504

Qy      408 AGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCT 467
              |    |||||||||||||||   ||||||||   |        |  ||||  ||||| |
Db      505 CCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGAT 564

Qy      468 CCAGGTGTCTGTCTGCTGC 486
              ||||||  |||||||||
Db      565 GAAGGTGTTCGTCTGCTGC 583


RESULT  12
US-09-057-121-1
; Sequence 1, Application US/09057121
; Patent No. 5969110
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,121
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,124
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1037 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  hek-L A2
;    FEATURE:
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;       NAME/KEY:  CDS
;       LOCATION:  83..799
;     FEATURE:
;       NAME/KEY:  sig_peptide
;       LOCATION:  83..139
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  140..796
US-09-057-121-1

  Query Match             16.3%;  Score 103.4;  DB 2;  Length 1037;
  Best Local Similarity   54.3%;  Pred. No. 6.2e-19;
  Matches  271;  Conservative    0;  Mismatches  201;  Indels   27;  Gaps    2;

Qy       15 GACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
            | |  |||   || ||| ||||||||  |||||   | | || |    |    || | ||
Db       85 GGCGGCGGCTCCGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCT 144

Qy       75 CGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
             | |      |   | ||||      |   ||| || |  || |||||||||  |   ||
Db      145 GGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAA 204

Qy      135 CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
            ||      |||  ||||  | |  |   ||| || ||  | | ||||| || || || ||
Db      205 CCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 264

Qy      195 TGTCTGCCCCCACTACGAAGGC------------------------CCAGGGCCCCCTGA 230
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Db      265 TTACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGG 324

Qy      231 GGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC 290
             ||  | |||  ||  |   |||||||||||  | |    |||||     ||||| | ||
Db      325 CGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGC 384

Qy      291 ---AGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCA 347
                 |||||  |  |  ||   || ||     |     |   ||     |||   |  |
Db      385 CAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAA 444

Qy      348 ATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407
             ||||| |||||| | ||||||| ||   | ||||| || ||||  ||||||    | ||
Db      445 GTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGG 504

Qy      408 AGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCT 467
              |    ||||||||||||||   ||||||||   |        |  ||||  ||||| |
Db      505 CCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGAT 564

Qy      468 CCAGGTGTCTGTCTGCTGC 486
              ||||||  |||||||||
Db      565 GAAGGTGTTCGTCTGCTGC 583

RESULT 13
US-09-358-734-1
; Sequence 1, Application US/09358734
; Patent No. 6274117
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/358,734
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,124
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1037 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  hek-L A2
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  83..799
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  83..139
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  140..796
US-09-358-734-1

  Query Match             16.3%;  Score 103.4;  DB 4;  Length 1037;
  Best Local Similarity   54.3%;  Pred. No. 6.2e-19;
  Matches  271;  Conservative    0;  Mismatches  201;  Indels   27;  Gaps    2;

Qy       15 GACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
            | |  |||   || ||| ||||||||  |||||   | | || |    |    || | ||
Db       85 GGCGGCGGCTCCGCTGCTGCTGCTGCTGCTCGTGCCCGTGCCGCTGCTGCCGCTGCT 144

Qy       75 CGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
             | |      |   | ||||      |   ||| || |  || |||||||||  |   ||
Db      145 GGCCCAAGGGCCCGGAGGGGCGCTGGGAAACCGGCATGCGGTGTACTGGAACAGCTCCAA 204

Qy      135 CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
            ||      |||  ||||  | |  |   ||| || ||  | | ||||| || || || ||
Db      205 CCAGCACCTGCGGCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATAT 264

Qy      195 TGTCTGCCCCCACTACGAAGGC------------------------CCAGGGCCCCCTGA 230
            |  |||||| |||||| |  ||                        || ||||||   |
Db      265 TTACTGCCCGCACTACAACAGCTCGGGGGTGGCCCCGGGGCGGACCGGGGCCCGGAGG 324

Qy      231 GGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC 290
             ||  | |||  ||  |   |||||||||||  | |    |||||     ||||| | ||
Db      325 CGGGGCAGAGCAGTACGTGCTGTACATGGTGAGCCGCAACGGCTACCGCACCTGCAACGC 384

Qy      291 ---AGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCA 347
                 |||||  |  |  ||   || ||     |     |   ||     |||   |  |
Db      385 CAGCCAGGGCTTCAAGCGCTGGGAGTGCAACCGGCCGCACGCCCCGCACAGCCCCATCAA 444
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Qy       348 ATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407
              ||||| |||||| | ||||||| ||   | ||||| || ||||  ||||||    | ||
Db       445 GTTCTCGGAGAAGTTCCAGCGCTACAGCGCCTTCTCTCTGGGCTACGAGTTCCACGCCGG 504

Qy       408 AGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCT 467
               |    ||||||||||||||   ||||||||   |        |  ||||  ||||| |
Db       505 CCACGAGTACTACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTCTGAGGAT 564

Qy       468 CCAGGTGTCTGTCTGCTGC 486
               ||||||  |||||||||
Db       565 GAAGGTGTTCGTCTGCTGC 583

RESULT 14
US-08-448-736-11
; Sequence 11, Application US/08448736
; Patent No. 5650504
;  GENERAL INFORMATION:
;    APPLICANT:  Bartley, Timothy Dudley
;    APPLICANT:  Fox, Gary Michael
;    APPLICANT:  Boyle, William James
;    APPLICANT:  Welcher, Andrew Avery
;    APPLICANT:  Parker, Vann Phillips
;    TITLE OF INVENTION:  Eck Receptor Ligands
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  Amgen Center
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 in., DS, 2.0 Mb
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh OS 7.0
;      SOFTWARE:  Microsoft Word Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/448,736
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/145,616
;      FILING DATE:  09-NOV-1993
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1480  nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double-stranded
;      TOPOLOGY:  linear
US-08-448-736-11

  Query Match             16.0%;  Score 101.8;  DB 1;  Length 1480;
  Best Local Similarity   56.9%;  Pred. No. 1.9e-18;
  Matches  253;  Conservative    0;  Mismatches  177;  Indels   15;  Gaps    3;

Qy        56 TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAG 115
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Db        81 TCCTCTGGGCCCCTCTCTTGGGTCTGTGCTGCAGTCTGGCCGCTGCTGATCGCCACACCG 140

Qy       116 TCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCC 175
             ||| |||||||      || |||| ||| |     |  |||  |    |  |  ||   |
Db       141 TCTTCTGGAACAGTTCAAATCCCAAGTTCCGGAATGAGGACTACACCATACATGTGCAGC 200

Qy       176 TCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGG---CCCAGGGCCCCCTGAGG 232
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Db       261 CCATGGAGCAGTACATACTGTACCTGGTGGAGCATGAGGAGTACCAGCTGTGCCAGCCCC 320
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Db       378 AGAAGCTGTCTGAGAAGTTCCAGCGCTTCACACCTTTCACCCTGGGCAAGGAGTTCAAAG 437

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; Sequence 11, Application US/08452779
; Patent No. 5716934
;  GENERAL INFORMATION:
;    APPLICANT:  Bartley, Timothy Dudley
;    APPLICANT:  Fox, Gary Michael
;    APPLICANT:  Boyle, William James
;    APPLICANT:  Welcher, Andrew Avery
;    APPLICANT:  Parker, Vann Phillips
;    TITLE OF INVENTION:  Eck Receptor Ligands
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  Amgen Center
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 in., DS, 2.0 Mb
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh OS 7.0
;      SOFTWARE:  Microsoft Word Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/452,779
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/145,616
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1480  nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double-stranded
;      TOPOLOGY:  linear
US-08-452-779-11

  Query Match             16.0%;  Score 101.8;  DB 1;  Length 1480;
  Best Local Similarity   56.9%;  Pred. No. 1.9e-18;
  Matches  253;  Conservative    0;  Mismatches  177;  Indels   15;  Gaps    3;

Qy        56 TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAG 115
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Search completed: September 27, 2002, 22:43:03
Job time: 8659 sec
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                      GenCore version 4.5
             Copyright (c) 1993 - 2000  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          September 28, 2002, 01:28:23 ; Search time 3673.16 Seconds
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Title:           US-09-904-954-3
Perfect score:   636
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters:      43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

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    3     636      100.0    636 18  US-09-440-302A-839         Sequence 839, App
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ALIGNMENTS

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;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09282
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
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;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  636 base pairs
;      TYPE:  nucleic acid
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;      TOPOLOGY:  linear
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360

Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420

Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480

Qy      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540

Qy      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600

Qy      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
            ||||||||||||||||||||||||||||||||||||
Db      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636


RESULT   2
US-08-161-132-3
; Sequence 3, Application US/08161132
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
```

```
;       STATE:  WASHINGTON
;       COUNTRY:  USA
;       ZIP:  98101
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/161,132
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/114,426
;       FILING DATE:  30-AUG-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/109,745
;       FILING DATE:  20-AUG-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SEESE, KATHRYN A.
;       REGISTRATION NUMBER:  32,172
;       REFERENCE/DOCKET NUMBER:  2814-B
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 587-0430
;       TELEFAX:  (206) 233-0644
;       TELEX:  756822
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  636 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     IMMEDIATE SOURCE:
;       CLONE:  hek-L C6
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  94..630
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  28..633
;     FEATURE:
;       NAME/KEY:  sig_peptide
;       LOCATION:  28..93
US-08-161-132-3

  Query Match             100.0%;  Score 636;  DB 5;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-145;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60

Qy       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120

Qy      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180

Qy      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240

Qy      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
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```
Qy      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360

Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420

Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480

Qy      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540

Qy      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600

Qy      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
            ||||||||||||||||||||||||||||||||||||
Db      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636


RESULT   3
US-09-440-302A-839
; Sequence 839, Application US/09440302A
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey E.
;  TITLE OF INVENTION: Human Neurobiology Array
;  FILE REFERENCE: CLON-006CIP11
;  CURRENT APPLICATION NUMBER: US/09/440,302A
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 1193
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 839
;   LENGTH: 636
;   .TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-440-302A-839

  Query Match             100.0%;  Score 636;  DB 18;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-145;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctc 60

Qy       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 tgggccgcgttcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 120

Qy      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 tggaactccagtaaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaac 180

Qy      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 gattacctagacattgtctgcccccactacgaaggcccagggccccctgagggccccgag 240

Qy      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 acgtttgctttgtacatggtggactggccaggctatgagtcctgccaggcagagggcccc 300

Qy      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 cgggcctacaagcgctgggtgtgctccctgccctttggccatgttcaattctcagagaag 360
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Qy    361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 attcagcgcttcacacctttctccctcggctttgagttcttacctggagagacttactac 420

Qy    421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 tacatctcggtgcccactccagagagttctggccagtgcttgaggctccaggtgtctgtc 480

Qy    481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 tgctgcaaggagaggaagtctgagtcagcccatcctgttgggagccctggagagagtggc 540

Qy    541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 acatcagggtggcgagggggggacactcccagccccctctgtctcttgctattactgctg 600

Qy    601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
          ||||||||||||||||||||||||||||||||||||
Db    601 cttctgattcttcgtcttctgcgaattctgtgagcc 636


RESULT   4
US-09-904-954-3
; Sequence 3, Application US/09904954
;   GENERAL INFORMATION:
;        APPLICANT: BECKMANN, M. P.
;                   CERRETTI, DOUGLAS P.
;        TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
;                            RECEPTOR HEK
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: IMMUNEX CORPORATION
;             STREET: 51 UNIVERSITY STREET
;             CITY: SEATTLE
;             STATE: WASHINGTON
;             COUNTRY: USA
;             ZIP: 98101
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: Apple Macintosh
;             OPERATING SYSTEM: Apple System 7.1
;             SOFTWARE: Microsoft Word for Apple, Version 5.1a
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/904,954
;             FILING DATE: 12-Jul-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/240,124
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 08/114,426
;             FILING DATE: 30-AUG-1993
;             APPLICATION NUMBER: US 08/109,745
;             FILING DATE: 20-AUG-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SEESE, KATHRYN A.
;             REGISTRATION NUMBER: 32,172
;             REFERENCE/DOCKET NUMBER: 2814-C
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 587-0430
;             TELEFAX: (206) 233-0644
;             TELEX: 756822
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 636 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA to mRNA
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        IMMEDIATE SOURCE:
;             CLONE: hek-L C6
;        FEATURE:
;             NAME/KEY:  mat_peptide
;             LOCATION:  94..630
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  28..633
;        FEATURE:
;             NAME/KEY:  sig_peptide
;             LOCATION:  28..93
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-904-954-3


  Query Match             100.0%;  Score 636;  DB 34;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-145;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60

Qy     61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120

Qy    121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180

Qy    181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240

Qy    241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300

Qy    301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360

Qy    361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420

Qy    421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480

Qy    481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540

Qy    541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600

Qy    601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
          ||||||||||||||||||||||||||||||||||||
Db    601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636


RESULT   5
US-09-652-122-4283
; Sequence 4283, Application US/09652122
; GENERAL INFORMATION:
;  APPLICANT:  Shyjan, Andrew W.
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.1194-001
;  CURRENT APPLICATION NUMBER: US/09/652,122
;  CURRENT FILING DATE:  2000-08-30
;  PRIOR APPLICATION NUMBER:  60/151,421
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;  PRIOR FILING DATE:  1999-08-30
;  NUMBER OF SEQ ID NOS:  5020
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 4283
;   LENGTH: 1247
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-652-122-4283

  Query Match             99.7%;  Score 634.4;  DB 25;  Length 1247;
  Best Local Similarity   99.8%;  Pred. No. 6.3e-145;
  Matches  635;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      50 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctc 109

Qy      61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     110 tgggccgcgttcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 169

Qy     121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     170 tggaactccagtaaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaac 229

Qy     181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     230 gattacctagacattgtctgcccccactacgaaggcccagggccccctgagggccccgag 289

Qy     241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     290 acgtttgctttgtacatggtggactggccaggctatgagtcctgccaggcagagggcccc 349

Qy     301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     350 cgggcctacaagcgctgggtgtgctccctgccctttggccatgttcaattctcagagaag 409

Qy     361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
           ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     410 attcagcgcttcacacccttctccctcggctttgagttcttacctggagagacttactac 469

Qy     421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     470 tacatctcggtgcccactccagagagttctggccagtgcttgaggctccaggtgtctgtc 529

Qy     481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     530 tgctgcaaggagaggaagtctgagtcagcccatcctgttgggagccctggagagagtggc 589

Qy     541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     590 acatcagggtggcgagggggggacactcccagccccctctgtctcttgctattactgctg 649

Qy     601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
           ||||||||||||||||||||||||||||||||||||
Db     650 cttctgattcttcgtcttctgcgaattctgtgagcc 685

RESULT   6
US-09-698-010-11684
; Sequence 11684, Application US/09698010
; GENERAL INFORMATION:
;  APPLICANT:  Williamson, Mark
;  APPLICANT:  Shyjan, Andrew W.
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.2029-001
;  CURRENT APPLICATION NUMBER: US/09/698,010
;  CURRENT FILING DATE:  2000-10-27
;  PRIOR APPLICATION NUMBER:  60/162,358
;  PRIOR FILING DATE:  1999-10-29
;  NUMBER OF SEQ ID NOS:  15684
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;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 11684
;   LENGTH: 1247
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-698-010-11684

  Query Match             99.7%;  Score 634.4;  DB 27;  Length 1247;
  Best Local Similarity   99.8%;  Pred. No. 6.3e-145;
  Matches  635;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      50 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctc 109

Qy      61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     110 tgggccgcgttcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 169

Qy     121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     170 tggaactccagtaaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaac 229

Qy     181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     230 gattacctagacattgtctgcccccactacgaaggcccagggccccctgagggccccgag 289

Qy     241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     290 acgtttgctttgtacatggtggactggccaggctatgagtcctgccaggcagagggcccc 349

Qy     301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     350 cgggcctacaagcgctgggtgtgctccctgccctttggccatgttcaattctcagagaag 409

Qy     361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
           ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     410 attcagcgcttcacacccttctccctcggctttgagttcttacctggagagacttactac 469

Qy     421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     470 tacatctcggtgcccactccagagagttctggccagtgcttgaggctccaggtgtctgtc 529

Qy     481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     530 tgctgcaaggagaggaagtctgagtcagcccatcctgttgggagccctggagagagtggc 589

Qy     541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     590 acatcagggtggcgagggggggacactcccagccccctctgtctcttgctattactgctg 649

Qy     601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
           ||||||||||||||||||||||||||||||||||||
Db     650 cttctgattcttcgtcttctgcgaattctgtgagcc 685

RESULT   7
US-09-700-000-4952
; Sequence 4952, Application US/09700000
; GENERAL INFORMATION:
;  APPLICANT:  Richardson, Jennifer
;  APPLICANT:  Shyjan, Andrew W.
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.2022-001
;  CURRENT APPLICATION NUMBER: US/09/700,000
;  CURRENT FILING DATE:  2000-10-30
;  PRIOR APPLICATION NUMBER:  60/162,619
;  PRIOR FILING DATE:  1999-10-29
;  NUMBER OF SEQ ID NOS:  7171
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 4952
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;   LENGTH: 1247
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-700-000-4952

  Query Match             99.7%;  Score 634.4;  DB 28;  Length 1247;
  Best Local Similarity   99.8%;  Pred. No. 6.3e-145;
  Matches  635;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       50 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctc 109

Qy       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      110 tgggccgcgttcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 169

Qy      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      170 tggaactccagtaaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaac 229

Qy      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      230 gattacctagacattgtctgcccccactacgaaggcccagggccccctgagggccccgag 289

Qy      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      290 acgtttgctttgtacatggtggactggccaggctatgagtcctgccaggcagagggcccc 349

Qy      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      350 cgggcctacaagcgctgggtgtgctccctgccctttggccatgttcaattctcagagaag 409

Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      410 attcagcgcttcacacccttctccctcggctttgagttcttacctggagagacttactac 469

Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      470 tacatctcggtgcccactccagagagttctggccagtgcttgaggctccaggtgtctgtc 529

Qy      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      530 tgctgcaaggagaggaagtctgagtcagcccatcctgttgggagccctggagagagtggc 589

Qy      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      590 acatcagggtggcgagggggggacactcccagccccctctgtctcttgctattactgctg 649

Qy      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
            ||||||||||||||||||||||||||||||||||||
Db      650 cttctgattcttcgtcttctgcgaattctgtgagcc 685

RESULT    8
US-09-760-443-311
; Sequence 311, Application US/09760443
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PJZ12
;  CURRENT APPLICATION NUMBER: US/09/760,443
;  CURRENT FILING DATE:  2001-01-16
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 2164
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 311
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (782)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (793)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (1069)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-760-443-311

  Query Match             97.7%;  Score 621.2;  DB 30;  Length 1273;
  Best Local Similarity   99.2%;  Pred. No. 1.1e-141;
  Matches  631;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       84 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctc 143

Qy       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      144 tgggccgcgttcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 203

Qy      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      204 tggaactccagtaaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaac 263

Qy      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
            |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db      264 gattacctagacattgtctgcccccactacgaaggcccarggccccctgagggccccgag 323

Qy      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      324 acgtttgctttgtacatggtggactggccaggctatgagtcctgccaggcagagggcccc 383

Qy      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      384 cgggcctacaagcgctgggtgtgctccctgccctttggccatgttcaattctcagagaag 443

Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
            |||||||||||||:||| |||||||||||||||:||||||||||||||||||||||||||
Db      444 attcagcgcttcamacccttctccctcggctttragttcttacctggagagacttactac 503

Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      504 tacatctcggtgcccactccagagagttctggccagtgcttgaggctccaggtgtctgtc 563

Qy      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      564 tgctgcaa-gagaggaagtctgagtcagcccatcctgttgggagccctggagagagtggc 622

Qy      541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      623 acatcagggtggcgagggggggacactcccagccccctctgtctcttgctattactgctg 682

Qy      601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
            ||||||||||||||||||||||||||||||||||||
Db      683 cttctgattcttcgtcttctgcgaattctgtgagcc 718

RESULT    9
US-09-306-609-7629
; Sequence 7629, Application US/09306609
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION: FROM A cDNA LIBRARY OF FETAL LIVER-SPLEEN
;  FILE REFERENCE: 20411-718CON2
;  CURRENT APPLICATION NUMBER: US/09/306,609
;  CURRENT FILING DATE: 1999-05-07
;  EARLIER APPLICATION NUMBER: US 09/168,296
;  EARLIER FILING DATE: 1998-10-07
;  EARLIER APPLICATION NUMBER: US 08/949,553
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;  EARLIER FILING DATE: 1997-10-09
;  NUMBER OF SEQ ID NOS: 13025
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7629
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(531)
;   OTHER INFORMATION: n = A,T,C or G
US-09-306-609-7629


  Query Match             73.8%;  Score 469.4;  DB 17;  Length 531;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-104;
  Matches  481;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy       12 CCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTT 71
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctctgggccgcgtt 60

Qy       72 CCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAG 131
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 cctcggctcccctctgcgcgggggctccagcctccgccacgtagtctactggaactccag 120

Qy      132 TAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGA 191
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 taaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaacgattacctaga 180

Qy      192 CATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTT 251
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 cattgtctgcccccactacgaaggcccagggccccctgagggccccgagacgtttgcttt 240

Qy      252 GTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAA 311
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 gtacatggtggactggccaggctatgagtcctgccaggcagagggcccccgggcctacaa 300

Qy      312 GCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTT 371
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 gcgctgggtgtgctccctgccctttggccatgttcaattctcagagaagattcagcgctt 360

Qy      372 CACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGT 431
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 cacacccttctccctcggctttgagttcttacctggagagacttactactacatctcggt 420

Qy      432 GCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGGA 491
            ||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||||||
Db      421 gcccactccagagagttctgg-cagtgcttgaggctccangtgtctgtctgctgcaagga 479

Qy      492 GAGGA 496
            || ||
Db      480 ganga 484

RESULT 10
US-09-522-251-7629
; Sequence 7629, Application US/09522251
; GENERAL INFORMATION:
;  APPLICANT: Drmanac, Radoje T.
;  APPLICANT: Labat, Ivan
;  APPLICANT: Stache-Crain, Birgit
;  APPLICANT: Dickson, Mark C.
;  APPLICANT: Jones, Lee W.
;  APPLICANT: Garcia, Veronica E.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION: FROM A cDNA LIBRARY OF FETAL LIVER-SPLEEN
;  FILE REFERENCE: 718CIP
;  CURRENT APPLICATION NUMBER: US/09/522,251
;  CURRENT FILING DATE: 2000-03-09
;  EARLIER APPLICATION NUMBER: 09/306,609
;  EARLIER FILING DATE: 1999-05-07
;  EARLIER APPLICATION NUMBER: 09/168,296
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;  EARLIER FILING DATE: 1998-10-07
;  EARLIER APPLICATION NUMBER: 60/150,686
;  EARLIER FILING DATE: 1997-10-09
;  NUMBER OF SEQ ID NOS: 13025
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7629
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(531)
;   OTHER INFORMATION: n = A,T,C or G
US-09-522-251-7629


  Query Match             73.8%;  Score 469.4;  DB 19;  Length 531;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-104;
  Matches  481;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy       12 CCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTT 71
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctctgggccgcgtt 60

Qy       72 CCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAG 131
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 cctcggctcccctctgcgcgggggctccagcctccgccacgtagtctactggaactccag 120

Qy      132 TAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGA 191
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 taaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaacgattacctaga 180

Qy      192 CATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTT 251
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 cattgtctgcccccactacgaaggcccagggccccctgagggccccgagacgtttgcttt 240

Qy      252 GTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAA 311
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 gtacatggtggactggccaggctatgagtcctgccaggcagagggcccccgggcctacaa 300

Qy      312 GCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTT 371
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 gcgctgggtgtgctccctgccctttggccatgttcaattctcagagaagattcagcgctt 360

Qy      372 CACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGT 431
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 cacacccttctccctcggctttgagttcttacctggagagacttactactacatctcggt 420

Qy      432 GCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGGA 491
            ||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||||||
Db      421 gcccactccagagagttctgg-cagtgcttgaggctccangtgtctgtctgctgcaagga 479

Qy      492 GAGGA 496
            || ||
Db      480 ganga 484


RESULT 11
US-10-025-600-7629
; Sequence 7629, Application US/10025600
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM A cDNA LIBRARY OF FETAL LIVER-SPLEEN
;  FILE REFERENCE: 20411-718CON2
;  CURRENT APPLICATION NUMBER: US/10/025,600
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/306,609
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-07
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/168,296
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/949,553
;  PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-09
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;  NUMBER OF SEQ ID NOS: 13025
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7629
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(531)
;   OTHER INFORMATION: n = A,T,C or G
US-10-025-600-7629


  Query Match             73.8%;  Score 469.4;  DB 37;  Length 531;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-104;
  Matches  481;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy      12 CCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTT 71
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctctgggccgcgtt 60

Qy      72 CCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAG 131
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 cctcggctcccctctgcgcgggggctccagcctccgccacgtagtctactggaactccag 120

Qy     132 TAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGA 191
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 taaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaacgattacctaga 180

Qy     192 CATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTT 251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 cattgtctgcccccactacgaaggcccagggccccctgagggccccgagacgtttgcttt 240

Qy     252 GTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAA 311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 gtacatggtggactggccaggctatgagtcctgccaggcagagggcccccgggcctacaa 300

Qy     312 GCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTT 371
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 gcgctgggtgtgctccctgccctttggccatgttcaattctcagagaagattcagcgctt 360

Qy     372 CACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGT 431
           |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db     361 cacacccttctccctcggctttgagttcttacctggagagacttactactacatctcggt 420

Qy     432 GCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGGA 491
           ||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||||||
Db     421 gcccactccagagagttctgg-cagtgcttgaggctccangtgtctgtctgctgcaagga 479

Qy     492 GAGGA 496
           || ||
Db     480 ganga 484

RESULT 12
US-09-205-070-27545
; Sequence 27545, Application US/09205070
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS cDNA
;  TITLE OF INVENTION: LIBRARIES
;  FILE REFERENCE: 20411-748
;  CURRENT APPLICATION NUMBER: US/09/205,070
;  CURRENT FILING DATE: 1998-12-03
;  NUMBER OF SEQ ID NOS: 45207
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27545
;   LENGTH: 532
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(532)
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;   OTHER INFORMATION: n = A,T,C or G
US-09-205-070-27545

  Query Match             73.8%;  Score 469.4;  DB 16;  Length 532;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-104;
  Matches  481;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy      12 CCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTT 71
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 ccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctctgggccgcgtt 61

Qy      72 CCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAG 131
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 cctcggctcccctctgcgcgggggctccagcctccgccacgtagtctactggaactccag 121

Qy     132 TAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGA 191
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 taaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaacgattacctaga 181

Qy     192 CATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTT 251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 cattgtctgcccccactacgaaggcccagggccccctgagggccccgagacgtttgcttt 241

Qy     252 GTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAA 311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 gtacatggtggactggccaggctatgagtcctgccaggcagagggcccccgggcctacaa 301

Qy     312 GCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTT 371
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     302 gcgctgggtgtgctccctgccctttggccatgttcaattctcagagaagattcagcgctt 361

Qy     372 CACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGT 431
           |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db     362 cacacccttctccctcggctttgagttcttacctggagagacttactactacatctcggt 421

Qy     432 GCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGGA 491
           ||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||||||
Db     422 gcccactccagagagttctgg-cagtgcttgaggctccangtgtctgtctgctgcaagga 480

Qy     492 GAGGA 496
           || ||
Db     481 ganga 485

RESULT 13
US-09-340-623-27545
; Sequence 27545, Application US/09340623
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS cDNA
;  TITLE OF INVENTION: LIBRARIES
;  FILE REFERENCE: 20411-748CON1
;  CURRENT APPLICATION NUMBER: US/09/340,623
;  CURRENT FILING DATE: 1999-06-28
;  EARLIER APPLICATION NUMBER: US 09/205,070
;  EARLIER FILING DATE: 1998-12-03
;  NUMBER OF SEQ ID NOS: 45207
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27545
;   LENGTH: 532
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(532)
;   OTHER INFORMATION: n = A,T,C or G
US-09-340-623-27545


  Query Match             73.8%;  Score 469.4;  DB 17;  Length 532;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-104;
  Matches  481;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;
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Qy     12 CCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTT 71
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 ccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctctgggccgcgtt 61

Qy     72 CCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAG 131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 cctcggctcccctctgcgcgggggctccagcctccgccacgtagtctactggaactccag 121

Qy    132 TAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGA 191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 taaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaacgattacctaga 181

Qy    192 CATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTT 251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 cattgtctgcccccactacgaaggcccagggccccctgagggccccgagacgtttgcttt 241

Qy    252 GTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAA 311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 gtacatggtggactggccaggctatgagtcctgccaggcagagggcccccgggcctacaa 301

Qy    312 GCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTT 371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 gcgctgggtgtgctccctgccctttggccatgttcaattctcagagaagattcagcgctt 361

Qy    372 CACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGT 431
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 cacacccttctccctcggctttgagttcttacctggagagacttactactacatctcggt 421

Qy    432 GCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGGA 491
          ||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||||||
Db    422 gcccactccagagagttctgg-cagtgcttgaggctccangtgtctgtctgctgcaagga 480

Qy    492 GAGGA 496
          || ||
Db    481 ganga 485


RESULT 14
US-09-898-888-27545
; Sequence 27545, Application US/09898888
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS cDNA
;  TITLE OF INVENTION:  LIBRARIES
;  FILE REFERENCE: 20411-748CON1
;  CURRENT APPLICATION NUMBER: US/09/898,888
;  CURRENT FILING DATE:  2001-07-03
;  PRIOR APPLICATION NUMBER: 09/340,623
;  PRIOR FILING DATE: 1999-06-28
;  NUMBER OF SEQ ID NOS: 45207
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27545
;   LENGTH: 532
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(532)
;   OTHER INFORMATION: n = A,T,C or G
US-09-898-888-27545


  Query Match             73.8%;  Score 469.4;  DB 33;  Length 532;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-104;
  Matches  481;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy     12 CCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTT 71
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 ccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctctgggccgcgtt 61

Qy     72 CCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAG 131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 cctcggctcccctctgcgcgggggctccagcctccgccacgtagtctactggaactccag 121

Qy    132 TAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGA 191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 taaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaacgattacctaga 181

Qy    192 CATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTT 251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 cattgtctgcccccactacgaaggcccagggccccctgagggccccgagacgtttgcttt 241

Qy    252 GTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAA 311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 gtacatggtggactggccaggctatgagtcctgccaggcagagggcccccgggcctacaa 301

Qy    312 GCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTT 371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 gcgctgggtgtgctccctgccctttggccatgttcaattctcagagaagattcagcgctt 361

Qy    372 CACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGT 431
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 cacacccttctccctcggctttgagttcttacctggagagacttactactacatctcggt 421

Qy    432 GCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGGA 491
          ||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||||||
Db    422 gcccactccagagagttctgg-cagtgcttgaggctccangtgtctgtctgctgcaagga 480

Qy    492 GAGGA 496
          || ||
Db    481 ganga 485


RESULT 15
US-09-898-888A-27545
; Sequence 27545, Application US/09898888A
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS cDNA
;  TITLE OF INVENTION:  LIBRARIES
;  FILE REFERENCE: 20411-748CON1
;  CURRENT APPLICATION NUMBER: US/09/898,888A
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/340,623
;  PRIOR FILING DATE: 1999-06-28
;  PRIOR APPLICATION NUMBER: US 09/205,070
;  PRIOR FILING DATE: 1998-12-03
;  NUMBER OF SEQ ID NOS: 45207
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27545
;   LENGTH: 532
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(532)
;   OTHER INFORMATION: n = A,T,C or G
US-09-898-888A-27545


  Query Match             73.8%;  Score 469.4;  DB 33;  Length 532;
  Best Local Similarity   99.2%;  Pred. No. 1.4e-104;
  Matches  481;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy     12 CCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTT 71
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 ccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctctgggccgcgtt 61

Qy     72 CCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAG 131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 cctcggctcccctctgcgcgggggctccagcctccgccacgtagtctactggaactccag 121

Qy    132 TAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGA 191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 taaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaacgattacctaga 181
```

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Qy      192 CATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTT 251
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      182 cattgtctgcccccactacgaaggcccagggccccctgagggccccgagacgtttgcttt 241

Qy      252 GTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAA 311
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      242 gtacatggtggactggccaggctatgagtcctgccaggcagagggcccccgggcctacaa 301

Qy      312 GCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTT 371
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      302 gcgctgggtgtgctccctgccctttggccatgttcaattctcagagaagattcagcgctt 361

Qy      372 CACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGT 431
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      362 cacacccttctccctcggctttgagttcttacctggagagacttactactacatctcggt 421

Qy      432 GCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGGA 491
            ||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||||||
Db      422 gcccactccagagagttctgg-cagtgcttgaggctccangtgtctgtctgctgcaagga 480

Qy      492 GAGGA 496
            || ||
Db      481 ganga 485


Search completed: September 28, 2002, 01:28:27
Job time: 14517 sec
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                    GenCore version 4.5
             Copyright (c) 1993 - 2000  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         September 28, 2002, 01:35:23 ; Search time 401.97 Seconds
                                               (without alignments)
                                               5139.396 Million cell updates/sec

Title:          US-09-904-954-3
Perfect score:  636
Sequence:       1 GCCAGACCAAACCGGACCTC..........TTCTGCGAATTCTGTGAGCC 636

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2167403 seqs, 1624121725 residues

Total number of hits satisfying chosen parameters:      4334806

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Pending_Patents_NA_New:*
               1:  /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
               2:  /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
               3:  /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
               4:  /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
               5:  /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
               6:  /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
               7:  /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
               8:  /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the total score of the result being printed,
      and is derived by analysis of the total score distribution.

                               SUMMARIES
                      %
Result               Query
  No.     Score      Match Length DB  ID                         Description
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    1       636      100.0    636  5  US-09-053-375B-187          Sequence 187, App
    2       636      100.0    636  5  US-09-440-302B-839          Sequence 839, App
    3     621.2       97.7   1273  6  US-10-206-021-271           Sequence 271, App
    4     621.2       97.7   1273  6  US-10-212-054-311           Sequence 311, App
    5       357       56.1    472  5  US-09-918-995-20569         Sequence 20569, A
    6       317       49.8    481  7  US-10-142-593-207           Sequence 207, App
    7     288.6       45.4   5831  6  US-10-206-021-924           Sequence 924, App
    8     288.6       45.4   5831  6  US-10-212-054-1809          Sequence 1809, Ap
    9       267       42.0    267  5  US-09-442-366A-548          Sequence 548, App
   10       267       42.0    267  5  US-09-440-302B-242          Sequence 242, App
   11     143.4       22.5    771  7  US-10-027-632-32020         Sequence 32020, A
   12     103.4       16.3    987  1  PCT-US02-25766-6624         Sequence 6624, Ap
   13     103.4       16.3    987  5  US-09-053-375B-186          Sequence 186, App
   14     103.4       16.3    987  5  US-09-440-302B-838          Sequence 838, App
   15     101.8       16.0   1480  1  PCT-US02-13644-14           Sequence 14, Appl
   16     101.8       16.0   1480  5  US-09-053-375B-1504         Sequence 1504, Ap
   17     101.8       16.0   1480  5  US-09-442-384B-743          Sequence 743, App
   18     101.8       16.0   1480  5  US-09-440-302B-837          Sequence 837, App
   19     101.8       16.0   1480  7  US-10-007-926A-227          Sequence 227, App
   20     101.8       16.0   1480  7  US-10-136-819-14            Sequence 14, Appl
   21     101.8       16.0   1480  7  US-10-171-311-49            Sequence 49, Appl
   22     101.8       16.0   1480  7  US-10-171-581-190           Sequence 190, App
   23     101.8       16.0   1496  1  PCT-US02-24563-287          Sequence 287, App
   24     101.8       16.0   1496  6  US-10-194-359-287           Sequence 287, App
   25     101.8       16.0   1496  6  US-10-192-007-287           Sequence 287, App
   26     101.8       16.0   1496  6  US-10-210-951-39            Sequence 39, Appl
   27     101.8       16.0   1496  6  US-10-211-858-39            Sequence 39, Appl
   28     101.8       16.0   1496  6  US-10-211-884-39            Sequence 39, Appl
   29     101.8       16.0   1496  6  US-10-230-417-287           Sequence 287, App
   30     101.8       16.0   1496  7  US-10-121-049-287           Sequence 287, App
   31     101.8       16.0   1496  7  US-10-121-050-287           Sequence 287, App
   32     101.8       16.0   1496  7  US-10-121-053-287           Sequence 287, App
   33     101.8       16.0   1496  7  US-10-121-043-287           Sequence 287, App
   34     101.8       16.0   1496  7  US-10-121-044-287           Sequence 287, App
   35     101.8       16.0   1496  7  US-10-121-047-287           Sequence 287, App
   36     101.8       16.0   1496  7  US-10-121-054-287           Sequence 287, App
   37     101.8       16.0   1496  7  US-10-121-056-287           Sequence 287, App
   38     101.8       16.0   1496  7  US-10-121-057-287           Sequence 287, App
   39     101.8       16.0   1496  7  US-10-121-058-287           Sequence 287, App
   40     101.8       16.0   1496  7  US-10-121-060-287           Sequence 287, App
   41     101.8       16.0   1496  7  US-10-121-063-287           Sequence 287, App
   42     101.8       16.0   1496  7  US-10-123-108-287           Sequence 287, App
   43     101.8       16.0   1496  7  US-10-123-154-287           Sequence 287, App
   44     101.8       16.0   1496  7  US-10-123-156-287           Sequence 287, App
   45     101.8       16.0   1496  7  US-10-123-157-287           Sequence 287, App

                               ALIGNMENTS

RESULT 1
US-09-053-375B-187
; Sequence 187, Application US/09053375B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Bibilashvilli, Robert
;  TITLE OF INVENTION: Nucleic Acid Arrays
;  FILE REFERENCE: CLON-006
;  CURRENT APPLICATION NUMBER: US/09/053,375B
;  CURRENT FILING DATE:  1998-08-31
;  NUMBER OF SEQ ID NOS: 1543
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 187
;   LENGTH: 636
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-053-375B-187

  Query Match             100.0%;  Score 636;  DB 5;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-142;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctc 60

Qy         61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 tgggccgcgttcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 120

Qy        121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 tggaactccagtaaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaac 180

Qy        181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 gattacctagacattgtctgcccccactacgaaggcccagggccccctgagggccccgag 240

Qy        241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 acgtttgctttgtacatggtggactggccaggctatgagtcctgccaggcagagggcccc 300

Qy        301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 cgggcctacaagcgctgggtgtgctccctgccctttggccatgttcaattctcagagaag 360

Qy        361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 attcagcgcttcacacctttctccctcggctttgagttcttacctggagagacttactac 420

Qy        421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 tacatctcggtgcccactccagagagttctggccagtgcttgaggctccaggtgtctgtc 480

Qy        481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 tgctgcaaggagaggaagtctgagtcagcccatcctgttgggagccctggagagagtggc 540

Qy        541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 acatcagggtggcgagggggggacactcccagccccctctgtctcttgctattactgctg 600

Qy        601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
                ||||||||||||||||||||||||||||||||||||
Db        601 cttctgattcttcgtcttctgcgaattctgtgagcc 636


RESULT   2
US-09-440-302B-839
; Sequence 839, Application US/09440302B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey E.
;  TITLE OF INVENTION: Human Neurobiology Array
;  FILE REFERENCE: CLON-006CIP11
;  CURRENT APPLICATION NUMBER: US/09/440,302B
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 1193
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 839
;   LENGTH: 636
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-440-302B-839


  Query Match             100.0%;  Score 636;  DB 5;  Length 636;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-142;
  Matches  636;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctc 60

Qy         61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 tgggccgcgttcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 120

Qy        121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 tggaactccagtaaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaac 180

Qy        181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 gattacctagacattgtctgcccccactacgaaggcccagggcccccctgagggccccgag 240

Qy        241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 acgtttgctttgtacatggtggactggccaggctatgagtcctgccaggcagagggcccc 300

Qy        301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 cgggcctacaagcgctgggtgtgctccctgccctttggccatgttcaattctcagagaag 360

Qy        361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 attcagcgcttcacacctttctccctcggctttgagttcttacctggagagacttactac 420
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Qy        421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 tacatctcggtgcccactccagagagttctggccagtgcttgaggctccaggtgtctgtc 480

Qy        481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 tgctgcaaggagaggaagtctgagtcagcccatcctgttgggagccctggagagagtggc 540

Qy        541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 acatcagggtggcgagggggggacactcccagccccctctgtctcttgctattactgctg 600

Qy        601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
                ||||||||||||||||||||||||||||||||||||
Db        601 cttctgattcttcgtcttctgcgaattctgtgagcc 636


RESULT   3
US-10-206-021-271
; Sequence 271, Application US/10206021
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ51C1N
;  CURRENT APPLICATION NUMBER: US/10/206,021
;  CURRENT FILING DATE:  2002-07-29
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 937
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 271
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (782)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (793)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1069)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-206-021-271


  Query Match             97.7%;  Score 621.2;  DB 6;  Length 1273;
  Best Local Similarity   99.2%;  Pred. No. 2.8e-138;
  Matches  631;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctc 143

Qy         61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 tgggccgcgttcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 203

Qy        121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 tggaactccagtaaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaac 263

Qy        181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
                |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        264 gattacctagacattgtctgcccccactacgaaggcccarggcccccctgagggccccgag 323

Qy        241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 acgtttgctttgtacatggtggactggccaggctatgagtcctgccaggcagagggcccc 383

Qy        301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     384 cgggcctacaagcgctgggtgtgctccctgccctttggccatgttcaattctcagagaag 443

Qy     361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
             |||||||||||||:||| |||||||||||||||:||||||||||||||||||||||||||
Db     444 attcagcgcttcamacccttctccctcggctttragttcttacctggagagacttactac 503

Qy     421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     504 tacatctcggtgcccactccagagagttctggccagtgcttgaggctccaggtgtctgtc 563

Qy     481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     564 tgctgcaa-gagaggaagtctgagtcagcccatcctgttgggagccctggagagagtggc 622

Qy     541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     623 acatcagggtggcgagggggggacactcccagccccctctgtctcttgctattactgctg 682

Qy     601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
             ||||||||||||||||||||||||||||||||||||
Db     683 cttctgattcttcgtcttctgcgaattctgtgagcc 718


RESULT   4
US-10-212-054-311
; Sequence 311, Application US/10212054
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PJZ12C1N
;  CURRENT APPLICATION NUMBER: US/10/212,054
;  CURRENT FILING DATE:  2002-08-06
;  NUMBER OF SEQ ID NOS: 2164
;  Prior application removed - See File Wrapper or Palm
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 311
;   LENGTH: 1273
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (782)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (793)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1069)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-212-054-311

  Query Match             97.7%;  Score 621.2;  DB 6;  Length 1273;
  Best Local Similarity   99.2%;  Pred. No. 2.8e-138;
  Matches  631;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      84 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctc 143

Qy      61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     144 tgggccgcgttcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 203

Qy     121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     204 tggaactccagtaaccccaggttgcttcgaggagacgccgtggtggagctgggcctcaac 263

Qy     181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
             |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
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Db     264 gattacctagacattgtctgcccccactacgaaggcccarggcccccctgagggccccgag 323

Qy     241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     324 acgtttgctttgtacatggtggactggccaggctatgagtcctgccaggcagagggcccc 383

Qy     301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     384 cgggcctacaagcgctgggtgtgctccctgccctttggccatgttcaattctcagagaag 443

Qy     361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
             |||||||||||||:||| |||||||||||||||:||||||||||||||||||||||||||
Db     444 attcagcgcttcamacccttctccctcggctttragttcttacctggagagacttactac 503

Qy     421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     504 tacatctcggtgcccactccagagagttctggccagtgcttgaggctccaggtgtctgtc 563

Qy     481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     564 tgctgcaa-gagaggaagtctgagtcagcccatcctgttgggagccctggagagagtggc 622

Qy     541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     623 acatcagggtggcgagggggggacactcccagccccctctgtctcttgctattactgctg 682

Qy     601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
             ||||||||||||||||||||||||||||||||||||
Db     683 cttctgattcttcgtcttctgcgaattctgtgagcc 718


RESULT   5
US-09-918-995-20569
; Sequence 20569, Application US/09918995
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20569
;   LENGTH: 472
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(472)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-20569


  Query Match             56.1%;  Score 357;  DB 5;  Length 472;
  Best Local Similarity   98.4%;  Pred. No. 1.8e-75;
  Matches  360;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     271 GGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTG 330
             ||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 ggagacgagtcctgccaggcagagggcccccgggcctacaagcgctgggtgtgctccctg 81

Qy     331 CCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGC 390
             ||||||||||||||||||||||||||||||| ||||||||||||||| ||||||||||||
Db      82 ccctttggccatgttcaattctcagagaagagtcagcgcttcacacccttctccctcggc 141

Qy     391 TTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCT 450
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     142 tttgagttcttacctggagagacttactactacatctcggtgcccactccagagagttct 201

Qy     451 GGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGGAGAGGAAGTCTGAGTCAGCC 510
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 ggccagtgcttgaggctccaggtgtctgtctgctgcaaggagaggaagtctgagtcagcc 261

Qy    511 CATCCTGTTGGGAGCCCTGGAGAGAGTGGCACATCAGGGTGGCGAGGGGGGGACACTCCC 570
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    262 catcctgttgggagccctggagagagtggcacatcanggtggcgagggggggacactccc 321

Qy    571 AGCCCCCTCTGTCTCTTGCTATTACTGCTGCTTCTGATTCTTCGTCTTCTGCGAATTCTG 630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 agcccctctgtctcttgctattactgctgcttctgattcttcgtcttctgcgaattctg 381

Qy    631 TGAGCC 636
          ||||||
Db    382 tgagcc 387


RESULT   6
US-10-142-593-207
; Sequence 207, Application US/10142593
; GENERAL INFORMATION:
;  APPLICANT: Abuin, Alejandro
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: Novel Mutated Mammalian Cells and
;  TITLE OF INVENTION:  Animals
;  FILE REFERENCE: LEX-0339-USA
;  CURRENT APPLICATION NUMBER: US/10/142,593
;  CURRENT FILING DATE:  2002-05-09
;  PRIOR APPLICATION NUMBER: US 60/290,495
;  PRIOR FILING DATE: 2001-05-11
;  NUMBER OF SEQ ID NOS: 352
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207
;   LENGTH: 481
;   TYPE: DNA
;   ORGANISM: mus musculus
US-10-142-593-207


  Query Match             49.8%;  Score 317;  DB 7;  Length 481;
  Best Local Similarity   82.3%;  Pred. No. 5.9e-66;
  Matches  394;  Conservative    0;  Mismatches   70;  Indels   15;  Gaps    2;

Qy    139 AGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGTC 198
          |||||||| |||||||| |||||||||||||||||| |||||||||||||||||||  ||
Db      3 aggttgctccgaggagatgccgtggtggagctgggcttcaacgattacctagacatcttc 62

Qy    199 TGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACATG 258
          ||||| || || ||| ||||||||||||| || ||||| || || ||||| || ||||||
Db     63 tgcccacattatgaaagcccagggcccccagaaggcccggaaacctttgcattatacatg 122

Qy    259 GTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGG 318
          ||||||||| ||||||| ||| |||||  |||||||||  |    |||| | ||||||||
Db    123 gtggactggtcaggctacgaggcctgcacggcagagggggcaaatgccttccagcgctgg 182

Qy    319 GTGTGCTCCCTGCCCTTTG---------GCCATGTTCAATTCTCAGAGAAGATTCAGCGC 369
             |||||  |||| ||||         ||| ||||| ||||||||| ||||||||||||
Db    183 aattgctcgatgccttttgcccctttcagccctgttcgattctcagaaaagattcagcgc 242

Qy    370 TTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCG 429
          | |||||| ||| | || |||||||||||||| |||||||||||||||||||||||||||
Db    243 tacacacccttcccgctgggctttgagttcttgcctggagagacttactactacatctcg 302

Qy    430 GTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAG 489
          ||||| ||||| |||||| |||||| |||| |||| ||||||||||||||||||||||||
Db    303 gtgccgactccggagagtcctggccggtgcctgagactccaggtgtctgtctgctgcaag 362

Qy    490 GAGAGGAAGTC------TGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGCACA 543
          |||||   |||      ||||||||| |||||||||||||| |||||||| || || ||
Db    363 gagagcgggtcatcacatgagtcagctcatcctgttgggagtcctggagaaagcggtacg 422

Qy    544 TCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTGCT 602
          || |||||||| || ||  || | ||||||||||| |||||||||||  | ||||||||
Db    423 tccgggtggcggggaggacacgcgcccagccccctgtgtctcttgctgctgctgctgct 481


RESULT   7
US-10-206-021-924
; Sequence 924, Application US/10206021
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ51C1N
;  CURRENT APPLICATION NUMBER: US/10/206,021
;  CURRENT FILING DATE:  2002-07-29
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 937
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 924
;   LENGTH: 5831
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-206-021-924


  Query Match             45.4%;  Score 288.6;  DB 6;  Length 5831;
  Best Local Similarity   98.6%;  Pred. No. 4.3e-59;
  Matches  291;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    138 CAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGT 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3002 caggttgcttcgaggagacgccgtggtggagctgggcctcaacgattacctagacattgt 3061

Qy    198 CTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACAT 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3062 ctgcccccactacgaaggcccagggcccccctgagggccccgagacgtttgctttgtacat 3121

Qy    258 GGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTG 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3122 ggtggactggccaggctatgagtcctgccaggcagagggcccccgggcctacaagcgctg 3181

Qy    318 GGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACC 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3182 ggtgtgctccctgccctttggccatgttcaattctcagagaagattcagcgcttcacacc 3241

Qy    378 TTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGTG 432
           |||||||||||||||||||||||||||||||||||||||||||||||||  | |
Db   3242 cttctccctcggctttgagttcttacctggagagacttactactacatctgtgag 3296


RESULT   8
US-10-212-054-1809
; Sequence 1809, Application US/10212054
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PJZ12C1N
;  CURRENT APPLICATION NUMBER: US/10/212,054
;  CURRENT FILING DATE:  2002-08-06
;  NUMBER OF SEQ ID NOS: 2164
;  Prior application removed - See File Wrapper or Palm
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1809
;   LENGTH: 5831
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-212-054-1809


  Query Match             45.4%;  Score 288.6;  DB 6;  Length 5831;
  Best Local Similarity   98.6%;  Pred. No. 4.3e-59;
  Matches  291;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    138 CAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGT 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3002 caggttgcttcgaggagacgccgtggtggagctgggcctcaacgattacctagacattgt 3061
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Qy    198 CTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACAT 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3062 ctgcccccactacgaaggcccagggccccctgagggccccgagacgtttgctttgtacat 3121

Qy    258 GGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTG 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3122 ggtggactggccaggctatgagtcctgccaggcagagggcccccgggcctacaagcgctg 3181

Qy    318 GGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACC 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3182 ggtgtgctccctgccctttggccatgttcaattctcagagaagattcagcgcttcacacc 3241

Qy    378 TTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGGTG 432
           |||||||||||||||||||||||||||||||||||||||||||||||||  | |
Db   3242 cttctccctcggctttgagttcttacctggagagacttactactacatctgtgag 3296

RESULT   9
US-09-442-366A-548
; Sequence 548, Application US/09442366A
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey E.
;  TITLE OF INVENTION: Human Array
;  FILE REFERENCE: CLON-006CIP13
;  CURRENT APPLICATION NUMBER: US/09/442,366A
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 2216
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 548
;   LENGTH: 267
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic gene fragment
US-09-442-366A-548

  Query Match             42.0%;  Score 267;  DB 5;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-54;
  Matches  267;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    169 CTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCT 228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ctgggcctcaacgattacctagacattgtctgcccccactacgaaggcccagggccccct 60

Qy    229 GAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAG 288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gagggccccgagacgtttgctttgtacatggtggactggccaggctatgagtcctgccag 120

Qy    289 GCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAA 348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gcagagggcccccgggcctacaagcgctgggtgtgctccctgccctttggccatgttcaa 180

Qy    349 TTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGA 408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ttctcagagaagattcagcgcttcacacctttctccctcggctttgagttcttacctgga 240

Qy    409 GAGACTTACTACTACATCTCGGTGCCC 435
          |||||||||||||||||||||||||||
Db    241 gagacttactactacatctcggtgccc 267

RESULT  10
US-09-440-302B-242
; Sequence 242, Application US/09440302B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey E.
;  TITLE OF INVENTION: Human Neurobiology Array
;  FILE REFERENCE: CLON-006CIP11
;  CURRENT APPLICATION NUMBER: US/09/440,302B
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 1193
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 242
;   LENGTH: 267
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302B-242

  Query Match             42.0%;  Score 267;  DB 5;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-54;
  Matches  267;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    169 CTGGGCCTCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCT 228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ctgggcctcaacgattacctagacattgtctgcccccactacgaaggcccagggccccct 60

Qy    229 GAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAG 288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gagggccccgagacgtttgctttgtacatggtggactggccaggctatgagtcctgccag 120

Qy    289 GCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAA 348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gcagagggcccccgggcctacaagcgctgggtgtgctccctgccctttggccatgttcaa 180

Qy    349 TTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGA 408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ttctcagagaagattcagcgcttcacacctttctccctcggctttgagttcttacctgga 240

Qy    409 GAGACTTACTACTACATCTCGGTGCCC 435
          |||||||||||||||||||||||||||
Db    241 gagacttactactacatctcggtgccc 267

RESULT  11
US-10-027-632-32020
; Sequence 32020, Application US/10027632
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32020
;   LENGTH: 771
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-32020
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  Query Match             22.5%;  Score 143.4;  DB 7;  Length 771;
  Best Local Similarity   99.3%;  Pred. No. 1.2e-24;
  Matches  144;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    398 gccagaccaaaccggacctcgggggcgatgcggctgctgcccctgctgcggactgtcctc 457

Qy     61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    458 tgggccgcgttcctcggctcccctctgcgcgggggctccagcctccgccacgtagtctac 517

Qy    121 TGGAACTCCAGTAACCCCAGGTTGC 145
          |||||||||||||||||||||| ||
Db    518 tggaactccagtaaccccaggtagc 542

RESULT  12
PCT-US02-25766-6624
; Sequence 6624, Application PC/TUS0225766
; GENERAL INFORMATION:
;  APPLICANT: GENE LOGIC, INC.
;  APPLICANT:  MUNGER, William E
;  APPLICANT:  FAULK, Ronald
;  APPLICANT:  SUN, Hongwei
;  APPLICANT:  SASAI, Hitoshi
;  APPLICANT:  WAGA, Iwao
;  APPLICANT:  YAMAMOTO, Jun
;  TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
;  FILE REFERENCE: 44921-5068-WO
;  CURRENT APPLICATION NUMBER: PCT/US02/25766
;  CURRENT FILING DATE:  2002-08-14
;  PRIOR APPLICATION NUMBER: US 60/311,837
;  PRIOR FILING DATE: 2001-08-14
;  NUMBER OF SEQ ID NOS: 13946
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6624
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. U14187
PCT-US02-25766-6624

  Query Match             16.3%;  Score 103.4;  DB 1;  Length 987;
  Best Local Similarity   54.3%;  Pred. No. 4.1e-15;
  Matches  271;  Conservative    0;  Mismatches  201;  Indels   27;  Gaps    2;

Qy     15 GACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
          | |  |||   || ||| ||||||||  |||||   | | || |    |    || | ||
Db     60 ggcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgct 119

Qy     75 CGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
           | |      |   | ||||      |   ||| || |  || |||||||||  |   ||
Db    120 ggcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaa 179

Qy    135 CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
          ||      |||  ||||  | |  |   ||| || ||  | | ||||| || || || ||
Db    180 ccagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatat 239

Qy    195 TGTCTGCCCCCACTACGAAGGC------------------------CCAGGGCCCCCTGA 230
          |  |||||| |||||| |  ||                        || ||||||   |
Db    240 ttactgcccgcactacaacagctcgggggtgggccccggggcgggaccggggcccggagg 299

Qy    231 GGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC 290
           ||  | |||  ||  |   ||||||||||| |  |    |||||     ||||| | ||
Db    300 cggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgc 359

Qy    291 ---AGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCA 347
               |||||  |  |  ||   || ||     |     |   ||     |||   |  |
Db    360 cagccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaa 419

Qy    348 ATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407
           ||||| |||||| | ||||||| ||   | ||||| || ||||  ||||||    | ||
Db    420 gttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgccgg 479

Qy    408 AGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCT 467
            |    ||||||||||||||   ||||||||   |        |  ||||  ||||| |
Db    480 ccacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggat 539

Qy    468 CCAGGTGTCTGTCTGCTGC 486
            ||||||  |||||||||
Db    540 gaaggtgttcgtctgctgc 558

RESULT  13
US-09-053-375B-186
; Sequence 186, Application US/09053375B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Bibilashvilli, Robert
;  TITLE OF INVENTION: Nucleic Acid Arrays
;  FILE REFERENCE: CLON-006
;  CURRENT APPLICATION NUMBER: US/09/053,375B
;  CURRENT FILING DATE:  1998-08-31
;  NUMBER OF SEQ ID NOS: 1543
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 186
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-053-375B-186

  Query Match             16.3%;  Score 103.4;  DB 5;  Length 987;
  Best Local Similarity   54.3%;  Pred. No. 4.1e-15;
  Matches  271;  Conservative    0;  Mismatches  201;  Indels   27;  Gaps    2;

Qy     15 GACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
          | |  |||   || ||| ||||||||  |||||   | | || |    |    || | ||
Db     60 ggcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgct 119

Qy     75 CGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
           | |      |   | ||||      |   ||| || |  || |||||||||  |   ||
Db    120 ggcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaa 179

Qy    135 CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
          ||      |||  ||||  | |  |   ||| || ||  | | ||||| || || || ||
Db    180 ccagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatat 239

Qy    195 TGTCTGCCCCCACTACGAAGGC------------------------CCAGGGCCCCCTGA 230
          |  |||||| |||||| |  ||                        || ||||||   |
Db    240 ttactgcccgcactacaacagctcgggggtgggccccggggcgggaccggggcccggagg 299

Qy    231 GGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC 290
           ||  | |||  ||  |   ||||||||||| |  |    |||||     ||||| | ||
Db    300 cggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgc 359

Qy    291 ---AGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCA 347
               |||||  |  |  ||   || ||     |     |   ||     |||   |  |
Db    360 cagccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaa 419

Qy    348 ATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407
           ||||| |||||| | ||||||| ||   | ||||| || ||||  ||||||    | ||
Db    420 gttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgccgg 479

Qy    408 AGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCT 467
            |    ||||||||||||||   ||||||||   |        |  ||||  ||||| |
Db    480 ccacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggat 539

Qy    468 CCAGGTGTCTGTCTGCTGC 486
            ||||||  |||||||||
Db    540 gaaggtgttcgtctgctgc 558
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RESULT 14
US-09-440-302B-838
; Sequence 838, Application US/09440302B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey E.
;  TITLE OF INVENTION: Human Neurobiology Array
;  FILE REFERENCE: CLON-006CIP11
;  CURRENT APPLICATION NUMBER: US/09/440,302B
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 1193
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 838
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-440-302B-838

  Query Match             16.3%;  Score 103.4;  DB 5;  Length 987;
  Best Local Similarity   54.3%;  Pred. No. 4.1e-15;
  Matches  271;  Conservative    0;  Mismatches  201;  Indels   27;  Gaps    2;

Qy     15 GACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCT 74
          | |  |||   || ||| ||||||||  |||||   | | || |    |    || | ||
Db     60 ggcggcggctccgctgctgctgctgctgctgctcgtgcccgtgccgctgctgccgctgct 119

Qy     75 CGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAA 134
           | |      |   | ||||      |   ||| || |  || |||||||||  |   ||
Db    120 ggcccaagggcccggaggggcgctgggaaaccggcatgcggtgtactggaacagctccaa 179

Qy    135 CCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACAT 194
          ||      |||  ||||  | |  |   ||| || ||  | | ||||| || || || ||
Db    180 ccagcacctgcggcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatat 239

Qy    195 TGTCTGCCCCCACTACGAAGGC------------------------CCAGGGCCCCCTGA 230
          |  |||||| |||||| |  ||                        || ||||||   |
Db    240 ttactgcccgcactacaacagctcgggggtgggccccggggcgggaccggggcccggagg 299

Qy    231 GGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGC 290
           ||  | |||  ||  |   |||||||||||  | |    |||||     ||||| | ||
Db    300 cggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgcaacgc 359

Qy    291 ---AGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCA 347
               |||||  |  |  ||   || ||     |     |   ||     |||   |  |
Db    360 cagccagggcttcaagcgctgggagtgcaaccggccgcacgccccgcacagccccatcaa 419

Qy    348 ATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGG 407
           ||||| |||||| | ||||||| ||   | ||||| || ||||  ||||||    | ||
Db    420 gttctcggagaagttccagcgctacagcgccttctctctgggctacgagttccacgccgg 479

Qy    408 AGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCT 467
            |    ||||||||||||||   ||||||||   |        |  ||||  ||||| |
Db    480 ccacgagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggat 539

Qy    468 CCAGGTGTCTGTCTGCTGC 486
            ||||||  |||||||||
Db    540 gaaggtgttcgtctgctgc 558

RESULT 15
PCT-US02-13644-14
; Sequence 14, Application PC/TUS0213644
; GENERAL INFORMATION:
;  APPLICANT: Chien, Kenneth
;  APPLICANT:  Hoshijima, Masahiko
;  TITLE OF INVENTION: Non-viral vesicle vector for cardiac specific gene delivery
;  FILE REFERENCE: 6627-PA1198
;  CURRENT APPLICATION NUMBER: PCT/US02/13644
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: 60/287,423
;  PRIOR FILING DATE: 2001-04-30
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 1480
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-13644-14

  Query Match             16.0%;  Score 101.8;  DB 1;  Length 1480;
  Best Local Similarity   56.9%;  Pred. No. 1e-14;
  Matches  253;  Conservative    0;  Mismatches  177;  Indels   15;  Gaps    3;

Qy     56 TCCTCTGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAG 115
          ||||||||||| |  || | ||           |   || | |       ||||||   |
Db     81 tcctctgggcccctctcttgggtctgtgctgcagtctggccgctgctgatcgccacaccg 140

Qy    116 TCTACTGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCC 175
          ||| |||||||      || |||| ||| |     |  |||  |    |  |  ||   |
Db    141 tcttctggaacagttcaaatcccaagttccggaatgaggactacaccatacatgtgcagc 200

Qy    176 TCAACGATTACCTAGACATTGTCTGCCCCCACTACGAAGG---CCCAGGGCCCCCTGAGG 232
          | || || ||| | |||||  |||| || ||||| ||||    | | | | |    |  |
Db    201 tgaatgactacgtggacatcatctgtccgcactatgaagatcactctgtggcagacgctg 260

Qy    233 GCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAG 292
           |   |||  ||      ||||| |||||||       |  ||  ||   |||||| |
Db    261 ccatggagcagtacatactgtacctggtggagcatgaggagtaccagctgtgccagcccc 320

Qy    293 AGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTT---------TGGCCATG 343
          ||    ||  || | |    ||||||  ||||  || ||||           |||||  |
Db    321 ag---tccaaggaccaagtccgctggcagtgcaaccggcccagtgccaagcatggcccgg 377

Qy    344 TTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTAC 403
             |  | || |||||| | |||||||||||||||||| |||| |||    ||||||  |
Db    378 agaagctgtctgagaagttccagcgcttcacacctttcaccctgggcaaggagttcaaag 437

Qy    404 CTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGA 463
            ||| | |  ||||||||||||||    ||||  |   ||  |   | ||  |||||||
Db    438 aaggacacagctactactacatctccaaacccatccaccagcatgaagaccgctgcttga 497

Qy    464 GGCTCCAGGTGTCTGTCTGCTGCAA 488
          || |  ||||| ||||| |  ||||
Db    498 ggttgaaggtgactgtcagtggcaa 522


Search completed: September 28, 2002, 01:35:28
Job time: 12728 sec
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                        GenCore version 4.5
              Copyright (c) 1993 - 2000  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          September 27, 2002, 22:03:08 ; Search time 2180.79 Seconds
                                               (without alignments)
                                               3936.217 Million cell updates/sec

Title:           US-09-904-954-3
Perfect score:   636
Sequence:        1 GCCAGACCAAACCGGACCTC..........TTCTGCGAATTCTGTGAGCC 636

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters:      27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
                1:  em_estba:*
                2:  em_esthum:*
                3:  em_estin:*
                4:  em_estmu:*
                5:  em_estov:*
                6:  em_estpl:*
                7:  em_estro:*
                8:  em_htc:*
                9:  gb_est1:*
                10:  gb_est2:*
                11:  gb_htc:*
                12:  gb_gss:*
                13:  em_gss_hum:*
                14:  em_gss_inv:*
                15:  em_gss_pln:*
                16:  em_gss_vrt:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result            Query
  No.   Score     Match Length DB  ID                        Description
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     1   622.4     97.9    912  10  BI868252                  BI868252 603392205
     2   610.4     96.0    707  10  BE883793                  BE883793 601506189
     3     597     93.9    838  10  BE890843                  BE890843 601431292
     4   456.4     71.8    493  10  BG747752                  BG747752 602705246
     5   456.4     71.8    495  10  BG748489                  BG748489 602706466
     6   442.6     69.6   1255  11  AK012195                  AK012195 Mus muscu
     7   440.4     69.2    482  10  BG338638                  BG338638 602436387
     8   414.4     65.2    751  10  BF792518                  BF792518 602253627
     9   404.2     63.6    778  10  BF138971                  BF138971 601784106
    10   400.4     63.0   1054  10  BI663095                  BI663095 603286494
    11   399.4     62.8    561   9  AW784975                 AW784975 115339 MA
    12   396.6     62.4    542  10  BE750737                  BE750737 202345 MA
    13     392     61.6    554   9  BE236077                 BE236077 143746 MA
    14   384.8     60.5    963  10  BI646617                  BI646617 603276523
    15   378.8     59.6    565   9  BE032073                 BE032073 130886 MA
    16     365     57.4    375   9  AW405707                 AW405707 UI-HF-BL0
    17   359.2     56.5    567  10  BE899787                  BE899787 182909 MA
    18   356.8     56.1    544   9  AV608466                 AV608466 AV608466
    19   340.6     53.6    541   9  AI663168                 AI663168 uk23f02.y
    20   327.8     51.5    464   9  AI664495                 AI664495 uk25a03.y
    21     321     50.5    458  10  BF189993                  BF189993 235888 MA
    22   311.4     49.0    469   9  AW741367                 AW741367 ur50g07.y
    23   291.6     45.8    476   9  BE234774                 BE234774 142009 MA
    24   274.4     43.1    837  10  BI258895                  BI258895 602970424
    25   274.2     43.1    453   9  AA002297                 AA002297 mg42d03.r
    26   253.4     39.8    409   9  AA289704                 AA289704 mp12h03.r
    27     252     39.6    506  10  BF441035                  BF441035 257144 MA
    28     250     39.3    870  10  BE780161                  BE780161 601468029
    29     248     39.0    334  10  BF442110                  BF442110 258680 MA
c   30   242.2     38.1    298  10  BF224394                  BF224394 hr76a10.x
    31   236.4     37.2    338   9  AW315678                 AW315678 13228 MAR
    32   231.2     36.4    482  10  BF441034                  BF441034 257143 MA
    33   216.4     34.0    600  10  BI986340                  BI986340 3164-27 M
    34   211.6     33.3    353   9  AW462601                 AW462601 BP230009B
    35   209.4     32.9    635  10  BI083742                  BI083742 602875475
    36   199.4     31.4    442   9  AA015379                 AA015379 mg94g11.r
    37     196     30.8    233   9  AA312329                 AA312329 EST183005
    38   188.4     29.6    373   9  AA003996                 AA003996 mg80d02.r
    39   187.6     29.5    391  10  W12777                    W12777 ma87a10.r1
    40   187.4     29.5    492  10  BM258125                  BM258125 522820 MA
    41   181.2     28.5    530  10  BF470931                  BF470931 UI-M-BH3-
    42   172.2     27.1    676   9  AL661297                 AL661297 AL661297
    43   171.2     26.9    179   9  AA296663                 AA296663 EST112224
    44   161.4     25.4    586  10  BJ074808                  BJ074808 BJ074808
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                              ALIGNMENTS


RESULT   1
BI868252
LOCUS       BI868252                 912 bp    mRNA    linear   EST 11-OCT-2001
DEFINITION  603392205F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402208 5',
            mRNA sequence.
ACCESSION   BI868252
VERSION     BI868252.1  GI:16041925
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12025  row: j  column: 01
            High quality sequence stop: 806.
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_90"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.7 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
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BASE COUNT      175 a    282 c    264 g    191 t
ORIGIN


  Query Match             97.9%;  Score 622.4;  DB 10;  Length 912;
  Best Local Similarity   99.7%;  Pred. No. 9.9e-137;
  Matches  634;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 71

Qy         61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
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Db         72 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 131

Qy        121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
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Db        132 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 191

Qy        181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
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Db        192 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCA-GGCCCCCTGAGGGCCCCGAG 250

Qy        241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
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Db        251 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 310

Qy        301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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Db        311 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 370

Qy        361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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Db        371 ATTCAGCGCTTCACACCCTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 430

Qy        421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
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Db        431 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 490

Qy        481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
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Db        491 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 550

Qy        541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
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Db        551 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 610

Qy        601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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Db        611 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 646


RESULT   2
BE883793
LOCUS       BE883793                 707 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601506189F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3907510 5',
            mRNA sequence.
ACCESSION   BE883793
VERSION     BE883793.1  GI:10332569
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 707)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
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             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9718  row: b  column: 23
            High quality sequence stop: 706.
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                     /tissue_type="leiomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
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                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2.1 kb.  "
BASE COUNT      119 a    228 c    204 g    156 t
ORIGIN


  Query Match             96.0%;  Score 610.4;  DB 10;  Length 707;
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  Matches  633;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy          1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db         22 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 81

Qy         61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
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Db         82 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 141

Qy        121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
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Db        142 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 201

Qy        181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
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Db        202 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCA-GGCCCCCTGAGGGCCCCGAG 260

Qy        241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 320

Qy        301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 380

Qy        361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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Db        381 ATTCAGCGCTTCACACCCTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 440

Qy        421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
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Db        441 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 500

Qy        481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
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Db        501 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 560

Qy        541 ACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTG 600
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Db        561 ACATCAGGGTGGCGAGGGGGGGACACTCCCAG-CCCCTCTGTCTCTTGCTATTACTGCTG 619

Qy        601 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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Db        620 CTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 655


RESULT   3
BE890843
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LOCUS       BE890843                 838 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601431292F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916487 5',
            mRNA sequence.
ACCESSION   BE890843
VERSION     BE890843.1  GI:10349570
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 838)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9741  row: h  column: 24
            High quality sequence stop: 707.
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_72"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      135 a    265 c    256 g    182 t
ORIGIN


  Query Match             93.9%;  Score 597;  DB 10;  Length 838;
  Best Local Similarity   98.1%;  Pred. No. 9.6e-131;
  Matches  625;  Conservative    0;  Mismatches   10;  Indels    2;  Gaps    2;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db       44 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 103

Qy       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      104 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 163

Qy      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      164 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 223

Qy      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
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Db      224 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCA-GGCCCCCTGAGGGCCCCGAG 282

Qy      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      283 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 342

Qy      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
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Db      343 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 402

Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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Db      403 ATTCAGCGCTTCACACCCTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 462

Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 480
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Db      463 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTC 522

Qy      481 TGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGC 540
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Qy      541 ACATCAGGTGGCGA-GGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCT 599
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Db      583 ACATCAGGTGGCGACGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGTG 642

Qy      600 GCTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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Db      643 CTTCTGATTTCTTCGTCTTCTGCGAATTCTGTGAGCC 679


RESULT   4
BG747752
LOCUS       BG747752                 493 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602705246F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842011 5',
            mRNA sequence.
ACCESSION   BG747752
VERSION     BG747752.1  GI:14058405
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 493)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1675  row: l  column: 12
            High quality sequence stop: 493.
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                     /db_xref="taxon:9606"
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library.'|"
BASE COUNT       79 a    167 c    144 g    103 t
ORIGIN


  Query Match             71.8%;  Score 456.4;  DB 10;  Length 493;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-97;
  Matches  457;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db       36 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 95

Qy       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
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Qy      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
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Db      156 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 215

Qy      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
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Db      336 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 395

Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
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Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTG 458
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Db      456 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTG 493


RESULT   5
BG748489
LOCUS       BG748489                 495 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602706466F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842977 5',
            mRNA sequence.
ACCESSION   BG748489
VERSION     BG748489.1  GI:14059142
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 495)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1678  row: d  column: 18
            High quality sequence stop: 495.
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                     /clone_lib="NIH_MGC_43"
                     /tissue_type="normal pigmented retinal epithelium"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library. |"
BASE COUNT       79 a    168 c    144 g    104 t
ORIGIN
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  Query Match             71.8%;  Score 456.4;  DB 10;  Length 495;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-97;
  Matches  457;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db       38 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 97

Qy       61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       98 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 157

Qy      121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      158 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 217

Qy      181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      218 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 277

Qy      241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      278 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 337

Qy      301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      338 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAG 397

Qy      361 ATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 420
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      398 ATTCAGCGCTTCACACCCTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTAC 457

Qy      421 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTG 458
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Db      458 TACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTG 495


RESULT   6
AK012195
LOCUS       AK012195                1255 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
            enriched library, clone:2610529M21:ephrin A4, full insert sequence.
ACCESSION   AK012195
VERSION     AK012195.1  GI:12848791
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) 10 days embryo cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:2610529M21.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2  (sites)
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3  (sites)
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
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            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4  (sites)
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5  (bases 1 to 1255)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
FEATURES             Location/Qualifiers
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                     /db_xref="MGD:MGI:1910658"
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                     /clone="2610529M21"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="10 days embryo"
     gene            83..703
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                     /note="data source:MGD, source key:MGI:106643,
                     evidence:ISS
                     ephrin A4
                     putative"
                     /codon_start=1
                     /protein_id="BAB28092.1"
                     /db_xref="GI:12848792"
                     /translation="MRLLPLLRTVLWAALLGSRLPGCSSLRHPIYWNSSNPRLLRGDA
                     VVELGFNDYLDIFCPHYESPGPPEGPETFALYIVDWSGYEACTAEGANSFQRWNCSMP
                     FAPFSPVRFSEKIQRYTPFPLGFEFLPGETYYISVPTPESPGRCLRLQVSVCCKESG
                     SSHESAHPVGSPGESGTSGWRGGHAPSPLCLLLLLLLPILRLLRVL"
     polyA_signal    1231..1236
                     /note="putative"
     polyA_site      1255
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BASE COUNT      248 a    374 c    357 g    275 t      1 others
ORIGIN


  Query Match             69.6%;  Score 442.6;  DB 11;  Length 1255;
  Best Local Similarity   82.5%;  Pred. No. 3.2e-94;
  Matches  537;  Conservative    0;  Mismatches   99;  Indels   15;  Gaps    2;
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Qy          1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db         56 GCCAGACCAGACTGGACCCCAGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTGCTC 115

Qy         61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
              ||||||||| | |||||||| |  ||||  ||| |||||||||||||||||  | |||||
Db        116 TGGGCCGCGCTGCTCGGCTCGCGCCTGCCGGGGTGCTCCAGCCTCCGCCACCCAATCTAC 175

Qy        121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
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Db        176 TGGAACTCCTCTAACCCCAGGTTGCTCCGAGGAGATGCCGTGGTGGAGCTGGGCTTCAAC 235

Qy        181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
              ||||||||||||||  ||||||| || || ||| ||||||||||||| || ||||| || 
Db        236 GATTACCTAGACATCTTCTGCCCACATTATGAAAGCCCAGGGCCCCCAGAAGGCCCGGAA 295

Qy        241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
              || ||||| || ||||| ||||||||| ||||||| ||| |||||  |||||||||  | 
Db        296 ACCTTTGCATTATACATCGTGGACTGGTCAGGCTACGAGGCCTGCACGGCAGAGGGGGCA 355

Qy        301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTG---------GCCATGTTCAATTC 351
                   || | ||||||||   |||||  |||| ||||         ||| ||||| ||||
Db        356 AATAGCTTCCAGCGCTGGAATTGCTCGATGCCTTTTGCCCCTTTCAGCCCTGTTCGATTC 415

Qy        352 TCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAG 411
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Db        416 TCAGAAAAGATTCAGCGCTACACACCCTTCCCGCTGGGCTTTGAGTTCTTGCCTGGAGAG 475

Qy        412 ACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAG 471
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Db        476 ACTTACTACTACATCTCGGTGCCGACTCCGGAGAGTCCTGGCCGGTGCCTGAGACTCCAG 535

Qy        472 GTGTCTGTCTGCTGCAAGGAGAGGAAGTC------TGAGTCAGCCCATCCTGTTGGGAGC 525
              |||||||||||||||||||||||   |||      ||||||||| |||||||||||||| 
Db        536 GTGTCTGTCTGCTGCAAGGAGAGCGGGTCATCACATGAGTCAGCTCATCCTGTTGGGAGT 595

Qy        526 CCTGGAGAGAGTGGCACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTC 585
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Db        596 CCTGGAGAAAGCGGTACGTCCGGGTGGCGGGGAGGACACGCGCCCAGCCCCCTGTGTCTC 655

Qy        586 TTGCTATTACTGCTGCTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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Db        656 TTGCTGCTGCTGCTGCTCCCAATCCTCCGTCTCCTGAGAGTTCTGTGAGCC 706


RESULT   7
BG338638
LOCUS       BG338638                 482 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602436387F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4554429 5',
            mRNA sequence.
ACCESSION   BG338638
VERSION     BG338638.1  GI:13145076
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 482)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1253  row: m  column: 22
            High quality sequence stop: 482.
FEATURES             Location/Qualifiers
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                    /tissue_type="leiomyosarcoma cell line"
                    /lab_host="DH10B (phage-resistant)"
                    /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
                    EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                    into EcoRI/XhoI sites using the following 5' adaptor:
                    GGCACGAG(G). Size-selected >500bp for average insert size
                    1.8kb. Library constructed by Ling Hong in the laboratory
                    of Gerald M. Rubin (University of California, Berkeley)
                    using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                    II RT (Life Technologies). Note: this is a NIH_MGC
                    Library."
BASE COUNT       78 a    161 c    144 g     99 t
ORIGIN


  Query Match             69.2%;  Score 440.4;  DB 10;  Length 482;
  Best Local Similarity   99.6%;  Pred. No. 7.4e-94;
  Matches  452;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy        5 GACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGG 64
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Db       30 GACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGG 89

Qy       65 CCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGA 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       90 CCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGA 149

Qy      125 ACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      150 ACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATT 209

Qy      185 ACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGT 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      210 ACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGT 269

Qy      245 TTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGG 304
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Db      270 TTGC-TTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGG 328

Qy      305 CCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTC 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      329 CCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTC 388

Qy      365 AGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACA 424
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Db      389 AGCGCTTCACACCCTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACA 448

Qy      425 TCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTG 458
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Db      449 TCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTG 482


RESULT   8
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LOCUS       BF792518                 751 bp    mRNA    linear   EST 12-JAN-2001
DEFINITION  602253627F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4345734 5',
            mRNA sequence.
ACCESSION   BF792518
VERSION     BF792518.1  GI:12097572
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 751)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
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COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9966  row: f  column: 07
            High quality sequence stop: 737.
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                     /tissue_type="adrenal cortex carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
                     primed. Average insert size 1.229 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      148 a    217 c    222 g    164 t
ORIGIN


  Query Match             65.2%;  Score 414.4;  DB 10;  Length 751;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-87;
  Matches  415;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        1 GGCCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGT 60

Qy      281 CCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCC 340
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Db       61 CCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTGGCC 120

Qy      341 ATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCT 400
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Db      121 ATGTTCAATTCTCAGAGAAGATTCAGCGCTTCACACCCTTCTCCCTCGGCTTTGAGTTCT 180

Qy      401 TACCTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCT 460
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Db      181 TACCTGGAGAGACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCT 240

Qy      461 TGAGGCTCCAGGTGTCTGTCTGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTG 520
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Db      241 TGAGGCTCCAGGTGTCTGTCTGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTG 300

Qy      521 GGAGCCCTGGAGAGAGTGGCACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCT 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      581 GTCTCTTGCTATTACTGCTGCTTCTGATTCTTCGTCTTCTGCGAATTCTGTGAGCC 636
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RESULT   9
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LOCUS       BF138971                 778 bp    mRNA    linear   EST 24-OCT-2000
DEFINITION  601784106F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4012153 5',
            mRNA sequence.
ACCESSION   BF138971
VERSION     BF138971.1  GI:10978114
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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REFERENCE   1  (bases 1 to 778)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by:Incyte Genomics, Inc.
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9252  row: k  column: 02
            High quality sequence stop: 667.
FEATURES             Location/Qualifiers
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                     /clone_lib="NCI_CGAP_Lu30"
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                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; transgenic model WNT-1, expression driven by
                     MMTV-LTR enhancer; Cloned unidirectionally.  Primer: Oligo
                     dT.   Library constructed by Life Technologies.
                     Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT      143 a    235 c    239 g    161 t
ORIGIN


  Query Match             63.6%;  Score 404.2;  DB 10;  Length 778;
  Best Local Similarity   83.3%;  Pred. No. 3.1e-85;
  Matches  499;  Conservative    0;  Mismatches   88;  Indels   12;  Gaps    3;

Qy          1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db         15 GGCAGACCAGACTGGACC-CCAGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTGCTC 73

Qy         61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
              ||||||||| | |||||||| |  ||||  ||| ||||||||||||||||    |||||
Db         74 TGGGCCGCGCTGCTCGGCTCGCGCCTGCCGGGGTGCTCCAGCCTCCGCCACCCAATCTAC 133

Qy        121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
              |||||||||  |||||||||||||||| ||||||||| |||||||||||||||||| |||||
Db        134 TGGAACTCCTCTAACCCCAGGTTGCTCCGAGGAGATGCCGTGGTGGAGCTGGGCTTCAAC 193

Qy        181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
              ||||||||||||||  ||||||| || || ||| ||||||||||||| || ||||| ||
Db        194 GATTACCTAGACATCTTCTGCCCACATTATGAAAGCCCAGGGCCCCCAGAAGGCCCGGAA 253

Qy        241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
              || ||||| || ||||||||||||||||| ||||||| ||| |||||  |||||||||  |
Db        254 ACCTTTGCATTATACATGGTGGACTGGTCAGGCTACGAGGCCTGCACGGCAGAGGGGGCA 313

Qy        301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTG---------GCCATGTTCAATTC 351
                 |||| | ||||||||   |||||  |||| ||||         ||| ||||| ||||
Db        314 AATGCCTTCCAGCGCTGGAATTGCTCGATGCCTTTTGCCCCTTTCAGCCCTGTTCGATTC 373

Qy        352 TCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAG 411
              ||||| |||||||||||||| |||||| ||| | || |||||||||||||| |||||||||
Db        374 TCAGAAAAGATTCAGCGCTACACACCCTTCCCGCTGGGCTTTGAGTTCTTGCCTGGAGAG 433

Qy        412 ACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAG 471
              ||||||||||||||||||||||| ||||| |||||| |||||| |||| |||| ||||||
Db        434 ACTTACTACTACATCTCGGTGCCGACTCCGGAGAGTCCTGGCCGGTGCCTGAGACTCCAG 493

Qy        472 GTGTCTGTCTGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGA 531
              |||||||||||||||||||||||   ||| |||||||| |||||||||||||| ||||||
Db        494 GTGTCTGTCTGCTGCAAGGAGAGCGGGTCGGAGTCAGCTCATCCTGTTGGGAGTCCTGGA 553
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Qy        532 GAGAGTGGCACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCT 590
              || || || || || |||||||  |||| |||||  | |   ||||| |||||||||||
Db        554 GAAAGCGGTACGTCCGGGTGGC--GGGGAGGACAGGCGCCAGCCCCTGTGTCTCTTGCT 610


RESULT  10
BI663095
LOCUS       BI663095                1054 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603286494F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5320846 5',
            mRNA sequence.
ACCESSION   BI663095
VERSION     BI663095.1  GI:15577328
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1054)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11813  row: k  column: 23
            High quality sequence stop: 778.
FEATURES             Location/Qualifiers
     source          1..1054
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5320846"
                     /clone_lib="NCI_CGAP_Mam6"
                     /sex="female, virgin"
                     /tissue_type="infiltrating ductal carcinoma"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      208 a    333 c    322 g    191 t
ORIGIN


  Query Match             63.0%;  Score 400.4;  DB 10;  Length 1054;
  Best Local Similarity   82.4%;  Pred. No. 2.7e-84;
  Matches  537;  Conservative    0;  Mismatches   96;  Indels   19;  Gaps    6;

Qy          1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
              ||||||||| || ||||| |  |||||||||||||||||||||||||||||||||| |||
Db         25 GCCAGACCAGACTGGACC-CCAGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTGCTC 83

Qy         61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
              ||||||||| | |||||||| |  ||||  ||| ||||||||||||||||    |||||
Db         84 TGGGCCGCGCTGCTCGGCTCGCGCCTGCCGGGGTGCTCCAGCCTCCGCCACCCAATCTAC 143

Qy        121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
              |||||||||  |||||||||||||||| ||||||||| |||||||||||||||||| |||||
Db        144 TGGAACTCCTCTAACCCCAGGTTGCTCCGAGGAGATGCCGTGGTGGAGCTGGGCTTCAAC 203

Qy        181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
              ||||||||||||||  ||||||| || || ||| ||||| ||||||| || ||||| ||
Db        204 GATTACCTAGACATCTTCTGCCCACATTATGAAAGCCCA-GGCCCCCAGAAGGCCCGGAA 262

Qy        241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
              || ||||| || ||||||||||||||||| ||||||| ||| |||||  |||||||||  |
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Db    263 ACCTTTGCATTATACATGGTGGACTGGTCAGGCTACGAGGCCTGCACGGCAGAGGGGGCA 322

Qy    301 CGGGCCTACAAGCGCTGGGTGTGCTCCCTGCCCTTTG---------GCCATGTTCAATTC 351
             |||| | ||||||||   |||||  |||| ||||         ||| ||||| ||||
Db    323 AATGCCTTCCAGCGCTGGAATTGCTCGATGCCTTTTGCCCCTTTCAGCCCTGTTCGATTC 382

Qy    352 TCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAG 411
          ||||| ||||||||||||| |||||| ||| | || |||||||||||||| |||||||||
Db    383 TCAGAAAAGATTCAGCGCTACACACCCTTCCCGCTGGGCTTTGAGTTCTTGCCTGGAGAG 442

Qy    412 ACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAG 471
          ||||||||||||||||||||||| ||||| |||||| |||||| |||| |||| ||||||
Db    443 ACTTACTACTACATCTCGGTGCCGACTCCGGAGAGTCCTGGCCGGTGCCTGAGACTCCAG 502

Qy    472 GTGTCTGTCTGCTGCAAGGAGAGGAAGTC------TGAGTCAGCCCATCCTGTTGGGAGC 525
          |||||||||||||||||||||||   |||      ||||||||| |||||||||||||| 
Db    503 GTGTCTGTCTGCTGCAAGGAGAGCGGGTCATCACATGAGTCAGCTCATCCTGTTGGGAGT 562

Qy    526 CCTGGAGAGAGTGGCACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTC 585
          |||||||| || || || || |||||||| || ||  || | ||||| ||||| ||||||
Db    563 CCTGGAGAAAGCGGTACGTCCGGGTGGCGGGGAGGACACGCGCCCAG-CCCCTGTGTCTC 621

Qy    586 TTGCTATTACTGCTGCTTCTGATTCTTCG-TCTTCTGCGAATTCTGTGAGCC 636
          |||||  | |||||||| |  || || || ||| ||| || |||||||||||
Db    622 TTGCTGCTGCTGCTGCTCCCAATCCTCCGTTCTCCTGAGAGTTCTGTGAGCC 673

RESULT  11
AW784975
LOCUS       AW784975                 561 bp    mRNA    linear   EST 09-JUL-2000
DEFINITION  115339 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   AW784975
VERSION     AW784975.1  GI:7841751
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 48  row: C  column: 4
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1..561
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 1PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
BASE COUNT       93 a    181 c    174 g    113 t
ORIGIN
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  Query Match             62.8%;  Score 399.4;  DB 9;  Length 561;
  Best Local Similarity   87.5%;  Pred. No. 3.8e-84;
  Matches  463;  Conservative    0;  Mismatches   56;  Indels   10;  Gaps    2;

Qy      1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
          ||||||| ||||| |||| |||||||||||||||||| ||||||||||||||||||||||
Db     33 GCCAGACTAAACCAGACCCCGGGGGCGATGCGGCTGCAGCCCCTGCTGCGGACTGTCCTC 92

Qy     61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
          ||||||||| ||||| ||||||||||| | ||| ||||  | ||||||||||  ||||| 
Db     93 TGGGCCGCGCTCCTCAGCTCCCCTCTGAGAGGGAGCTCTGGTCTCCGCCACGAGGTCTAT 152

Qy    121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||| 
Db    153 TGGAACTCCAGTAACCCCAGGCTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAG 212

Qy    181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
          ||||||||||||||  ||||||| ||||| ||  |||||||||||||||||||||| |||
Db    213 GATTACCTAGACATCTTCTGCCCACACTATGAGAGCCCAGGGCCCCCTGAGGGCCCGGAG 272

Qy    241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
          || ||||| || ||||||||||||||| | ||||||||| |||||||||| ||||| || 
Db    273 ACCTTTGCCTTATACATGGTGGACTGGTCGGGCTATGAGGCCTGCCAGGCGGAGGGGCCA 332

Qy    301 CGGGCCTACAAGCGCTGGGTGTGCTCCC---------TGCCCTTTGGCCATGTTCAATTC 351
           | |||| ||||||||||| ||||||||           |||||||||| ||| | ||||
Db    333 GGTGCCTTCAAGCGCTGGGAGTGCTCCCGCCCCTTTGCTCCCTTTGGCCCTGTGCGATTC 392

Qy    352 TCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAG 411
          |||||||||||||||||||||||||| |||||||| ||||| |||||||| |||||||||
Db    393 TCAGAGAAGATTCAGCGCTTCACACCCTTCTCCCTGGGCTTCGAGTTCTTGCCTGGAGAG 452

Qy    412 ACTTACTACTACATCTCGGTGCCCACTCC-AGAGAGTTCTGGCCAGTGCTTGAGGCTCCA 470
          || |||||||||||||| ||||| |||||  |||||| ||||||||||||||||||||||
Db    453 ACCTACTACTACATCTCAGTGCCAACTCCGGGAGAGTCCTGGCCAGTGCTTGAGGCTCCA 512

Qy    471 GGTGTCTGTCTGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTT 519
          ||||||||||||||||||||||   ||| ||||||| ||||||||||||
Db    513 GGTGTCTGTCTGCTGCAAGGAGGACAAGCCTGAGTCGGCCCATCCTGTT 561

RESULT  12
BE750737
LOCUS       BE750737                 542 bp    mRNA    linear   EST 25-APR-2001
DEFINITION  202345 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE750737
VERSION     BE750737.1  GI:10164729
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 542)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
```

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            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 113  row: B  column: 13
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .542
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 4BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from day 20 and day 40
                     embryos."
BASE COUNT       94 a    177 c    161 g    110 t
ORIGIN

  Query Match             62.4%;  Score 396.6;  DB 10;  Length 542;
  Best Local Similarity   85.4%;  Pred. No. 1.7e-83;
  Matches  457;  Conservative    0;  Mismatches   69;  Indels    9;  Gaps    1;

Qy      1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
          ||||||||| ||| ||||| |||||||||||||||||| ||||||||||| ||||||||||
Db      7 GCCAGACCACACCAGACCTAGGGGGCGATGCGGCTGCAGCCCCTGCTGCAGACTGTCCTC 66

Qy     61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
          ||||||| | ||||| ||||||||||||| |||||||   |||||||||  |  ||||||
Db     67 TGGGCCGTGCTCCTCAGCTCCCCTCTGCGAGGGGGCTGTGGCCTCCGCCTTGCGGTCTAC 126

Qy    121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||| |||| 
Db    127 TGGAACTCCAGTAACCCCAGGCTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCTTCAAG 186

Qy    181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
          ||||||||||||||  ||||||| ||||| ||  | ||||||||||||||||||||||||
Db    187 GATTACCTAGACATCATCTGCCCACACTATGAGAGTCCAGGGCCCCCTGAGGGCCCCGAG 246

Qy    241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
          || || || || ||| | ||||||||| | |||||  || |||||||||| ||||| || 
Db    247 ACATTCGCATTATACGTAGTGGACTGGGCGGGCTACAAGGCCTGCCAGGCTGAGGGGCCG 306

Qy    301 CGGGCCTACAAGCGCTGGGTGTGCTCCC---------TGCCCTTTGGCCATGTTCAATTC 351
           | |||| ||||||||||| ||||||||           |||||||||| ||||| ||| 
Db    307 AGTGCCTTCAAGCGCTGGGAGTGCTCCCGCCCCTTCGCTCCCTTTGGCCCTGTTCGATTT 366

Qy    352 TCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAG 411
           ||||||||||||||||||||||||| |||||||| ||| | |||||||| || ||||||
Db    367 CCAGAGAAGATTCAGCGCTTCACACCCTTCTCCCTTGGCATGGAGTTCTTGCCCGGAGAG 426

Qy    412 ACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAG 471
          || |||||||||||||| ||||| ||||| | |||| |||||||||||||||||||||||
Db    427 ACCTACTACTACATCTCAGTGCCAACTCCGGGGAGTCCTGGCCAGTGCTTGAGGCTCCAG 486

Qy    472 GTGTCTGTCTGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCC 526
          |||||| ||||||||||||||   ||  ||||||||||||||||||| |||||||
Db    487 GTGTCTATCTGCTGCAAGGAGGACAAACCTGAGTCAGCCCATCCTGTCGGGAGCC 541

RESULT  13
BE236077
LOCUS       BE236077               554 bp    mRNA    linear   EST 10-JUL-2000
DEFINITION  143746 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BE236077
VERSION     BE236077.1  GI:9020795
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 554)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 85  row: N  column: 6
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .554
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 1PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
BASE COUNT       92 a    181 c    171 g    110 t
ORIGIN

  Query Match             61.6%;  Score 392;  DB 9;  Length 554;
  Best Local Similarity   87.2%;  Pred. No. 2.1e-82;
  Matches  457;  Conservative    0;  Mismatches   55;  Indels   12;  Gaps    2;

Qy      1 GCCAGACCAAACCGGACCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTC 60
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Db     34 GCCAGACTAAACCAGACCCCGGGGGCGATGCGGCTGCAGCCCCTGCTGCGGACTGTCCTC 93

Qy     61 TGGGCCGCGTTCCTCGGCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTAC 120
          ||||||||| ||||| ||||||||||| | ||| ||||  | ||||||||||  ||||| 
Db     94 TGGGCCGCGCTCCTCAGCTCCCCTCTGAGAGGGAGCTCTGGTCTCCGCCACGAGGTCTAT 153

Qy    121 TGGAACTCCAGTAACCCCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAC 180
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||| 
Db    154 TGGAACTCCAGTAACCCCAGGCTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAG 213

Qy    181 GATTACCTAGACATTGTCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAG 240
          ||||||||||||||  ||||||| ||||| ||  |||||||||||||||||||||| |||
Db    214 GATTACCTAGACATCTTCTGCCCACACTATGAGAGCCCAGGGCCCCCTGAGGGCCCGGAG 273

Qy    241 ACGTTTGCTTTGTACATGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCC 300
          || ||||| || ||||||||||||||| | ||||||||| |||||||||| ||||| || 
Db    274 ACCTTTGCCTTATACATGGTGGACTGGTCGGGCTATGAGGCCTGCCAGGCGGAGGGGCCA 333

Qy    301 CGGGCCTACAAGCGCTGGGTGTGCTCCC---------TGCCCTTTGGCCATGTTCAATTC 351
           | |||| ||||||||||| ||||||||           |||||||||| ||| | ||||
Db    334 GGTGCCTTCAAGCGCTGGGAGTGCTCCCGCCCCTTTGCTCCCTTTGGCCCTGTGCGATTC 393

Qy    352 TCAGAGAAGATTCAGCGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAG 411
          |||||||||||||||||||||||||| |||||||| ||||| |||||||| |||||||||
Db    394 TCAGAGAAGATTCAGCGCTTCACACCCTTCTCCCTGGGCTTCGAGTTCTTGCCTGGAGAG 453

Qy    412 ACTTACTACTACATCTCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAG 471
          || |||||||||||||   |||| ||||| |||||| |||||||||||||||||||||||
Db    454 ACCTACTACTACATCT---TGCCAACTCCGGAGAGTCCTGGCCAGTGCTTGAGGCTCCAG 510

Qy    472 GTGTCTGTCTGCTGCAAGGAGAGGAAGTCTGAGTCAGCCCATCC 515
          |||||||||||||||||||||   ||| ||||||| ||||||||
Db    511 GTGTCTGTCTGCTGCAAGGAGGACAAGCCTGAGTCGGCCCATCC 554
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RESULT  14
BI646617
LOCUS       BI646617                963 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603276523F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5317037 5',
            mRNA sequence.
ACCESSION   BI646617
VERSION     BI646617.1  GI:15560853
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 963)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11803  row: m  column: 06
            High quality sequence stop: 764.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5317037"
                     /clone_lib="NIH_CGAP_Mam3"
                     /tissue_type="tumor, gross tissue"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert 2 kb. Library constructed by Life
                     Technologies, catalog #12017-018. Investigators providing
                     samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference
                     for transgenic model: Xu et al., Nature Genetics 22, 37-43
                     (1999). Note: this is a NCI_CGAP Library."
BASE COUNT      191 a    295 c    284 g    193 t
ORIGIN


  Query Match             60.5%;  Score 384.8;  DB 10;  Length 963;
  Best Local Similarity   81.5%;  Pred. No. 1.3e-80;
  Matches  512;  Conservative    0;  Mismatches   97;  Indels   19;  Gaps    5;

Qy     17 CCTCGGGGGCGATGCGGCTGCTGCCCCTGCTGCGGACTGTCCTCTGGGCCGCGTTCCTCG 76
          ||  || |    |||||||||||||||||||||||||||| |||||||||||| | ||||
Db     66 CCCAGGTGCGACTGCGGCTGCTGCCCCTGCTGCGGACTGTGCTCTGGGCCGCGCTGCTCG 125

Qy     77 GCTCCCCTCTGCGCGGGGGCTCCAGCCTCCGCCACGTAGTCTACTGGAACTCCAGTAACC 136
          |||| |  ||||  ||| |||||||||||||||||  | ||||||||||||||  |||||
Db    126 GCTCGCGCCTGCCGGGGTGCTCCAGCCTCCGCCACCCAATCTACTGGAACTCCTCTAACC 185

Qy    137 CCAGGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTG 196
          |||||||||| |||||||| |||||||||||||||||| |||||||||||||||||||  
Db    186 CCAGGTTGCTCCGAGGAGATGCCGTGGTGGAGCTGGGCTTCAACGATTACCTAGACATCT 245

Qy    197 TCTGCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACA 256
          ||||||| || || ||| ||||||||||||| || ||||| || || ||||| || ||||
Db    246 TCTGCCCACATTATGAAAGCCCAGGGCCCCCAGAAGGCCCGGAAACCTTTGCATTATACA 305

Qy    257 TGGTGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCT 316
          ||||||||||| ||||||| ||| |||||  |||||||||  |    |||| | ||||||
Db    306 TGGTGGACTGGTCAGGCTACGAGGCCTGCACGGCAGAGGGGGCAAATGCCTTCCAGCGCT 365

Qy    317 GG-GTGTGCTCCCTGCCCTTTG---------GCCATGTTCAATTCTCAGAGAAGATTCAG 366
          ||  | |||||  |||| ||||         ||| ||||| ||||||||| |||||||||
Db    366 GGAATTTGCTCGATGCCTTTTGCCCCTTTCAGCCCTGTTCGATTCTCAGAAAAGATTCAG 425
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Qy    367 CGCTTCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATC 426
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Db    426 CGCTACACACCCTTCCCGCTGGGCTTTGAGTTCTTGCCTGGAGAGACTTACTACTACATC 485

Qy    427 TCGGTGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGC 486
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Db    486 TCGGTGCCGACTCCGGAGAGTCCTGGCCGGTGCCTGAGACTCCAGGTGTCTGTCTGCTGC 545

Qy    487 AAGGAGAGGAAGTC------TGAGTCAGCCCATCCTGTTGGGAGCCCTGGAG--AGAGTG 538
          ||||||||   |||      ||||||||| |||||||||||||| |||||||  | || |
Db    546 AAGGAGAGCGGGTCATCACATGAGTCAGCTCATCCTGTTGGGAGTCCTGGAGCAAAAGCG 605

Qy    539 GCACATCAGGGTGGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTAC-TG 597
          | || || |||||||| || ||  || | ||||||||||| |||||||||||  | | ||
Db    606 GTACGTCCGGGTGGCGGGGAGGACACGCGCCCAGCCCCCTGTGTCTCTTGCTGCTGCTTG 665

Qy    598 CTGCTTCTGATTCTTCGTCTTCTGCGAA 625
          ||||| |  || || ||||| ||| |||
Db    666 CTGCTCCCAATCCTCCGTCTCCTGAGAA 693


RESULT  15
BE032073
LOCUS       BE032073                565 bp    mRNA    linear   EST 09-JUL-2000
DEFINITION  130886 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BE032073
VERSION     BE032073.1  GI:8327082
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 565)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 69. row: H  column: 17
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .565
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 1PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
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                     and 30 embryos."
BASE COUNT       86 a    185 c    178 g    116 t
ORIGIN


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  Best Local Similarity   87.6%;  Pred. No. 2.8e-79;
  Matches  429;  Conservative    0;  Mismatches   52;  Indels    9;  Gaps    1;

Qy    140 GGTTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAACGATTACCTAGACATTGTCT 199
```

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          || ||||||||||||||||||||||||||||||||||||| ||||||||||||||  |||
Db     75 GGCTGCTTCGAGGAGACGCCGTGGTGGAGCTGGGCCTCAAGGATTACCTAGACATCTTCT 134

Qy    200 GCCCCCACTACGAAGGCCCAGGGCCCCCTGAGGGCCCCGAGACGTTTGCTTTGTACATGG 259
          |||| ||||| ||  |||||||||||||||||||||| ||||| ||||| || |||||||
Db    135 GCCCACACTATGAGAGCCCAGGGCCCCCTGAGGGCCCGGAGACCTTTGCCTTATACATGG 194

Qy    260 TGGACTGGCCAGGCTATGAGTCCTGCCAGGCAGAGGGCCCCCGGGCCTACAAGCGCTGGG 319
          |||||||| | ||||||||| |||||||||| ||||| ||  | |||| |||||||||||
Db    195 TGGACTGGTCGGGCTATGAGGCCTGCCAGGCGGAGGGGCCAGGTGCCTTCAAGCGCTGGG 254

Qy    320 TGTGCTCCC---------TGCCCTTTGGCCATGTTCAATTCTCAGAGAAGATTCAGCGCT 370
           ||||||||           |||||||||| ||| | |||||||||||||||||||||||
Db    255 AGTGCTCCCGCCCCTTTGCTCCCTTTGGCCCTGTGCGATTCTCAGAGAAGATTCAGCGCT 314

Qy    371 TCACACCTTTCTCCCTCGGCTTTGAGTTCTTACCTGGAGAGACTTACTACTACATCTCGG 430
          ||||||| |||||||| ||||| |||||||| ||||||||||| |||||||||||||| |
Db    315 TCACACCCTTCTCCCTGGGCTTCGAGTTCTTGCCTGGAGAGACCTACTACTACATCTCAG 374

Qy    431 TGCCCACTCCAGAGAGTTCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGG 490
          |||| ||||| |||||| ||||||||||||||||||||||||||||||||||||||||||
Db    375 TGCCAACTCCGGAGAGTCCTGGCCAGTGCTTGAGGCTCCAGGTGTCTGTCTGCTGCAAGG 434

Qy    491 AGAGGAAGTCTGAGTCAGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGCACATCAGGGT 550
          ||   ||| ||||||| ||||||||||||||||||||||||||||||||||| |||||||
Db    435 AGGACAAGCCTGAGTCGGCCCATCCTGTTGGGAGCCCTGGAGAGAGTGGCACGTCAGGGT 494

Qy    551 GGCGAGGGGGGGACACTCCCAGCCCCCTCTGTCTCTTGCTATTACTGCTGCTTCTGATTC 610
          ||| |||||||| |||||||||||||||||||||||||||  | |||||||| |  ||||
Db    495 GGCAAGGGGGGGCCACTCCCAGCCCCCTCTGTCTCTTGCTCCTGCTGCTGCTCCCAATTC 554

Qy    611 TTCGTCTTCT 620
          | ||||| ||
Db    555 TGCGTCTCCT 564


Search completed: September 27, 2002, 22:03:14
Job time: 6600 sec
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                    GenCore version 4.5
              Copyright (c) 1993 - 2000  Compugen Ltd.

OM protein - protein search, using sw model

Run on:          September 28, 2002, 01:36:51 ; Search time 74.08 Seconds
                                                (without alignments)
                                                301.375 Million cell updates/sec

Title:           US-09-904-954-4
Perfect score:   1091
Sequence:        1 MRLLPLLRTVLWAAFLGSPL..........SPLCLLLLLLLLILRLLRIL 201

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters:      747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_032802:*
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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                 SUMMARIES
                     %
Result               Query
  No.    Score       Match Length DB  ID                    Description
-----------------------------------------------------------------------------
    1     1091   100.0    201  16  AAR71482              Human hek-L protei
    2    380.5    34.9    228  17  AAR97854              Human AL-1, a liga
    3    380.5    34.9    228  17  AAW02586              Lerk-7 protein.  H
    4    380.5    34.9    228  17  AAW00035              HEK4 binding prote
    5    380.5    34.9    335  22  ABG27837              Novel human diagno
    6    366.5    33.6    234  16  AAR82605              Eph transmembrane
    7    364.5    33.4    238  16  AAR71481              Human hek-L protei
    8      359    32.9    200  17  AAR94767              Chicken EPH recept
    9      359    32.9    200  19  AAW71007              Amino acid sequenc
   10      343    31.4    204  22  AAU12315              Human PRO202 polyp
   11      343    31.4    204  22  AAB50974              Human PRO202 prote
   12    342.5    31.4    209  17  AAR94766              Mouse EPH receptor
   13    342.5    31.4    209  19  AAW71006              Amino acid sequenc
   14    340.5    31.2    213  20  AAY06822              Human LERK-6 polyp
   15    335.5    30.8    205  22  AAB50990              Human PRO202 prote
   16    335.5    30.8    218  21  AAB54058              Human pancreatic c
   17    334.5    30.7    205  13  AAR23895              B61 protein sequen
   18    334.5    30.7    205  15  AAR53634              EBP.  Homo sapiens
   19    334.5    30.7    205  16  AAR82604              Eph transmembrane
   20    334.5    30.7    205  18  AAW04632              eck receptor bindi
   21    330.5    30.3    184  17  AAW02587              Lerk-6 protein.  M
   22    330.5    30.3    184  17  AAR91283              LERK-6 protein.  M
   23    330.5    30.3    184  20  AAY06820              Murine LERK-6 poly
   24    313.5    28.7    151  18  AAW18078              Truncated eck rece
   25    313.5    28.7    160  18  AAW18079              Truncated eck rece
   26    313.5    28.7    167  18  AAW18080              Truncated eck rece
   27    313.5    28.7    171  18  AAW18081              Truncated eck rece
   28    313.5    28.7    180  18  AAW18082              Truncated eck rece
   29      308    28.2    179  17  AAR94768              EPH receptor ligan
   30      308    28.2    179  19  AAW71008              Generic sequence f
   31    261.5    24.0    104  17  AAR91284              LERK-6 exon polype
   32    261.5    24.0    104  20  AAY06821              Amino acid sequenc
   33    169.5    15.5    340  18  AAW33699              AL-2-short (AL-2s)
   34    169.5    15.5    340  18  AAW31544              Human cytokine Ler
   35    169.5    15.5    340  18  AAW10637              NLERK2 ligand for
   36    169.5    15.5    340  18  AAW17081              EPH family ligand
   37    169.5    15.5    340  19  AAW46615              Human transmembran
   38    169.5    15.5    455  18  AAW33698              AL-2-long (AL-2l)
   39    166.5    15.3    331  17  AAW00288              Chicken Eph recept
   40      166    15.2    658  21  AAY96782              Ephrin-B2-Ephrin-B
   41    164.5    15.1    334  17  AAW00287              Mouse Eph receptor
   42    164.5    15.1    336  17  AAR92742              Murine hepatoma tr
   43    158.5    14.5    652  22  ABB58621              Drosophila melanog
   44    158.5    14.5    652  22  ABB65548              Drosophila melanog
   45      156    14.3    333  17  AAW06337              Full length ligand

                                ALIGNMENTS

RESULT   1
AAR71482
ID   AAR71482 standard; Protein; 201 AA.
XX
AC   AAR71482;
XX
DT   03-OCT-1995  (first entry)
XX
DE   Human hek-L protein.
XX
KW   Ligand; cell surface; tyrosine kinase receptor; tumorigenesis;
KW   immunogen.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /note= "signal peptide"
FT   Protein         23..201
XX
PN   WO9506065-A.
XX
PD   02-MAR-1995.
XX
PF   17-AUG-1994;   94WO-US09282.
XX
PR   20-AUG-1993;   93US-0109745.
PR   30-AUG-1993;   93US-0114426.
PR   03-DEC-1993;   93US-0161132.
PR   09-MAY-1994;   94US-0240124.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Beckmann MP,  Cerretti DP;
```

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XX
DR   WPI; 1995-106811/14.
DR   N-PSDB; AAQ85888.
XX
PT   New isolated DNA encoding hek-L protein or its fusion products  -
PT   useful as assay reagent or for carrying therapeutic and
PT   diagnostic compounds to leukaemia cells.
XX
PS   Claim 21; Page 38; 45pp; English.
XX
CC   The sequence is that of a novel protein designated hek-L, a protein
CC   that can bind hek (a cell surface receptor tyrosine kinase).  Hek-L
CC   is the first known ligand for hek and can be used to study cellular
CC   processes regulated by hek (which may be involved in tumorigenesis).
CC   It is also an immunogen for antibody production, as a reagent for
CC   detecting hek or hek-L in in vitro assays, to determine binding of
CC   hek proteins, to purify hek proteins, and to carry diagnostic or
CC   cytotoxic agents to particular leukaemia cells that express the hek
CC   antigen.  Hek-L also binds the elk tyrosine kinase receptors.
CC   See also AAR71481.
XX
SQ   Sequence   201 AA;


  Query Match             100.0%;  Score 1091;  DB 16;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-111;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 mrllpllrtvlwaaflgsplrggsslrhvvywnssnprllrgdavvelglndyldivcph 60

Qy         61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 yegpgppegpetfalymvdwpgyescqaegpraykrwvcslpfghvqfsekiqrftpfsl 120

Qy        121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 gfeflpgetyyyisvptpessgqclrlqvsvcckerksesahpvgspgesgtsgwrggdt 180

Qy        181 PSPLCLLLLLLLLILRLLRIL 201
              |||||||||||||||||||||
Db        181 psplclllllllllilrllril 201


RESULT   2
AAR97854
ID   AAR97854 standard; Protein; 228 AA.
XX
AC   AAR97854;
XX
DT   05-JAN-1997  (first entry)
XX
DE   Human AL-1, a ligand for eph-related tyrosine kinase receptor REK7.
XX
KW   AL-1; REK7; eph-related tyrosine kinase receptor; ligand;
KW   neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Sig_peptide
FT   Modified-site   37..39
FT                   /label= Glycosylation
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   162..164
FT                   /label= Glycosylation
FT                   /note= "potential N-glycosylation site"
FT   Binding-site    203..204
FT                   /label= GPI
FT                   /note= "potential attachment site for
FT                          glycophosphatidyl-inositol"
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FT   Domain          214..228
FT                   /label= Hydrophobic_domain
XX
PN   WO9613518-A1.
XX
PD   09-MAY-1996.
XX
PF   26-OCT-1995;   95WO-US14016.
XX
PR   07-JUN-1995;   95US-0486449.
PR   27-OCT-1994;   94US-0330128.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Caras IW,  Winslow JW;
XX
DR   WPI; 1996-239448/24.
DR   N-PSDB; AAT18897.
XX
PT   AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in
PT   treatment and diagnosis of neuronal disorders and
PT   angiogenesis-related conditions.
XX
PS   Claim 1; Page 54; 75pp; English.
XX
CC   Human AL-1 (AAR97854) neurotrophic factor is a ligand for eph-related
CC   tyrosine kinase receptor REK7 (AAR97853).  Its amino acid sequence
CC   was deduced from a cDNA clone (AAT18897) isolated from a human foetal
CC   brain cDNA library.  Recombinant, mature AL-1 can be produced in
CC   transformed host cells.  It may be useful in promoting the
CC   development, maintenance or regeneration of neurons in vivo, and
CC   can be utilised in methods for the diagnosis and/or treatment of
CC   neurological disorders.  It can also be used to promote or enhance
CC   angiogenesis.  Antagonists and agonists of AL-1, as well as
CC   antibodies raised against AL-1, also have therapeutic applns.
XX
SQ   Sequence   228 AA;


  Query Match             34.9%;  Score 380.5;  DB 17;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 3.5e-33;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy          1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
              : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db          4 vemltlvflvlwmcvfsqdpgskavadryavywnssnprfqrgdyhidvcindyldvfcp 63

Qy         60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
              |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db         64 hyedsvpedkteryvlymvnfdgysacd-htskgfkrwecnrphspngplkfsekfqlft 122

Qy        117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
              |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db        123 pfslgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigvhdrvfdvndkve 182

Qy        155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
                 |   :: |    |    : |     ||  |  || :|| |:  || :
Db        183 nslepaddtvhesaep----srgenaaqtpripsrllaillfllamlltl 228


RESULT   3
AAW02586
ID   AAW02586 standard; Protein; 228 AA.
XX
AC   AAW02586;
XX
DT   28-NOV-1996  (first entry)
XX
DE   Lerk-7 protein.
XX
KW   Lerk-6; hek; elk; cell surface receptor; culture; reagent;
KW   neuron; disorder; injury; delivery agent; diagnostic; therapeutic;
KW   Lerk-7; probe; cytokine.
```

```
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= signal_peptide
FT   Protein         1..228
FT                   /label= precursor_protein
FT   Domain          1..133
FT                   /label= extracellular_receptor-binding_domain
FT   Region          134..183
FT                   /label= spacer_region
FT   Region          194..208
FT                   /note= "C-terminal stretch of hydrophobic residues"
FT   Binding-site    183
FT                   /label= GPI_attachment_site
XX
PN   WO9617925-A1.
XX
PD   13-JUN-1996.
XX
PF   05-DEC-1995;   95WO-US15781.
XX
PR   01-MAR-1995;   95US-0396946.
PR   06-DEC-1994;   94US-0351025.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1996-287171/29.
DR   N-PSDB; AAT32699.
XX
PT   New isolated human Lerk-7 cytokine - which binds to cell surface
PT   receptors elk, hek and eck, useful for delivering agents to cells or
PT   for treating neural disorders
XX
PS   Claim 1; Page 37-38; 49pp; English.
XX
CC   The present sequence is that of human Lerk-7 protein. Lerk-7 is
CC   predicted to be anchored to the cell surface via
CC   glycosyl-phosphatidylinositol (GPI) linkage. A GPI anchor attaches to the
CC   exposed C-terminal amino acid of the processed mature protein, usually
CC   after cleavage upstream, often about 10-12 amino acids, of the N-terminus
CC   of the hydrophobic domain. Lerk-7 coding sequence (AAT32699) was isolated
CC   using a probe derived from the murine Lerk-6 DNA (AAT32700). The Lerk-7
CC   gene and protein can be used for studying the role of Lerk-7 in
CC   conjunction with elk, hek and eck receptors. They can also be used for
CC   delivering diagnostic or therapeutic agents to cells, e.g. cancer cells.
CC   The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic
CC   properties and can be used to treat neural tissue disorders.
XX
SQ   Sequence   228 AA;


  Query Match             34.9%;  Score 380.5;  DB 17;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 3.5e-33;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy      1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
          : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db      4 vemltlvflvlwmcvfsqdpgskavadryavywnssnprfqrgdyhidvcindyldvfcp 63

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
          |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db     64 hyedsvpedkteryvlymvnfdgysacd-htskgfkrwecnrphspngplkfsekfqlft 122

Qy    117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
          |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db    123 pfslgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigvhdrvfdvndkve 182

Qy    155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
             |   ::  |    |    : |     ||  |  || :|| |:  || :
```

```
Db    183 nslepaddtvhesaep----srgenaaqtpripsrllaillfllamlltl 228

RESULT 4
AAW00035
ID   AAW00035 standard; Protein; 228 AA.
XX
AC   AAW00035;
XX
DT   24-OCT-1996  (first entry)
XX
DE   HEK4 binding protein.
XX
KW   HEK4 binding protein; HEK4 receptor; EPH-like receptor;
KW   protein tyrosine kinase; ligand; growth; differentiation; cancer;
KW   nervous system disorder; therapy; antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= Sig_peptide
FT   Protein         20..228
FT                   /label= Mat_protein
XX
PN   WO9623000-A1.
XX
PD   01-AUG-1996.
XX
PF   16-JAN-1996;   96WO-US01079.
XX
PR   27-JAN-1995;   95US-0379802.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Bartley TD,  Fox GM;
XX
DR   WPI; 1996-362633/36.
DR   N-PSDB; AAT34292.
XX
PT   Ligand for EPH-like receptors, partic. the HEK4 receptor - useful to
PT   modulate growth and differentiation of, e.g. liver and kidney cells,
PT   and to treat cancer and nervous system disorders
XX
PS   Claim 8; Page 39-40; 65pp; English.
XX
CC   Human HEK4 binding protein (HEK4 BP) (AAW00035) binds to and activates
CC   HEK4 and ECK receptors.  Its amino acid sequence was deduced from
CC   a cDNA clone (AAT34292) isolated from a human placenta cDNA library.
CC   Expression vectors and host cells can be used for the prodn. of
CC   biologically active HEK BP.  It is useful for modulating the growth
CC   and/or differentiation of EPH sub-family receptor-bearing cells,
CC   esp. in liver, kidney, lung, skin or neural tissues.  It can be
CC   used to treat neural system disorders and in the regeneration of
CC   damaged or depleted tissues.  Antagonists are useful for cancer
CC   treatment.  HEK4 BP can also be used to raise antibodies.
XX
SQ   Sequence   228 AA;


  Query Match             34.9%;  Score 380.5;  DB 17;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 3.5e-33;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy      1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
          : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db      4 vemltlvflvlwmcvfsqdpgskavadryavywnssnprfqrgdyhidvcindyldvfcp 63

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
          |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db     64 hyedsvpedkteryvlymvnfdgysacd-htskgfkrwecnrphspngplkfsekfqlft 122

Qy    117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
```

```
           |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db    123 pfslgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigvhdrvfdvndkve 182

Qy    155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
             |   :: |    |    : |     ||  |  || :|| |:  || :
Db    183 nslepaddtvhesaep----srgenaaqtpripsrllaillfllamlltl 228


RESULT   5
ABG27837
ID   ABG27837 standard; Protein; 335 AA.
XX
AC   ABG27837;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #27828.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS92024.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 58196; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   335 AA;

  Query Match             34.9%;  Score 380.5;  DB 22;  Length 335;
  Best Local Similarity   38.3%;  Pred. No. 5.8e-33;
```

```
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy      1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
          : :| |:  |||   |   |     : |: |||||||||  |||  ::: :||||| : ||
Db    111 vemltlvflvlwmcvfsqdpgskavadryavywnssnprfqrgdyhidvcindyldvfcp 170

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
          |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db    171 hyedsvpedkteryvlymvnfdgysacd-htskgfkrwecnrphspngplkfsekfqlft 229

Qy    117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
          |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db    230 pfslgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigvhdrvfdvndkve 289

Qy    155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
             |   :: |    |    : |     ||  |  || :|| |:  || :
Db    290 nslepaddtvhesaep----srgenaaqtpripsrllaillfllamlltl 335


RESULT   6
AAR82605
ID   AAR82605 standard; Protein; 234 AA.
XX
AC   AAR82605;
XX
DT   16-MAY-1996  (first entry)
XX
DE   Eph transmembrane tyrosine kinase family ligand, Efl-2.
XX
KW   Efl-2; EHK1-L; Eph transmembrane tyrosine kinase family ligand;
KW   neurological disorder; identification; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT                   /label= signal_peptide
FT   Region          218..235
FT                   /note= "carboxy terminal hydrophobic
FT                          GPI-recognition tail"
FT   Misc-difference 158
FT                   /note= "residue borders main conserved regions"
XX
PN   WO9527060-A2.
XX
PD   12-OCT-1995.
XX
PF   04-APR-1995;   95WO-US04208.
XX
PR   21-OCT-1994;   94US-0327423.
PR   04-APR-1994;   94US-0222075.
PR   12-APR-1994;   94US-0229402.
PR   01-SEP-1994;   94US-0299567.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Aldrich TH,  Davis S,  Gale N,  Goldfarb M,  Maisonpierre PC;
PI   Yancopoulos GD;
XX
DR   WPI; 1995-358635/46.
DR   N-PSDB; AAT03883.
XX
PT   Ligands which bind Eph family receptors - used in the diagnosis of
PT   neurological disorders
XX
PS   Disclosure; Fig 2; 58pp; English.
XX
CC   Efl-2 (also known as EHK-1L) is an Eph transmembrane tyrosine kinase
CC   family ligand. It has homology with B61 (Efl-1) (see AAR82604). Efl-2
CC   ends in a C-terminal hydrophobic sequence that appears to to be a
CC   recognition sequence allowing it to be GPI-linked and thus lacking in
CC   an intracellular domain. Efl-2 is useful for identifying other ligands
CC   for Ehk-1, -2, -3, Eck and Elk receptors.   The ligands are useful in
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CC   promoting a differential function and/or influencing the phenotye,
CC   such as growth and/or proliferation, of receptor bearing cells. They
CC   may be used in the diagnosis, and treatment of neurological disorders.
XX
SQ   Sequence   234 AA;

  Query Match             33.6%;  Score 366.5;  DB 16;  Length 234;
  Best Local Similarity   45.6%;  Pred. No. 1.2e-31;
  Matches   77;  Conservative   16;  Mismatches   67;  Indels    9;  Gaps    3;

Qy          3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
              || ||  |     |     |    || |||||||  | |    |:: :|||||| ||||
Db          8 lllllvpvpllpllaqgpggalgnrhavywnssnqhlrregytvqvnvndyldiycphyn 67

Qy         63 ----GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRF 115
                  ||||  | | : ||||   || :| |   : :||| |:    |   ::|||| ||:
Db         68 ssgagpgpgggaeqyvlymvsrngyrtcnas--qgfkrwecnrphaphspikfsekfqry 125

Qy        116 TPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
              : ||||:||  |  ||||| ||     :|||::| |||         ||
Db        126 safslgyefhagheyyyistpthnlhwkclrmkvfvccastshsgekpv 174


RESULT   7
AAR71481
ID   AAR71481 standard; Protein; 238 AA.
XX
AC   AAR71481;
XX
DT   03-OCT-1995  (first entry)
XX
DE   Human hek-L protein.
XX
KW   Ligand; cell surface; tyrosine kinase receptor; tumorigenesis;
KW   immunogen.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Protein         20..238
XX
PN   WO9506065-A.
XX
PD   02-MAR-1995.
XX
PF   17-AUG-1994;   94WO-US09282.
XX
PR   20-AUG-1993;   93US-0109745.
PR   30-AUG-1993;   93US-0114426.
PR   03-DEC-1993;   93US-0161132.
PR   09-MAY-1994;   94US-0240124.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Beckmann MP,  Cerretti DP;
XX
DR   WPI; 1995-106811/14.
DR   N-PSDB; AAQ85887.
XX
PT   New isolated DNA encoding hek-L protein or its fusion products  -
PT   useful as assay reagent or for carrying therapeutic and
PT   diagnostic compounds to leukaemia cells.
XX
PS   Claim 21; Page 36; 45pp; English.
XX
CC   The sequence is that of a novel protein designated hek-L, a protein
CC   that can bind hek (a cell surface receptor tyrosine kinase).  Hek-L
CC   is the first known ligand for hek and can be used to study cellular
CC   processes regulated by hek (which may be involved in tumorigenesis).
CC   It is also an immunogen for antibody production, as a reagent for
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CC   detecting hek or hek-L in in vitro assays, to determine binding of
CC   hek proteins, to purify hek proteins, and to carry diagnostic or
CC   cytotoxic agents to particular leukaemia cells that express the hek
CC   antigen.  Hek-L also binds the elk tyrosine kinase receptors.
CC   See also AAR71482.
XX
SQ   Sequence   238 AA;

  Query Match             33.4%;  Score 364.5;  DB 16;  Length 238;
  Best Local Similarity   44.5%;  Pred. No. 2.1e-31;
  Matches   77;  Conservative   16;  Mismatches   67;  Indels   13;  Gaps    3;

Qy          3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
              || ||  |     |     |    || |||||||  | |    |:: :|||||| ||||
Db          8 lllllvpvpllpllaqgpggalgnrhavywnssnqhlrregytvqvnvndyldiycphyn 67

Qy         63 --------GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEK 111
                      ||||  | | : ||||   || :| |   : :||| |:    |   ::||||
Db         68 ssgvgpgagpgpgggaeqyvlymvsrngyrtcnas--qgfkrwecnrphaphspikfsek 125

Qy        112 IQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
               ||:: ||||:||  |  ||||| ||     :|||::| |||         ||
Db        126 fqrysafslgyefhagheyyyistpthnlhwkclrmkvfvccastshsgekpv 178


RESULT   8
AAR94767
ID   AAR94767 standard; Protein; 200 AA.
XX
AC   AAR94767;
XX
DT   02-JUL-1996  (first entry)
XX
DE   Chicken EPH receptor ligand Elf-1.
XX
KW   Elf-1; EPH receptor ligand; dementia; tachycardia; therapy;
KW   diagnosis; transgenic animal.
XX
OS   Gallus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..21
FT                   /label= Sig_peptide
FT   Protein         22..200
FT                   /label= Mat_protein
FT   Region          61..150
FT                   /label= Cys4_motif
FT   Region          33..157
FT                   /label= Core_sequence_motif
XX
PN   WO9609384-A1.
XX
PD   28-MAR-1996.
XX
PF   19-SEP-1995;   95WO-US11869.
XX
PR   27-FEB-1995;   95US-0393462.
PR   19-SEP-1994;   94US-0308814.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1996-188446/19.
DR   N-PSDB; AAT15009.
XX
PT   Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis
PT   and treatment of disorders associated with the Elf-1 gene, e.g.
PT   dementia, tachycardia , etc.
XX
PS   Claim 1; Page 88-89; 107pp; English.
XX
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CC   A novel chicken EPH receptor ligand, Elf-1 (AAR94767), is involved in
CC   the formation and maintenance of ordered spatial arrangements of
CC   differentiated tissue.  It is the product of a cDNA clone (AAT15009)
CC   obtd. from an embryo cDNA expression library.  This cDNA is used for
CC   the prodn. of recombinant Elf-1, which can be used to modulate
CC   proliferation, survival and/or differentiation of cells and tissues,
CC   and to stimulate or antagonise intracellular signal transduction
CC   pathways mediated by the EPH-type receptor.
XX
SQ   Sequence   200 AA;


  Query Match             32.9%;  Score 359;  DB 17;  Length 200;
  Best Local Similarity   45.1%;  Pred. No. 6.5e-31;
  Matches   78;  Conservative   23;  Mismatches   62;  Indels   10;  Gaps    5;

Qy      3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
          |  ::   :|:   |  :    | |: |||| ||||  |||  ||: :|||||| |||||
Db     10 laaivgvcvwsddpgkvi----sdryavywnrsnprfhrgdytvevsindyldiycphye 65

Qy     63 GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRFTPFS 119
           | | |  | : ||||:: |: ||     : :||| |:    | | ::|||| | |||||
Db     66 eplpaermeryvlymvnyeghascd-hrqkgfkrwecnrpdspsgplkfsekfqlftpfs 124

Qy    120 LGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSESAHPVGSPGES 170
          ||||| ||  |||||   |    : ||:|:| |    :   ||  |: :   |
Db    125 lgfefrpgheyyyisasppnvvdrpclklkvyvrptndslyespepiftsnns 177


RESULT   9
AAW71007
ID   AAW71007 standard; Protein; 200 AA.
XX
AC   AAW71007;
XX
DT   20-OCT-1998  (first entry)
XX
DE   Amino acid sequence of an avian Elf-1 protein.
XX
KW   Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP;
KW   tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation;
KW   intracellular signalling; increased; survival; neuronal cell;
KW   neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour;
KW   artificial liver; cartilage; bone formation.
XX
OS   Gallus sp.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 61..150
FT                   /note= "contains a Cys4 motif"
FT   Misc-difference 35..157
FT                   /note= "contains a core sequence motif"
XX
PN   US5795734-A.
XX
PD   18-AUG-1998.
XX
PF   31-MAY-1995;   95US-0455001.
XX
PR   31-MAY-1995;   95US-0455001.
PR   19-SEP-1994;   94US-0308814.
PR   27-FEB-1995;   95US-0393462.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1998-466665/40.
DR   N-PSDB; AAV42927.
XX
PT   Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor
PT   - for production of Elf-1 protein, useful for regulating
PT   proliferation, differentiation, and survival of cells
```

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XX
PS   Claim 1; Columns 75-78; 53pp; English.
XX
CC   The present sequence represents an avian EPH receptor ligand designated
CC   Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a
CC   tyrosine kinase ligand, which is linked to the membrane through a
CC   phosphatidylinositol linkage. It shares some homology to 2 other EPH
CC   receptor ligands, B61 and LERK-2. The Elf-1 protein modulates
CC   proliferation, differentiation and survival of EPH receptor-expressing
CC   cells by stimulating or antagonising intracellular signalling mediated
CC   by the EPH receptor. Typical of many potential applications are
CC   increasing survival of neuronal cells in culture (e.g. where intended for
CC   transplantation), also therapeutically in increase neuron survival
CC   (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent
CC   nervous system and lymphatic tumours, to induce differentiation of
CC   hepatocytes to form an artificial liver, to induce cartilage and bone
CC   formation.
XX
SQ   Sequence   200 AA;


  Query Match             32.9%;  Score 359;  DB 19;  Length 200;
  Best Local Similarity   45.1%;  Pred. No. 6.5e-31;
  Matches   78;  Conservative   23;  Mismatches   62;  Indels   10;  Gaps    5;

Qy      3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
          |  ::   :|:   |  :    | |: |||| ||||  |||  ||: :|||||| |||||
Db     10 laaivgvcvwsddpgkvi----sdryavywnrsnprfhrgdytvevsindyldiycphye 65

Qy     63 GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRFTPFS 119
           | | |  | : ||||:: |: ||     : :||| |:    | | ::|||| | |||||
Db     66 eplpaermeryvlymvnyeghascd-hrqkgfkrwecnrpdspsgplkfsekfqlftpfs 124

Qy    120 LGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSESAHPVGSPGES 170
          ||||| ||  |||||   |    : ||:|:| |    :   ||  |: :   |
Db    125 lgfefrpgheyyyisasppnvvdrpclklkvyvrptndslyespepiftsnns 177


RESULT  10
AAU12315
ID   AAU12315 standard; Protein; 204 AA.
XX
AC   AAU12315;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human PRO202 polypeptide sequence.
XX
KW   Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW   breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW   cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW   adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200140466-A2.
XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US32678.
XX
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   09-DEC-1999;   99US-0170262.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30911.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31243.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
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PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US04914.
PR   24-FEB-2000; 2000WO-US05004.
PR   01-MAR-2000; 2000WO-US05601.
PR   20-MAR-2000; 2000WO-US07377.
PR   21-MAR-2000; 2000WO-US07532.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   10-NOV-2000; 2000WO-US30873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   N-PSDB; AAS21387.
XX
PT   Isolated, secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing
PT   PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT   lung, breast, prostate, cervical  -
XX
PS   Claim 12; Fig 288; 813pp; English.
XX
CC   AAU12172-AAU12446 represent novel human secretory and transmembrane
CC   PRO polypeptides. The PRO polypeptides are useful to detect other
CC   PRO polypeptides, to link bioactive molecules to cells expressing
CC   PRO polypeptides, to modulate biological activities of cells expressing
CC   PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample.
CC   Some of the 275 sequences are also useful to stimulate the release of
CC   tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC   proliferation or differentiation of chondrocytes, the proliferation or
CC   gene expression in pericyte cells, the release of proteoglycans from
CC   cartilage, the proliferation of inner ear utricular supporting cells or
CC   of T-lymphocytes, the release of a cytokine from peripheral blood
CC   monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC   the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC   skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC   to factor VIIA. The PRO polypeptides can be used in assays to identify
CC   molecules involved in binding interactions. The polynucleotides encoding
CC   PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy.
XX
SQ   Sequence   204 AA;


  Query Match             31.4%;  Score 343;  DB 22;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 3.7e-29;
  Matches   79;  Conservative   26;  Mismatches   73;  Indels   26;  Gaps    5;

Qy         11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
              |||  ||      :: || |:||||||:    |  : : ||||:||:|||||
Db          4 lwapllglccslaaadrhtvfwnssnpkfrnedytihvqlndyvdiicphyedhsadaam 63

Qy         71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
              | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||  |
Db         64 eqyilylveheeyqlcqpqs-kdqvrwqcnrpsakhgpeklsekfqrftpftlgkefkeg 122

Qy        128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----- 182
               :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db        123 hsyyyiskpihqhedrclrlkvtvsgkithspqah--dnpqekrla----addpevrvlh 176

Qy        183 -----------PLCLLLLLLLLIL 195
```

```
                         ||   :||| |:|
Db        177 sighsaaprlfplawtvlllplll 200


RESULT  11
AAB50974
ID   AAB50974 standard; Protein; 204 AA.
XX
AC   AAB50974;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO202 protein.
XX
KW   Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
KW   antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW   PRO agonist; cancer; inflammatory disorder; immunological disorder.
XX
OS   Homo sapiens.
XX
PN   WO200073348-A2.
XX
PD   07-DEC-2000.
XX
PF   30-MAY-2000; 2000WO-US14941.
XX
PR   02-JUN-1999;   99WO-US12252.
PR   22-JUN-1999;   99US-0140650.
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   29-OCT-1999;   99US-0162506.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30999.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   02-MAR-2000; 2000WO-US05841.
PR   03-MAR-2000; 2000US-0187202.
PR   10-MAR-2000; 2000WO-US06319.
PR   15-MAR-2000; 2000WO-US06884.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W,  Kabakoff RC;
PI   Shelton DL,  Smith V,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-016509/02.
DR   N-PSDB; AAC91576.
XX
PT   Twenty eight nucleic acids encoding PRO polypeptides which are useful
PT   for treating various tumors, e.g. breast cancer, and other
PT   inflammatory, angiogenic and immunological disorders -
XX
PS   Claim 31; Fig 48; 188pp; English.
XX
CC   The present sequence is one of twenty eight novel PRO polypeptides. The
CC   PRO polypeptides and their agonists, including antibodies, peptides, and
CC   small molecule agonists, may be used to treat various tumours, e.g.,
CC   cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
CC   cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
CC   central nervous system cancer, melanoma or leukaemia. They are also
CC   useful for treating other disorders such as neuronal, glial, astrocytal,
CC   hypothalamic and other glandular, macrophagal, epithelial, stromal and
CC   blastocoelic disorders, and inflammatory, angiogenic and immunological
CC   disorders.
```

```
XX
SQ   Sequence   204 AA;

  Query Match             31.4%;  Score 343;  DB 22;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 3.7e-29;
  Matches   79;  Conservative   26;  Mismatches   73;  Indels   26;  Gaps    5;

Qy      11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
           |||  ||      :: || |:||||||:    |  : : ||||:||:|||||
Db       4 lwapllglccslaaadrhtvfwnssnpkfrnedytihvqlndyvdiicphyedhsadaam 63

Qy      71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
           | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||  |
Db      64 eqyilylveheeyqlcqpqs-kdqvrwqcnrpsakhgpeklsekfqrftpftlgkefkeg 122

Qy     128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----- 182
            :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db     123 hsyyyiskpihqhedrclrlkvtvsgkithspqah--dnpqekrla----addpevrvlh 176

Qy     183 -----------PLCLLLLLLLLIL 195
                      ||   :||| |:|
Db     177 sighsaaprlfplawtvlllplll 200

RESULT  12
AAR94766
ID   AAR94766 standard; Protein; 209 AA.
XX
AC   AAR94766;
XX
DT   02-JUL-1996  (first entry)
XX
DE   Mouse EPH receptor ligand Elf-1.
XX
KW   Elf-1; EPH receptor ligand; dementia; tachycardia; therapy;
KW   diagnosis; transgenic animal.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Sig_peptide
FT   Protein         21..209
FT                   /label= Mat_protein
FT   Region          69..159
FT                   /label= Cys4_motif
FT   Region          35..166
FT                   /label= Core_sequence_motif
FT   Modified-site   38
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   170
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   184
FT                   /note= "potential N-glycosylation site"
XX
PN   WO9609384-A1.
XX
PD   28-MAR-1996.
XX
PF   19-SEP-1995;   95WO-US11869.
XX
PR   27-FEB-1995;   95US-0393462.
PR   19-SEP-1994;   94US-0308814.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1996-188446/19.
DR   N-PSDB; AAT15008.
XX
PT   Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis
```

```
PT   and treatment of disorders associated with the Elf-1 gene, e.g.
PT   dementia, tachycardia , etc.
XX
PS   Claim 1; Page 86; 107pp; English.
XX
CC   A novel mouse EPH receptor ligand, Elf-1 (AAR94766), is involved in
CC   the formation and maintenance of ordered spatial arrangements of
CC   differentiated tissue.  It is the product of a cDNA clone (AAT15008)
CC   obtd. from an embryo mid- and hind-brain cDNA expression library.
CC   This cDNA is used for the prodn. of recombinant Elf-1, which can
CC   be used to modulate proliferation, survival and/or differentiation
CC   of cells and tissues, and to stimulate or antagonise intracellular
CC   signal transduction pathways mediated by the EPH-type receptor.
XX
SQ   Sequence   209 AA;

  Query Match             31.4%;  Score 342.5;  DB 17;  Length 209;
  Best Local Similarity   42.5%;  Pred. No. 4.4e-29;
  Matches   90;  Conservative   20;  Mismatches   67;  Indels   35;  Gaps   10;

Qy       3 LLPLLRTVLWAAFLGSPLRG-------GSSLRHVVYWNSSNPRLL------RGDAVVELG 49
           |||||  :|       |||         :: |: |||| ||||         |   ||:
Db       8 llpllllll-------plrarnedparanadryavywnrsnprfqvsavgdgggytvevs 60

Qy      50 LNDYLDIVCPHYEGPGPP-EGPETFALYMVDWPGYESCQAEGPRAYKRWVC---SLPFGH 105
           :|||||| ||||  | || |  | : ||||:  |: ||     | :||| |   : | |
Db      61 indyldiycphygaplppaermeryilymvngeghascd-hrqrgfkrwecnrpaapggp 119

Qy     106 VQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSESAHP 163
           ::|||| | |||||||||| ||  |||||   |    : ||||:| |    |   |:  |
Db     120 lkfsekfqlftpfslgfefrpgheyyyisatppnlvdrpclrlkvyvrptnetlyeapep 179

Qy     164 VGSPGESGTSGWRGGDTPSPLCLLLLLLLLIL 195
           : :   |  ||  |       | | |  : :|
Db     180 ift-snsscsglgg-------chlflttvpvl 203

RESULT  13
AAW71006
ID   AAW71006 standard; Protein; 209 AA.
XX
AC   AAW71006;
XX
DT   20-OCT-1998  (first entry)
XX
DE   Amino acid sequence of a mammalian Elf-1 protein.
XX
KW   Mouse; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand;
KW   B61; LERK-2; proliferation; differentiation; intracellular signalling;
KW   increased; survival; neuronal cell; neuron survival; treatment;
KW   Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage;
KW   bone formation.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /note= "signal peptide"
FT   Protein         21..209
FT                   /note= "mature protein"
FT   Modified-site   38
FT                   /note= "potential N-linked glycosylation site"
FT   Misc-difference 35..166
FT                   /note= "contains core sequence motif"
FT   Misc-difference 69..159
FT                   /note= "contains a Cys4 motif"
FT   Modified-site   170
FT                   /note= "potential N-linked glycosylation site"
FT   Modified-site   184
FT                   /note= "potential N-linked glycosylation site"
XX
PN   US5795734-A.
```

```
XX
PD   18-AUG-1998.
XX
PF   31-MAY-1995;   95US-0455001.
XX
PR   31-MAY-1995;   95US-0455001.
PR   19-SEP-1994;   94US-0308814.
PR   27-FEB-1995;   95US-0393462.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Cheng H,  Flanagan JG;
XX
DR   WPI; 1998-466665/40.
DR   N-PSDB; AAV42926.
XX
PT   Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor
PT   - for production of Elf-1 protein, useful for regulating
PT   proliferation, differentiation, and survival of cells
XX
PS   Claim 1; Fig 2A; 53pp; English.
XX
CC   The present sequence represents a mammalian EPH receptor ligand
CC   designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is
CC   a tyrosine kinase ligand, which is linked to the membrane through a
CC   phosphatidylinositol linkage. It shares some homology to 2 other EPH
CC   receptor ligands, B61 and LERK-2. The Elf-1 protein modulates
CC   proliferation, differentiation and survival of EPH receptor-expressing
CC   cells by stimulating or antagonising intracellular signalling mediated
CC   by the EPH receptor. Typical of many potential applications are
CC   increasing survival of neuronal cells in culture (e.g. where intended for
CC   transplantation), also therapeutically in increase neuron survival
CC   (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent
CC   nervous system and lymphatic tumours, to induce differentiation of
CC   hepatocytes to form an artificial liver, to induce cartilage and bone
CC   formation.
XX
SQ   Sequence   209 AA;

  Query Match             31.4%;  Score 342.5;  DB 19;  Length 209;
  Best Local Similarity   42.5%;  Pred. No. 4.4e-29;
  Matches   90;  Conservative   20;  Mismatches   67;  Indels   35;  Gaps   10;

Qy        3 LLPLLRTVLWAAFLGSPLRG-------GSSLRHVVYWNSSNPRLL------RGDAVVELG 49
            |||||  :|       |||         :: |: |||| ||||         |   ||:
Db        8 llpllllll-------plrarnedparanadryavywnrsnprfqvsavgdgggytvevs 60

Qy       50 LNDYLDIVCPHYEGPGPP-EGPETFALYMVDWPGYESCQAEGPRAYKRWVC---SLPFGH 105
            :|||||| ||||  | || |  | : ||||:  |: ||     | :||| |    :| |
Db       61 indyldiycphygaplppaermeryilymvngeghascd-hrqrgfkrwecnrpaapggp 119

Qy      106 VQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSESAHP 163
            ::|||| | |||||||||| ||  |||||   |    : ||||:| |    |   | : |
Db      120 lkfsekfqlftpfslgfefrpgheyyyisatppnlvdrpclrlkvyvrptnetlyeapep 179

Qy      164 VGSPGESGTSGWRGGDTPSPLCLLLLLLLLIL 195
            : :   |  ||  |       | | |  : :|
Db      180 ift-snsscsglgg-------chlflttvpvl 203

RESULT 14
AAY06822
ID   AAY06822 standard; Protein; 213 AA.
XX
AC   AAY06822;
XX
DT   24-JUN-1999  (first entry)
XX
DE   Human LERK-6 polypeptide.
XX
KW   LERK-6 polypeptide; hek receptor; elk receptor; human; murine; injury;
KW   cell proliferation; neural growth; neural tissue; neurological disease;
```

```
KW   neurodegenerative; excitotoxicity.
XX
OS   Homo sapiens.
XX
PN   WO9910495-A1.
XX
PD   04-MAR-1999.
XX
PF   27-AUG-1998;   98WO-US17772.
XX
PR   29-AUG-1997;   97US-0920440.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1999-243567/20.
DR   N-PSDB; AAX32767.
XX
PT   New cytokine designated LERK-6
XX
PS   Claim 6; Page 42; 46pp; English.
XX
CC   The invention relates murine and human LERK-6 polypeptides that bind to
CC   hek/elk receptors. Host cells transfected or transformed with vectors
CC   comprising the LERK-6 nucleic acid sequences are used for the recombinant
CC   production of the proteins. LERK-6 polypeptides may be useful in the
CC   enhancement, stimulation, proliferation or growth of cells expressing the
CC   hek or elk receptor. The ligand and receptor complex may be involved in
CC   neural growth, development and/or maintenance. LERK-6 can be used for
CC   treating disorders of neural tissue such as injury or neurological
CC   diseases, either chronic or acute. LERK-6 may be employed in treating
CC   neurodegenerative conditions where there is neural death, excitotoxicity.
CC   In addition, they may be administered to a mammal to exert a trophic
CC   effect on neural tissue. They can also be used as reagents for those
CC   conducting quality assurance studies e.g. to monitor shelf life and
CC   stability of elk protein under different conditions. The polypeptides can
CC   also be used as carriers for delivering agents attached to cells bearing
CC   the elk or hek cell surface receptor. The present sequence represents a
CC   human LERK-6 polypeptide.
XX
SQ   Sequence   213 AA;

  Query Match             31.2%;  Score 340.5;  DB 20;  Length 213;
  Best Local Similarity   41.7%;  Pred. No. 7.4e-29;
  Matches   90;  Conservative   21;  Mismatches   66;  Indels   39;  Gaps   10;

Qy        3 LLPLLRTVLWAAFLGSPL-----------RGGSSLRHVVYWNSSNPRLLRGDA------V 45
            |||||  :|       ||              :| |: |||| ||||   |
Db        8 llpllllll-------plppppfaraedaaransdryavywnrsnprfhagagddgggyt 60

Qy       46 VELGLNDYLDIVCPHYEGPGPP-EGPETFALYMVDWPGYESCQAEGPRAYKRWVC---SL 101
            ||: :|||||| ||||  | || |  | : ||||:  |: ||     | :||| |    :
Db       61 vevsindyldiycphygaplppaermehyvlymvngeghascd-hrqrgfkrwecnrpaa 119

Qy      102 PFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSE 159
            | | ::|||| | |||||||||| ||  |||||   | :  : ||||:| |    |   |
Db      120 pggplkfsekfqlftpfslgfefrpgheyyyisatppnavdrpclrlkvyvrptnetlye 179

Qy      160 SAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLIL 195
            :  |: :   | :|   ||      | | |  : :|
Db      180 apepiftsnnscss--pgg------crlflstipvl 207

RESULT 15
AAB50990
ID   AAB50990 standard; Protein; 205 AA.
XX
AC   AAB50990;
XX
DT   21-MAR-2001  (first entry)
XX
```

```
DE   Human PRO202 protein.
XX
KW   Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;
KW   vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;
KW   vulnerary; antianginal; gene therapy; cardiovascular disease;
KW   endothelial disorder; angiogenic disorder; cancer; periodontal disease;
KW   wound healing.
XX
OS   Homo sapiens.
XX
PN   WO200073445-A2.
XX
PD   07-DEC-2000.
XX
PF   17-MAY-2000; 2000WO-US13705.
XX
PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   28-JUL-1999;   99US-0146222.
PR   01-SEP-1999;   99WO-US20111.
PR   30-NOV-1999;   99WO-US28313.
PR   30-NOV-1999;   99WO-US28409.
PR   02-DEC-1999;   99WO-US28565.
PR   16-DEC-1999;   99WO-US30095.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   24-FEB-2000; 2000WO-US05004.
PR   02-MAR-2000; 2000WO-US05841.
PR   10-MAR-2000; 2000WO-US06319.
PR   15-MAR-2000; 2000WO-US06884.
PR   21-MAR-2000; 2000WO-US07532.
PR   30-MAR-2000; 2000WO-US08439.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Gurney AL,  Kuo SS,  Mark MR,  Marsters SA;
PI   Paoni NF,  Pitti RM,  Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2001-025251/03.
DR   N-PSDB; AAC90574.
XX
PT   Seventeen nucleic acids encoding PRO polypeptides which are useful in
PT   diagnosis and treatment of cardiovascular, endothelial or angiogenic
PT   disorders in a mammal -
XX
PS   Claim 71; Fig 24; 182pp; English.
XX
CC   The present sequence is one of seventeen novel PRO polypeptides. The PRO
CC   nucleic acids, polypeptides, agonists and antagonists are useful for
CC   treating cardiovascular, endothelial or angiogenic disorders in a mammal.
CC   Examples of these disorders include cardiac hypertrophy, trauma, cancer,
CC   age-related macular degeneration, atherosclerosis, hypertension, arterial
CC   restenosis, Reynaud's disease, rheumatoid arthritis,  angina, myocardial
CC   infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and
CC   antagonists are also used to prevent tumour angiogenesis and for treating
CC   periodontal diseases. They are also used to stimulate wound healing and
CC   tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO
CC   antibodies are useful for diagnosing a cardiovascular, endothelial or
CC   angiogenic disorder.
XX
SQ   Sequence   205 AA;

  Query Match             30.8%;  Score 335.5;  DB 22;  Length 205;
  Best Local Similarity   38.5%;  Pred. No. 2.5e-28;
  Matches   79;  Conservative   27;  Mismatches   72;  Indels   27;  Gaps    6;

Qy       11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
            |||  ||      :: || |:||||||:    |  : : ||||:||:|||||     :
Db        4 lwapllglccslaaadrhtvfwnssnpkfrnedytihvqlndyvdiicphyedhsvadaa 63

Qy       71 -ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLP 126
             | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||
Db       64 meqyilylveheeyqlcqpqs-kdqvrwqcnrpsakhgpeklsekfqrftpftlgkefke 122

Qy      127 GETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS---- 182
            | :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db      123 ghsyyyiskpihqhedrclrlkvtvsgkithspqah--dnpqekrla----addpevrvl 176

Qy      183 ------------PLCLLLLLLLLIL 195
                        ||   :||| |:|
Db      177 hsighsaaprlfplawtvlllplll 201


Search completed: September 28, 2002, 01:36:52
Job time: 10427 sec
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                        GenCore version 4.5
                Copyright (c) 1993 - 2000  Compugen Ltd.


OM protein - protein search, using sw model

Run on:         September 28, 2002, 01:37:42 ; Search time 29.18 Seconds
                                              (without alignments)
                                              168.250 Million cell updates/sec

Title:          US-09-904-954-4
Perfect score:  1091
Sequence:       1 MRLLPLLRTVLWAAFLGSPL..........SPLCLLLLLLLLILRLLRIL 201

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters:      231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

Database :       Issued_Patents_AA:*
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               4:  /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
               5:  /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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   Pred. No. is the number of results predicted by chance to have a
   score greater than or equal to the score of the result being printed,
   and is derived by analysis of the total score distribution.

                                 SUMMARIES
                    %
Result            Query
  No.    Score    Match Length DB ID                         Description
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    2     1091    100.0    201  1 US-08-453-943-4             Sequence 4, Appli
    3     1091    100.0    201  2 US-09-057-121-4             Sequence 4, Appli
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    6    380.5     34.9    228  1 US-08-440-815-4             Sequence 4, Appli
    7    380.5     34.9    228  3 US-08-379-802-2             Sequence 2, Appli
    8    380.5     34.9    228  3 US-09-048-129-2             Sequence 2, Appli
    9    380.5     34.9    228  4 US-09-048-079-2             Sequence 2, Appli
   10    380.5     34.9    228  4 US-08-486-449-4             Sequence 4, Appli
   11    380.5     34.9    228  5 PCT-US95-15781-5            Sequence 5, Appli
   12    368.5     33.8    234  1 US-08-299-567-5             Sequence 5, Appli
   13    364.5     33.4    238  1 US-08-240-124-2             Sequence 2, Appli
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   15    364.5     33.4    238  2 US-09-057-121-2             Sequence 2, Appli
   16    364.5     33.4    238  4 US-09-358-734-2             Sequence 2, Appli
   17      359     32.9    200  1 US-08-455-001-4             Sequence 4, Appli
   18      359     32.9    200  5 PCT-US95-11869-4            Sequence 4, Appli
   19    342.5     31.4    209  1 US-08-455-001-2             Sequence 2, Appli
   20    342.5     31.4    209  4 US-08-308-814-2             Sequence 2, Appli
   21    342.5     31.4    209  5 PCT-US95-11869-2            Sequence 2, Appli
   22    340.5     31.2    213  1 US-09-609-324A-10           Sequence 10, Appl
   23    340.5     31.2    213  2 US-08-920-440B-10           Sequence 10, Appl
   24    340.5     31.2    213  4 US-09-173-492-10            Sequence 10, Appl
   25    340.5     31.2    213  4 US-09-173-133-10            Sequence 10, Appl
   26    334.5     30.7    205  1 US-08-321-162-2             Sequence 2, Appli
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   32    334.5     30.7    205  2 US-08-445-065-12            Sequence 12, Appl
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   41    330.5     30.3    184  5 PCT-US95-15781-2            Sequence 2, Appli
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   44    261.5     24.0    104  1 US-09-609-324A-8            Sequence 8, Appli
   45    261.5     24.0    104  2 US-08-920-440B-8            Sequence 8, Appli


                                 ALIGNMENTS


RESULT   1
US-08-240-124-4
; Sequence 4, Application US/08240124
; Patent No. 5516658
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/240,124
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  201 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-240-124-4
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  Query Match             100.0%;  Score 1091;  DB 1;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-116;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60

Qy      61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120

Qy     121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180

Qy     181 PSPLCLLLLLLLLILRLLRIL 201
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Db     181 PSPLCLLLLLLLLILRLLRIL 201


RESULT   2
US-08-453-943-4
; Sequence 4, Application US/08453943
; Patent No. 5738844
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,943
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/240,124
;      FILING DATE:  09-MAY-1994
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  201 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;
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;    MOLECULE TYPE:  protein
US-08-453-943-4

  Query Match             100.0%;  Score 1091;  DB 1;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-116;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60

Qy      61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120

Qy     121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
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Db     121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180

Qy     181 PSPLCLLLLLLLLILRLLRIL 201
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RESULT   3
US-09-057-121-4
; Sequence 4, Application US/09057121
; Patent No. 5969110
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,121
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,124
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  201 amino acids
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;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-057-121-4

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Db        1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60

Qy       61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120

Qy      121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
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Db      121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180

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Db      181 PSPLCLLLLLLLLILRLLRIL 201


RESULT   4
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; Sequence 4, Application US/09358734
; Patent No. 6274117
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/358,734
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,124
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  201 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-358-734-4

  Query Match             100.0%;  Score 1091;  DB 4;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-116;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
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Db        1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60

Qy       61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120

Qy      121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
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Db      121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180

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Db      181 PSPLCLLLLLLLLILRLLRIL 201


RESULT   5
US-08-442-248-4
; Sequence 4, Application US/08442248
; Patent No. 5759863
;  GENERAL INFORMATION:
;    APPLICANT:  Caras, Ingrid W.
;    APPLICANT:  Winslow, John W.
;    TITLE OF INVENTION:  AL-1 Neurotrophic Factor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,248
;      FILING DATE:  15-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/330128
;      FILING DATE:  27-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  920C4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8674
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  228 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-442-248-4

  Query Match             34.9%;  Score 380.5;  DB 1;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 2.8e-35;
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Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
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Qy    117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK--------------- 154
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Db    123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy    155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
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Db    183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228


RESULT   6
US-08-440-815-4
; Sequence 4, Application US/08440815
; Patent No. 5798448
;  GENERAL INFORMATION:
;    APPLICANT:  Caras, Ingrid W.
;    APPLICANT:  Winslow, John W.
;    TITLE OF INVENTION:  AL-1 Neurotrophic Factor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/440,815
;      FILING DATE:  15-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/330128
;      FILING DATE:  27-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  920C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8674
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  228 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-440-815-4


  Query Match             34.9%;  Score 380.5;  DB 1;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 2.8e-35;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

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Db      4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
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Qy    117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK--------------- 154
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Db    123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy    155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
             |   :: |    |    : |     ||  |  || :|| |:  || :
Db    183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228


RESULT   7
US-08-379-802-2
; Sequence 2, Application US/08379802
; Patent No. 6057124
;  GENERAL INFORMATION:
;    APPLICANT:  Bartley, Timothy D.
;    APPLICANT:  Fox, Gary M.
;    TITLE OF INVENTION:  Ligands for EPH-Like Receptor
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/379,802
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-325
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  228 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-379-802-2


  Query Match             34.9%;  Score 380.5;  DB 3;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 2.8e-35;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy      1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
          : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db      4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
          |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db     64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy    117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK--------------- 154
          |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db    123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy    155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
             |   :: |    |    : |     ||  |  || :|| |:  || :
Db    183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228


RESULT   8
US-09-048-129-2
; Sequence 2, Application US/09048129
; Patent No. 6063903
```

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;  GENERAL INFORMATION:
;    APPLICANT:  Bartley, Timothy D.
;    APPLICANT:  Fox, Gary M.
;    TITLE OF INVENTION:  Ligands for EPH-Like Receptor
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/048,129
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/379,802
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-325
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  228 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-048-129-2

  Query Match             34.9%;  Score 380.5;  DB 3;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 2.8e-35;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy      1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
          : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db      4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
          |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db     64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy    117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
          |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db    123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy    155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
             |  ::  |    |    : |     ||  |  || :|| |:  || :
Db    183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228

RESULT   9
US-09-048-079-2
; Sequence 2, Application US/09048079
; Patent No. 6169167
;  GENERAL INFORMATION:
;    APPLICANT:  Bartley, Timothy D.
;    APPLICANT:  Fox, Gary M.
;    TITLE OF INVENTION:  Ligands for EPH-Like Receptor
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/048,079
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/379,802
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-325
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  228 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-048-079-2

  Query Match             34.9%;  Score 380.5;  DB 4;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 2.8e-35;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy      1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
          : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db      4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
          |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db     64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy    117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
          |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db    123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy    155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
             |  ::  |    |    : |     ||  |  || :|| |:  || :
Db    183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228

RESULT  10
US-08-486-449-4
; Sequence 4, Application US/08486449
; Patent No. 6280732
;  GENERAL INFORMATION:
;    APPLICANT:  Caras, Ingrid W.
;    APPLICANT:  Winslow, John W.
;    TITLE OF INVENTION:  AL-1 Neurotrophic Factor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 MB floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,449
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/330128
;      FILING DATE:  27-OCT-1994
```

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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  P0920P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8674
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  228 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-486-449-4


  Query Match             34.9%;  Score 380.5;  DB 4;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 2.8e-35;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy      1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
          : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db      4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
          |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db     64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy    117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
          |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db    123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy    155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
             |   :: |    |    : |     ||  |  || :|| |:  || :
Db    183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228


RESULT  11
PCT-US95-15781-5
; Sequence 5, Application PC/TUS9515781
;  GENERAL INFORMATION:
;    APPLICANT:  Cerretti, Douglas P.
;    TITLE OF INVENTION:  Cytokine Designated Lerk-7
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  System 7.1
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/15781
;      FILING DATE:  05-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/351,025
;      FILING DATE:  06-DEC-1994
;      CLASSIFICATION:
;      APPLICATION NUMBER:  US 08/396,946
;      FILING DATE:  01-MAR-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Anderson, Kathryn A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2829-WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
```

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;      TELEFAX:  (206) 233-0644
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  228 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-15781-5

  Query Match             34.9%;  Score 380.5;  DB 5;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 2.8e-35;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy      1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
          : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db      4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
          |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db     64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy    117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
          |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db    123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy    155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
             |   :: |    |    : |     ||  |  || :|| |:  || :
Db    183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228


RESULT  12
US-08-299-567-5
; Sequence 5, Application US/08299567
; Patent No. 5747033
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, et al.
;    TITLE OF INVENTION:  METHOD OF ENHANCING THE BIOLOGICAL
;    TITLE OF INVENTION:  ACTIVITY OF EPH FAMILY LIGANDS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Regeneron Pharmaceuticals, Inc.
;      STREET:  777 Old Saw Mill River Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10591-6707
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/299,567
;      FILING DATE:  01-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kempler, Gail M.
;      REGISTRATION NUMBER:  32,143
;      REFERENCE/DOCKET NUMBER:  REG 290
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  914-345-7400
;      TELEFAX:  914-345-7721
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  234 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-299-567-5
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  Query Match             33.8%;  Score 368.5;  DB 1;  Length 234;
  Best Local Similarity   45.6%;  Pred. No. 6.7e-34;
  Matches   77;  Conservative   17;  Mismatches   66;  Indels    9;  Gaps    3;

Qy       3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
           || ||  |     |     |    || |||||||  | |    |:: :|||||| ||||
Db       8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67

Qy      63 ----GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRF 115
               ||||  | | : ||||   || :| |   : :||| |:    |   ::|||| ||:
Db      68 SSGAGPGPGGGAEQYVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEKFQRY 125

Qy     116 TPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
           : ||||:||  | :||||| ||     :|||::| |||         ||
Db     126 SAFSLGYEFHAGHSYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 174


RESULT  13
US-08-240-124-2
; Sequence 2, Application US/08240124
; Patent No. 5516658
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/240,124
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  238 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-240-124-2

  Query Match             33.4%;  Score 364.5;  DB 1;  Length 238;
  Best Local Similarity   44.5%;  Pred. No. 1.9e-33;
  Matches   77;  Conservative   16;  Mismatches   67;  Indels   13;  Gaps    3;

Qy       3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
           || ||  |     |     |    || |||||||  | |    |:: :|||||| ||||
Db       8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67

Qy      63 --------GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEK 111
                   ||||  | | : ||||   || :| |   : :||| |:    |   ::||||
Db      68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEK 125

Qy     112 IQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
            ||:: ||||:||  |  ||||| ||     :|||::| |||         ||
Db     126 FQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 178


RESULT  14
US-08-453-943-2
; Sequence 2, Application US/08453943
; Patent No. 5738844
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,943
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/240,124
;      FILING DATE:  09-MAY-1994
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  238 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-453-943-2


  Query Match             33.4%;  Score 364.5;  DB 1;  Length 238;
  Best Local Similarity   44.5%;  Pred. No. 1.9e-33;
  Matches   77;  Conservative   16;  Mismatches   67;  Indels   13;  Gaps    3;

Qy       3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
           || ||  |     |     |    || |||||||  | |    |:: :|||||| ||||
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Db      8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67

Qy     63 --------GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEK 111
                  ||||  | | : ||||   || :| |   : :||| |:    |   ::||||
Db     68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEK 125

Qy    112 IQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
           ||:: ||||:||  |  ||||| ||     :|||::| |||         ||
Db    126 FQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 178


RESULT  15
US-09-057-121-2
; Sequence 2, Application US/09057121
; Patent No. 5969110
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,121
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/240,124
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  238 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-057-121-2

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  Matches   77;  Conservative   16;  Mismatches   67;  Indels   13;  Gaps    3;

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Search completed: September 28, 2002, 01:37:42
Job time: 10062 sec
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                     GenCore version 4.5
           Copyright (c) 1993 - 2000  Compugen Ltd.

OM protein - protein search, using sw model

Run on:          September 28, 2002, 01:43:26 ; Search time 251.33 Seconds
                                              (without alignments)
                                              281.495 Million cell updates/sec

Title:           US-09-904-954-4
Perfect score:   1091
Sequence:        1 MRLLPLLRTVLWAAFLGSPL..........SPLCLLLLLLLLILRLLRIL 201

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters:      3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_AA_Main:*
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                22:  /cgn2_6/ptodata/2/paa/US098_COMB.pep:*
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                26:  /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                               SUMMARIES
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  No.    Score   Match Length DB  ID                               Description
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    2     1091   100.0    201  5  US-08-161-132-4                 Sequence 4, Appli
    3     1091   100.0    201 23  US-09-904-954-4                  Sequence 4, Appli
    4     1073    98.4    201 16  US-09-214-631-8                  Sequence 8, Appli
    5   1067.5    97.8    200 11  US-08-730-700A-17                Sequence 17, Appl
    6   1067.5    97.8    200 20  US-09-621-595-17                 Sequence 17, Appl
    7      850    77.9    228 21  US-09-760-443-1064               Sequence 1064, Ap
    8    675.5    61.9    964 26  US-60-230-435-1232               Sequence 1232, Ap
    9      665    61.0    120 26  US-60-185-360-275                Sequence 275, App
   10      600    55.0    776 26  US-60-212-656-335                Sequence 335, App
   11      542    49.7     96 26  US-60-163-062-1186               Sequence 1186, Ap
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   20    380.5    34.9    228 19  US-09-570-327-2                  Sequence 2, Appli
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   35      351    32.2    233 11  US-08-730-700A-15                Sequence 15, Appl
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   39      349    32.0    237 11  US-08-730-700A-16                Sequence 16, Appl
   40      349    32.0    237 20  US-09-621-595-16                 Sequence 16, Appl
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   42      343    31.4    204 24  US-10-001-054-48                 Sequence 48, Appl
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   44    342.5    31.4    209  7  US-08-393-462-2                 Sequence 2, Appli
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                                ALIGNMENTS

RESULT   1
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; Sequence 4, Application PC/TUS9409282
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/09282
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,132
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
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;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  201 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US94-09282-4

  Query Match             100.0%;  Score 1091;  DB 1;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-101;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy       61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
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Qy      121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
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US-08-161-132-4
; Sequence 4, Application US/08161132
;  GENERAL INFORMATION:
;    APPLICANT:  BECKMANN, M. P.
;    APPLICANT:  CERRETTI, DOUGLAS P.
;    TITLE OF INVENTION:  CYTOKINE THAT BINDS THE CELL SURFACE
;    TITLE OF INVENTION:  RECEPTOR HEK
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMUNEX CORPORATION
;      STREET:  51 UNIVERSITY STREET
;      CITY:  SEATTLE
;      STATE:  WASHINGTON
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/161,132
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/114,426
;      FILING DATE:  30-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/109,745
;      FILING DATE:  20-AUG-1993
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SEESE, KATHRYN A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2814-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  201 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-161-132-4

  Query Match             100.0%;  Score 1091;  DB 5;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-101;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy       61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
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Qy      121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
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Db      121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180

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RESULT   3
US-09-904-954-4
; Sequence 4, Application US/09904954
;  GENERAL INFORMATION:
;       APPLICANT: BECKMANN, M. P.
;                  CERRETTI, DOUGLAS P.
;       TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
;                           RECEPTOR HEK
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: IMMUNEX CORPORATION
;            STREET: 51 UNIVERSITY STREET
;            CITY: SEATTLE
;            STATE: WASHINGTON
;            COUNTRY: USA
;            ZIP: 98101
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: Apple Macintosh
;            OPERATING SYSTEM: Apple System 7.1
;            SOFTWARE: Microsoft Word for Apple, Version 5.1a
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/904,954
;            FILING DATE: 12-Jul-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/240,124
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: US 08/114,426
;            FILING DATE: 30-AUG-1993
;            APPLICATION NUMBER: US 08/109,745
;            FILING DATE: 20-AUG-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SEESE, KATHRYN A.
;            REGISTRATION NUMBER: 32,172
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;            REFERENCE/DOCKET NUMBER: 2814-C
;        TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 587-0430
;            TELEFAX: (206) 233-0644
;            TELEX: 756822
;    INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 201 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-904-954-4

  Query Match            100.0%;  Score 1091;  DB 23;  Length 201;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-101;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
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Qy    121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
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Db    121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180

Qy    181 PSPLCLLLLLLLLILRLLRIL 201
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Db    181 PSPLCLLLLLLLLILRLLRIL 201


RESULT   4
US-09-214-631-8
; Sequence 8, Application US/09214631
; GENERAL INFORMATION:
;  APPLICANT: Holland, Sacha
;  APPLICANT: Mbamalu, Geraldine
;  APPLICANT: Pawson, Tony
;  TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
;  TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
;  TITLE OF INVENTION: TYROSINE KINASES
;  FILE REFERENCE: 11757.23USWO
;  CURRENT APPLICATION NUMBER: US/09/214,631
;  CURRENT FILING DATE: 1999-03-12
;  EARLIER APPLICATION NUMBER: PCT/CA97/00473
;  EARLIER FILING DATE: 1997-07-04
;  EARLIER APPLICATION NUMBER: 60/021,272
;  EARLIER FILING DATE: 1996-07-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 201
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-631-8

  Query Match            98.4%;  Score 1073;  DB 16;  Length 201;
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Qy      1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
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Db      1 MRLLPLLITVLWAAFLGSPLRGGSSLRHVVYWNSSNPRSLRGDAVVELGLNDYLDIVCPH 60

Qy     61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
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Qy    121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
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Qy    181 PSPLCLLLLLLLLILRLLRIL 201
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RESULT   5
US-08-730-700A-17
; Sequence 17, Application US/08730700A
;  GENERAL INFORMATION:
;    APPLICANT:  Pawson, Anthony
;    APPLICANT:  Henkemeyer, Mark
;    TITLE OF INVENTION:  Method of Activating a Novel Ligand
;    TITLE OF INVENTION:  Regulatory Pathway
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Room 970
;      STREET:  600 University Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1X5
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/730,700A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/005,518
;      FILING DATE:  13-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kurdydyk, Linda M.
;      REGISTRATION NUMBER:  34,971
;      REFERENCE/DOCKET NUMBER:  3153-196
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  416-586-3235
;      TELEFAX:  416-586-3110
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  200 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-730-700A-17

  Query Match            97.8%;  Score 1067.5;  DB 11;  Length 200;
  Best Local Similarity  99.0%;  Pred. No. 2.6e-99;
  Matches  199;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy      1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60

Qy     61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
          | |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db     61 YFGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKI-RFTPFSL 119

Qy    121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 179

Qy    181 PSPLCLLLLLLLLILRLLRIL 201
          |||||||||||||||||||||
```

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Db    180 PSPLCLLLLLLLLILRLLRIL 200


RESULT   6
US-09-621-595-17
; Sequence 17, Application US/09621595
;   GENERAL INFORMATION:
;        APPLICANT: Pawson, Anthony
;                   Henkemeyer, Mark
;        TITLE OF INVENTION: Method of Activating a Novel Ligand
;                            Regulatory Pathway
;        NUMBER OF SEQUENCES: 21
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Room 970
;             STREET: 600 University Avenue
;             CITY: Toronto
;             STATE: Ontario
;             COUNTRY: Canada
;             ZIP: M5G 1X5
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/621,595
;             FILING DATE: 21-Jul-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/730,700
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kurdydyk, Linda M.
;             REGISTRATION NUMBER: 34,971
;             REFERENCE/DOCKET NUMBER: 3153-196
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 416-586-3235
;             TELEFAX: 416-586-3110
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 200 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-621-595-17

  Query Match             97.8%;  Score 1067.5;  DB 20;  Length 200;
  Best Local Similarity   99.0%;  Pred. No. 2.6e-99;
  Matches  199;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy      1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60

Qy     61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
          | |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db     61 YFGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKI-RFTPFSL 119

Qy    121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 179

Qy    181 PSPLCLLLLLLLLILRLLRIL 201
          |||||||||||||||||||||
Db    180 PSPLCLLLLLLLLILRLLRIL 200


RESULT   7
US-09-760-443-1064
; Sequence 1064, Application US/09760443
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```
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PJZ12
;  CURRENT APPLICATION NUMBER: US/09/760,443
;  CURRENT FILING DATE:  2001-01-16
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 2164
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1064
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (101)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (152)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (159)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-443-1064

  Query Match             77.9%;  Score 850;  DB 21;  Length 228;
  Best Local Similarity   85.8%;  Pred. No. 3.2e-77;
  Matches  157;  Conservative    3;  Mismatches   23;  Indels    0;  Gaps    0;

Qy      1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     37 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 96

Qy     61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     97 YEGPXPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFXPFSL 156

Qy    121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
          || |||||||||||||||||||||||||||||||         :|:       |  ||
Db    157 GFXFLPGETYYYISVPTPESSGQCLRLQVSVCCKRGSLSQPILLGALERVAHQGGEGGTL 216

Qy    181 PSP 183
          |:|
Db    217 PAP 219


RESULT   8
US-60-230-435-1232
; Sequence 1232, Application US/60230435
; GENERAL INFORMATION:
;  APPLICANT:  Beasley, Ellen
;  TITLE OF INVENTION:  ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE:  CL000768
;  CURRENT APPLICATION NUMBER: US/60/230,435
;  CURRENT FILING DATE:  2000-09-06
;  NUMBER OF SEQ ID NOS:  2991
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1232
;   LENGTH: 964
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-230-435-1232


  Query Match             61.9%;  Score 675.5;  DB 26;  Length 964;
  Best Local Similarity   77.2%;  Pred. No. 8.6e-59;
  Matches  132;  Conservative    3;  Mismatches   21;  Indels   15;  Gaps    4;

Qy     16 LGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFAL 75
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      712 LGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFAL 771

Qy       76 YMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISV 135
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| :
Db      772 YMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYILL 831

Qy      136 PTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSG---WRGGDTPSP 183
                    |:| :  | | |   |   |  |  |   |    |     |||
Db      832 ------HGCVRERGLVACDE--CEDRLPGASQREGDQSSQCHWH----PSP 870

RESULT   9
US-60-185-360-275
; Sequence 275, Application US/60185360
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
;  TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
;  TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL000287
;  CURRENT APPLICATION NUMBER: US/60/185,360
;  CURRENT FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 342
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 275
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-185-360-275


  Query Match             61.0%;  Score 665;  DB 26;  Length 120;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-59;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       38 RLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRW 97
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 RLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRW 60

Qy       98 VCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKER 156
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 VCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKER 119

RESULT  10
US-60-212-656-335
; Sequence 335, Application US/60212656
; GENERAL INFORMATION:
;  APPLICANT:  Beasley, Ellen
;  TITLE OF INVENTION:  ISOLATED HUMAN PROTEASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE:  CL000673
;  CURRENT APPLICATION NUMBER: US/60/212,656
;  CURRENT FILING DATE:  2000-06-19
;  NUMBER OF SEQ ID NOS:  795
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 335
;   LENGTH: 776
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-212-656-335


  Query Match             55.0%;  Score 600;  DB 26;  Length 776;
  Best Local Similarity   84.3%;  Pred. No. 2.9e-51;
  Matches  107;  Conservative    4;  Mismatches   16;  Indels    0;  Gaps    0;

Qy       38 RLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRW 97
            :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      590 KLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRW 649

Qy       98 VCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERK 157
            ||||||||||||||||||||||||||||||||||||| ||     :|||::| |||
Db      650 VCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISTPTHNLHWKCLRMKVFVCCASTS 709

Qy      158 SESAHPV 164
                 ||
Db      710 HSGEKPV 716

RESULT  11
US-60-163-062-1186
; Sequence 1186, Application US/60163062
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTIENS AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL000134
;  CURRENT APPLICATION NUMBER: US/60/163,062
;  CURRENT FILING DATE: 1999-11-02
;  NUMBER OF SEQ ID NOS: 1302
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1186
;   LENGTH: 96
;   TYPE: PRT
;   ORGANISM: Human
US-60-163-062-1186


  Query Match             49.7%;  Score 542;  DB 26;  Length 96;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-46;
  Matches   96;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       38 RLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRW 97
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 RLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRW 60

Qy       98 VCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYI 133
            ||||||||||||||||||||||||||||||||||||
Db       61 VCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYI 96

RESULT  12
US-08-330-128-4
; Sequence 4, Application US/08330128
;  GENERAL INFORMATION:
;    APPLICANT:  Caras, Ingrid W.
;    APPLICANT:  Winslow, John W.
;    TITLE OF INVENTION:  AL-1 Neurotrophic Factor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/330,128
;      FILING DATE:  27-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Johnston, Sean A.
;      REGISTRATION NUMBER:  35,910
;      REFERENCE/DOCKET NUMBER:  920
;    TELECOMMUNICATION INFORMATION:
```

```
;       TELEPHONE:  415/225-3562
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  228 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-330-128-4

  Query Match             34.9%;  Score 380.5;  DB 7;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 1.1e-29;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy        1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
            : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db        4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

Qy       60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
            |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db       64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy      117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
            |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db      123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy      155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
               |   :: |    |    : |     ||  |  || :|| |:  || :
Db      183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228


RESULT  13
US-08-396-946-5
; Sequence 5, Application US/08396946
;   GENERAL INFORMATION:
;     APPLICANT:  Cerretti, Douglas P.
;     TITLE OF INVENTION:  Cytokine Designated Lerk-7
;     NUMBER OF SEQUENCES:  8
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Immunex Corporation
;       STREET:  51 University Street
;       CITY:  Seattle
;       STATE:  WA
;       COUNTRY:  USA
;       ZIP:  98101
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  Apple Macintosh
;       OPERATING SYSTEM:  System 7.1
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/396,946
;       FILING DATE:  01-MAR-1995
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/351,025
;       FILING DATE:  06-DEC-1994
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Anderson, Kathryn A.
;       REGISTRATION NUMBER:  32,172
;       REFERENCE/DOCKET NUMBER:  2829-A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 587-0430
;       TELEFAX:  (206) 233-0644
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  228 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-396-946-5
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  Query Match             34.9%;  Score 380.5;  DB 7;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 1.1e-29;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy        1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
            : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db        4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

Qy       60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
            |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db       64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy      117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
            |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db      123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy      155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
               |   :: |    |    : |     ||  |  || :|| |:  || :
Db      183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228


RESULT  14
US-08-440-567-4
; Sequence 4, Application US/08440567
;   GENERAL INFORMATION:
;     APPLICANT:  Caras, Ingrid W.
;     APPLICANT:  Winslow, John W.
;     TITLE OF INVENTION:  AL-1 Neurotrophic Factor
;     NUMBER OF SEQUENCES:  18
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Genentech, Inc.
;       STREET:  460 Point San Bruno Blvd
;       CITY:  South San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94080
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  patin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/440,567
;       FILING DATE:  15-MAY-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/330128
;       FILING DATE:  27-OCT-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Torchia, Timothy E.
;       REGISTRATION NUMBER:  36,700
;       REFERENCE/DOCKET NUMBER:  920C2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-8674
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  228 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-440-567-4


  Query Match             34.9%;  Score 380.5;  DB 8;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 1.1e-29;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy        1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
            : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db        4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63
```

```
Qy      60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
           |||   | :  | : ||||:: || :|     : :||| |: |     | ::|||| |.||
Db      64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy     117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
           |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db     123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy     155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
              |   :: |    |    : |     ||  |  || :|| |:  || :
Db     183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228


RESULT  15
US-08-442-245A-4
; Sequence 4, Application US/08442245A
;  GENERAL INFORMATION:
;    APPLICANT:  Caras, Ingrid W.
;    APPLICANT:  Winslow, John W.
;    TITLE OF INVENTION:  AL-1 Neurotrophic Factor
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,245A
;      FILING DATE:  15-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/330128
;      FILING DATE:  27-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  920C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8674
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  228 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-442-245A-4

  Query Match             34.9%;  Score 380.5;  DB 8;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 1.1e-29;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy       1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
           : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db       4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

Qy      60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
           |||   | :  | : ||||:: || :|     : :||| |: |     | ::|||| |.||
Db      64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy     117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
           |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db     123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy     155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
              |   :: |    |    : |     ||  |  || :|| |:  || :
Db     183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228


Search completed: September 28, 2002, 01:43:27
Job time: 892 sec
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                    GenCore version 4.5
         Copyright (c) 1993 - 2000  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         September 28, 2002, 01:45:54 ; Search time 125.93 Seconds
                                              (without alignments)
                                              431.292 Million cell updates/sec

Title:          US-09-904-954-4
Perfect score:  1091
Sequence:       1 MRLLPLLRTVLWAAFLGSPL..........SPLCLLLLLLLLILRLLRIL 201

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       962758 seqs, 270212090 residues

Total number of hits satisfying chosen parameters:      962758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_AA_New:*
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               2:  /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
               3:  /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
               4:  /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
               5:  /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
               6:  /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
               7:  /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result          Query
  No.   Score   Match Length DB  ID                        Description
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    1    1073    98.4    201  6  US-10-138-787-8            Sequence 8, Appli
    2     850    77.9    228  6  US-10-206-021-615          Sequence 615, App
    3     850    77.9    228  6  US-10-212-054-1064         Sequence 1064, Ap
    4   379.5    34.8    228  6  US-10-138-787-9            Sequence 9, Appli
    5   363.5    33.3    233  6  US-10-138-787-7            Sequence 7, Appli
    6     343    31.4    204  1  PCT-US02-24563-288         Sequence 288, App
    7     343    31.4    204  6  US-10-121-049-288          Sequence 288, App
    8     343    31.4    204  6  US-10-121-050-288          Sequence 288, App
    9     343    31.4    204  6  US-10-121-053-288          Sequence 288, App
   10     343    31.4    204  6  US-10-121-043-288          Sequence 288, App
   11     343    31.4    204  6  US-10-121-044-288          Sequence 288, App
   12     343    31.4    204  6  US-10-121-047-288          Sequence 288, App
   13     343    31.4    204  6  US-10-121-054-288          Sequence 288, App
   14     343    31.4    204  6  US-10-121-056-288          Sequence 288, App
   15     343    31.4    204  6  US-10-121-057-288          Sequence 288, App
   16     343    31.4    204  6  US-10-121-058-288          Sequence 288, App
   17     343    31.4    204  6  US-10-121-060-288          Sequence 288, App
   18     343    31.4    204  6  US-10-121-063-288          Sequence 288, App
   19     343    31.4    204  6  US-10-123-108-288          Sequence 288, App
   20     343    31.4    204  6  US-10-123-154-288          Sequence 288, App
   21     343    31.4    204  6  US-10-123-156-288          Sequence 288, App
   22     343    31.4    204  6  US-10-123-157-288          Sequence 288, App
   23     343    31.4    204  6  US-10-123-212-288          Sequence 288, App
   24     343    31.4    204  6  US-10-123-213-288          Sequence 288, App
   25     343    31.4    204  6  US-10-123-109-288          Sequence 288, App
   26     343    31.4    204  6  US-10-121-041-288          Sequence 288, App
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   27     343    31.4    204  6  US-10-121-045-288          Sequence 288, App
   28     343    31.4    204  6  US-10-121-046-288          Sequence 288, App
   29     343    31.4    204  6  US-10-121-051-288          Sequence 288, App
   30     343    31.4    204  6  US-10-121-040-288          Sequence 288, App
   31     343    31.4    204  6  US-10-121-048-288          Sequence 288, App
   32     343    31.4    204  6  US-10-121-052-288          Sequence 288, App
   33     343    31.4    204  6  US-10-121-061-288          Sequence 288, App
   34     343    31.4    204  6  US-10-121-042-288          Sequence 288, App
   35     343    31.4    204  6  US-10-121-055-288          Sequence 288, App
   36     343    31.4    204  6  US-10-121-059-288          Sequence 288, App
   37     343    31.4    204  6  US-10-124-822-288          Sequence 288, App
   38     343    31.4    204  6  US-10-123-903-288          Sequence 288, App
   39     343    31.4    204  6  US-10-124-817-288          Sequence 288, App
   40     343    31.4    204  6  US-10-124-819-288          Sequence 288, App
   41     343    31.4    204  6  US-10-124-823-288          Sequence 288, App
   42     343    31.4    204  6  US-10-125-704-288          Sequence 288, App
   43     343    31.4    204  6  US-10-123-215-288          Sequence 288, App
   44     343    31.4    204  6  US-10-123-235-288          Sequence 288, App
   45     343    31.4    204  6  US-10-123-236-288          Sequence 288, App

                              ALIGNMENTS

RESULT   1
US-10-138-787-8
; Sequence 8, Application US/10138787
; GENERAL INFORMATION:
;  APPLICANT: Holland, Sacha
;  APPLICANT:  Mbamalu, Geraldine
;  APPLICANT:  Pawson, Tony
;  TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
;  TITLE OF INVENTION:  BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
;  TITLE OF INVENTION:  TYROSINE KINASES
;  FILE REFERENCE: 11757.23USWO
;  CURRENT APPLICATION NUMBER: US/10/138,787
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: US/09/214,631
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: PCT/CA97/00473
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: 60/021,272
;  PRIOR FILING DATE: 1996-07-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 201
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-138-787-8


  Query Match             98.4%;  Score 1073;  DB 6;  Length 201;
  Best Local Similarity   98.5%;  Pred. No. 2.4e-97;
  Matches  198;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
                ||||||| |||||||||||||||||||||||||||||| |||||||||||||||||||||
Db          1 MRLLPLLITVLWAAFLGSPLRGGSSLRHVVYWNSSNPRSLRGDAVVELGLNDYLDIVCPH 60

Qy         61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
                |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db         61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRGYKRWVCSLPFGHVQFSEKIQRFTPFSL 120

Qy        121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180

Qy        181 PSPLCLLLLLLLLILRLLRIL 201
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Db        181 PSPLCLLLLLLLLILRLLRIL 201
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RESULT   2
US-10-206-021-615
; Sequence 615, Application US/10206021
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ51C1N
;  CURRENT APPLICATION NUMBER: US/10/206,021
;  CURRENT FILING DATE:  2002-07-29
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 937
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 615
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (101)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (152)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (159)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-206-021-615


  Query Match             77.9%;  Score 850;  DB 6;  Length 228;
  Best Local Similarity   85.8%;  Pred. No. 2.3e-75;
  Matches  157;  Conservative    3;  Mismatches   23;  Indels    0;  Gaps    0;

Qy      1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     37 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 96

Qy     61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     97 YEGPXPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFXPFSL 156

Qy    121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
          || |||||||||||||||||||||||||||||||         :|:       |  ||
Db    157 GFXFLPGETYYYISVPTPESSGQCLRLQVSVCCKRGSLSQPILLGALERVAHQGGEGGTL 216

Qy    181 PSP 183
          |:|
Db    217 PAP 219


RESULT   3
US-10-212-054-1064
; Sequence 1064, Application US/10212054
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PJZ12C1N
;  CURRENT APPLICATION NUMBER: US/10/212,054
;  CURRENT FILING DATE:  2002-08-06
;  NUMBER OF SEQ ID NOS: 2164
;  Prior application removed - See File Wrapper or Palm
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1064
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (101)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
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;   NAME/KEY: misc_feature
;   LOCATION: (152)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (159)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-212-054-1064


  Query Match             77.9%;  Score 850;  DB 6;  Length 228;
  Best Local Similarity   85.8%;  Pred. No. 2.3e-75;
  Matches  157;  Conservative    3;  Mismatches   23;  Indels    0;  Gaps    0;

Qy      1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     37 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 96

Qy     61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db     97 YEGPXPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFXPFSL 156

Qy    121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
          || |||||||||||||||||||||||||||||||         :|:       |  ||
Db    157 GFXFLPGETYYYISVPTPESSGQCLRLQVSVCCKRGSLSQPILLGALERVAHQGGEGGTL 216

Qy    181 PSP 183
          |:|
Db    217 PAP 219


RESULT   4
US-10-138-787-9
; Sequence 9, Application US/10138787
; GENERAL INFORMATION:
;  APPLICANT: Holland, Sacha
;  APPLICANT:  Mbamalu, Geraldine
;  APPLICANT:  Pawson, Tony
;  TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
;  TITLE OF INVENTION:  BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
;  TITLE OF INVENTION:  TYROSINE KINASES
;  FILE REFERENCE: 11757.23USWO
;  CURRENT APPLICATION NUMBER: US/10/138,787
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: US/09/214,631
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: PCT/CA97/00473
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: 60/021,272
;  PRIOR FILING DATE: 1996-07-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-138-787-9


  Query Match             34.8%;  Score 379.5;  DB 6;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 4.1e-29;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy      1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
          : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db      4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
          |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db     64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy    117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
          |||||||| ||  |:|||   |::  : ||:|:| |     | |
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Db    123 PFSLGFEFPPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy    155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
             |   :: |    |    : |     ||  |  || :|| |:  || :
Db    183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228

RESULT   5
US-10-138-787-7
; Sequence 7, Application US/10138787
; GENERAL INFORMATION:
;  APPLICANT: Holland, Sacha
;  APPLICANT:  Mbamalu, Geraldine
;  APPLICANT:  Pawson, Tony
;  TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
;  TITLE OF INVENTION:  BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
;  TITLE OF INVENTION:  TYROSINE KINASES
;  FILE REFERENCE: 11757.23USWO
;  CURRENT APPLICATION NUMBER: US/10/138,787
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: US/09/214,631
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: PCT/CA97/00473
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: 60/021,272
;  PRIOR FILING DATE: 1996-07-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-138-787-7

  Query Match             33.3%;  Score 363.5;  DB 6;  Length 233;
  Best Local Similarity   46.2%;  Pred. No. 1.6e-27;
  Matches   78;  Conservative   16;  Mismatches   56;  Indels   19;  Gaps    6;

Qy      3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
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Db     17 LLPLL--------AGGP-AGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67

Qy     63 ----GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRF 115
              ||||  | | : ||||   || :| |   : :||| |:    |   ::|||| ||:
Db     68 SSGAGPGPGGGAE-YVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEKFQRY 124

Qy    116 TPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
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Db    125 SAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 173

RESULT   6
PCT-US02-24563-288
; Sequence 288, Application PC/TUS0224563
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C331
;  CURRENT APPLICATION NUMBER: PCT/US02/24563
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
PCT-US02-24563-288

  Query Match             31.4%;  Score 343;  DB 1;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 1.4e-25;
  Matches   79;  Conservative   26;  Mismatches   73;  Indels   26;  Gaps    5;

Qy     11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
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Db      4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM 63

Qy     71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
          | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||  |
Db     64 EQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 122

Qy    128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----- 182
           :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db    123 HSYYYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPEVRVLH 176

Qy    183 -----------PLCLLLLLLLLIL 195
                     ||   :||| |:|
Db    177 SIGHSAAPRLFPLAWTVLLLPLLL 200

RESULT   7
US-10-121-049-288
; Sequence 288, Application US/10121049
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
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;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C17
;  CURRENT APPLICATION NUMBER: US/10/121,049
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-049-288

  Query Match            31.4%;  Score 343;  DB 6;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 1.4e-25;
  Matches   79;  Conservative   26;  Mismatches   73;  Indels   26;  Gaps    5;

Qy     11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
          |||  ||      :: || |:||||||:    |  : : ||||:||:|||||
Db      4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM 63

Qy     71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
          | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||  |
Db     64 EQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 122

Qy    128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----- 182
           :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db    123 HSYYYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPEVRVLH 176

Qy    183 -----------PLCLLLLLLLLIL 195
                     ||   :||| |:|
Db    177 SIGHSAAPRLFPLAWTVLLLPLLL 200

RESULT   8
US-10-121-050-288
; Sequence 288, Application US/10121050
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C20
;  CURRENT APPLICATION NUMBER: US/10/121,050
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-050-288
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  Query Match            31.4%;  Score 343;  DB 6;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 1.4e-25;
  Matches   79;  Conservative   26;  Mismatches   73;  Indels   26;  Gaps    5;

Qy     11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
          |||  ||      :: || |:||||||:    |  : : ||||:||:|||||
Db      4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM 63

Qy     71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
          | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||  |
Db     64 EQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 122

Qy    128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----- 182
           :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db    123 HSYYYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPEVRVLH 176

Qy    183 -----------PLCLLLLLLLLIL 195
                     ||   :||| |:|
Db    177 SIGHSAAPRLFPLAWTVLLLPLLL 200

RESULT   9
US-10-121-053-288
; Sequence 288, Application US/10121053
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C23
;  CURRENT APPLICATION NUMBER: US/10/121,053
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-053-288

  Query Match            31.4%;  Score 343;  DB 6;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 1.4e-25;
  Matches   79;  Conservative   26;  Mismatches   73;  Indels   26;  Gaps    5;

Qy     11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
          |||  ||      :: || |:||||||:    |  : : ||||:||:|||||
Db      4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM 63

Qy     71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
          | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||  |
Db     64 EQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 122

Qy    128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----- 182
           :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db    123 HSYYYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPEVRVLH 176

Qy    183 -----------PLCLLLLLLLLIL 195
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                      ||   :||| |:|
Db     177 SIGHSAAPRLFPLAWTVLLLPLLL 200


RESULT 10
US-10-121-043-288
; Sequence 288, Application US/10121043
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C15
;  CURRENT APPLICATION NUMBER: US/10/121,043
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-043-288


  Query Match             31.4%;  Score 343;  DB 6;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 1.4e-25;
  Matches   79;  Conservative   26;  Mismatches   73;  Indels   26;  Gaps    5;

Qy      11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
           |||  ||      :: || |:||||||:    |  : : ||||:||:|||||
Db       4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM 63

Qy      71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
           | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||  |
Db      64 EQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 122

Qy     128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----- 182
            :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db     123 HSYYYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPEVRVLH 176

Qy     183 -----------PLCLLLLLLLLIL 195
                      ||   :||| |:|
Db     177 SIGHSAAPRLFPLAWTVLLLPLLL 200


RESULT 11
US-10-121-044-288
; Sequence 288, Application US/10121044
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C5
;  CURRENT APPLICATION NUMBER: US/10/121,044
;  CURRENT FILING DATE:  2002-04-11
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-044-288


  Query Match             31.4%;  Score 343;  DB 6;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 1.4e-25;
  Matches   79;  Conservative   26;  Mismatches   73;  Indels   26;  Gaps    5;

Qy      11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
           |||  ||      :: || |:||||||:    |  : : ||||:||:|||||
Db       4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM 63

Qy      71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
           | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||  |
Db      64 EQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 122

Qy     128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----- 182
            :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db     123 HSYYYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPEVRVLH 176

Qy     183 -----------PLCLLLLLLLLIL 195
                      ||   :||| |:|
Db     177 SIGHSAAPRLFPLAWTVLLLPLLL 200


RESULT 12
US-10-121-047-288
; Sequence 288, Application US/10121047
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C4
;  CURRENT APPLICATION NUMBER: US/10/121,047
;  CURRENT FILING DATE:  2002-04-11
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
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;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-047-288


  Query Match             31.4%;  Score 343;  DB 6;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 1.4e-25;
  Matches   79;  Conservative   26;  Mismatches   73;  Indels   26;  Gaps    5;

Qy     11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
          |||  ||      :: || |:||||||:    |  : : ||||:||:|||||
Db      4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM 63

Qy     71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
          | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||  |
Db     64 EQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 122

Qy    128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----- 182
           :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db    123 HSYYYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPEVRVLH 176

Qy    183 -----------PLCLLLLLLLLIL 195
                     ||   :||| |:|
Db    177 SIGHSAAPRLFPLAWTVLLLPLLL 200


RESULT 13
US-10-121-054-288
; Sequence 288, Application US/10121054
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C14
;  CURRENT APPLICATION NUMBER: US/10/121,054
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-054-288


  Query Match             31.4%;  Score 343;  DB 6;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 1.4e-25;
  Matches   79;  Conservative   26;  Mismatches   73;  Indels   26;  Gaps    5;

Qy     11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
          |||  ||      :: || |:||||||:    |  : : ||||:||:|||||
Db      4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM 63

Qy     71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
          | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||  |
Db     64 EQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 122
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```
Qy    128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----- 182
           :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db    123 HSYYYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPEVRVLH 176

Qy    183 -----------PLCLLLLLLLLIL 195
                     ||   :||| |:|
Db    177 SIGHSAAPRLFPLAWTVLLLPLLL 200


RESULT 14
US-10-121-056-288
; Sequence 288, Application US/10121056
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C25
;  CURRENT APPLICATION NUMBER: US/10/121,056
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-056-288


  Query Match             31.4%;  Score 343;  DB 6;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 1.4e-25;
  Matches   79;  Conservative   26;  Mismatches   73;  Indels   26;  Gaps    5;

Qy     11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
          |||  ||      :: || |:||||||:    |  : : ||||:||:|||||
Db      4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM 63

Qy     71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
          | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||  |
Db     64 EQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 122

Qy    128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----- 182
           :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db    123 HSYYYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPEVRVLH 176

Qy    183 -----------PLCLLLLLLLLIL 195
                     ||   :||| |:|
Db    177 SIGHSAAPRLFPLAWTVLLLPLLL 200


RESULT 15
US-10-121-057-288
; Sequence 288, Application US/10121057
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
```

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;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C13
;  CURRENT APPLICATION NUMBER: US/10/121,057
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-121-057-288


  Query Match             31.4%;  Score 343;  DB 6;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 1.4e-25;
  Matches   79;  Conservative   26;  Mismatches   73;  Indels   26;  Gaps    5;

Qy         11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
              |||  ||      :: || |:||||||:    |  : : ||||:||:|||||
Db          4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM 63

Qy         71 ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLPG 127
              | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||  |
Db         64 EQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 122

Qy        128 ETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS----- 182
               :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db        123 HSYYYISKPIHQHEDRCLRLKVTVSGKITHSPQAH--DNPQEKRLA----ADDPEVRVLH 176

Qy        183 -----------PLCLLLLLLLLIL 195
                         ||   :||| |:|
Db        177 SIGHSAAPRLFPLAWTVLLLPLLL 200


Search completed: September 28, 2002, 01:45:54
Job time: 619 sec
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                    GenCore version 4.5
          Copyright (c) 1993 - 2000  Compugen Ltd.

OM protein - protein search, using sw model

Run on:          September 28, 2002, 01:38:54 ; Search time 49.23 Seconds
                                                (without alignments)
                                                392.321 Million cell updates/sec

Title:           US-09-904-954-4
Perfect score:   1091
Sequence:        1 MRLLPLLRTVLWAAFLGSPL..........SPLCLLLLLLLLILRLLRIL 201

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:      283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        PIR_71:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                  SUMMARIES
                  %
Result           Query
  No.    Score   Match Length DB  ID                      Description
-------------------------------------------------------------------------------
    1     1091   100.0    201  2  I38850                  LERK-4 - human
    2    380.5    34.9    228  2  I58170                  LERK-7 precursor -
    3      373    34.2    228  2  A57084                  repulsive axon gui
    4    364.5    33.4    238  2  I38849                  LERK-3 - human
    5    346.5    31.8    213  2  JE0322                  ephrin-A2 - human
    6    342.5    31.4    209  2  A54984                  ELF-1 protein prec
    7    334.5    30.7    205  2  A36377                  B61 protein precur
    8    164.5    15.1    336  2  I49766                  hepatoma transmemb
    9      156    14.3    333  2  I84743                  hepatoma transmemb
   10      146    13.4    346  2  S46993                  elk ligand - human
   11      145    13.3    345  2  I58406                  LERK-2 - rat
   12      144    13.2    345  2  I48780                  Stra1/Eplg2 protei
   13    132.5    12.1    462  2  T32645                  hypothetical prote
   14      113    10.4    237  2  T19914                  hypothetical prote
   15       87     8.0    628  2  I38000                  Lutheran blood gro
   16       85     7.8    164  2  F87296                  hypothetical prote
   17       85     7.8    268  2  S24377                  hypothetical prote
   18       84     7.7    325  2  I65354                  stem cell antigen
   19       84     7.7    382  2  I52565                  stem cell antigen
   20     83.5     7.7    577  1  VGBEGI                  glycoprotein E - s
   21       83     7.6    198  2  G42148                  GTP-binding protei
   22       82     7.5    206  2  A84664                  probable phytocyan
   23     80.5     7.4    564  2  I53106                  gene gli protein -
   24       80     7.3    351  2  I54347                  rod outer segment
   25       80     7.3    351  2  I68620                  rod outer segment
   26       80     7.3    472  2  AG3600                  cellulose synthase
   27       79     7.2    278  2  C84266                  hypothetical prote
   28       78     7.1    620  2  T30765                  hypothetical prote
   29     77.5     7.1    248  2  H70027                  carboxylesterase h
   30     77.5     7.1    261  2  B64783                  hypothetical prote
   31     77.5     7.1    294  2  T22639                  hypothetical prote
   32     77.5     7.1    310  2  T22641                  hypothetical prote
   33     77.5     7.1   1616  2  I37183                  gene APXL protein
   34       77     7.1    582  2  S10099                  transcription fact
   35       77     7.1    623  2  I46382                  ZP1 precursor - mo
   36       77     7.1    654  2  A34734                  transcription fact
   37       77     7.1    742  4  C34734                  transcription fact
   38       77     7.1    825  4  B34734                  transcription fact
   39     76.5     7.0    200  2  H84715                  probable phytocyan
   40       76     7.0    502  2  T01378                  nicotinic receptor
   41     75.5     6.9    219  2  A45384                  GTP-binding protei
   42     75.5     6.9    685  2  JC7570                  Delta-4 protein -
   43     75.5     6.9   1503  2  T43166                  alpha-2-macroglobu
   44     75.5     6.9   2115  2  S38480                  nonstructural prot
   45     75.5     6.9   6805  2  S20901                  titin - rabbit (fr

                                ALIGNMENTS

RESULT   1
I38850
LERK-4 - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C;Accession: I38850
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D
Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs en
A;Reference number: I38849; MUID:95140419
A;Accession: I38850
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-201 <RES>
A;Cross-references: EMBL:U14188; NID:g642834; PIDN:AAC50079.1; PID:g642835
C;Genetics:
A;Gene: GDB:EPLG4
A;Cross-references: GDB:438337; OMIM:601380
A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein


  Query Match             100.0%;  Score 1091;  DB 2;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-95;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60

Qy         61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120

Qy        121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180

Qy        181 PSPLCLLLLLLLLILRLLRIL 201
              |||||||||||||||||||||
Db        181 PSPLCLLLLLLLLILRLLRIL 201


RESULT   2
I58170
LERK-7 precursor - human
N;Alternate names: AL-1
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: I58170; G01812
R;Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P
Neuron 14, 973-981, 1995
```

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A;Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involved
A;Reference number: I58170; MUID:95267434
A;Accession: I58170
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-228 <RES>
A;Cross-references: GB:S77167; NID:g914184; PID:g914185
R;Kozlosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, D.P.; Carpenter, M.K.
submitted to the EMBL Data Library, May 1995
A;Reference number: G08477
A;Accession: G01812
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-228 <KOZ>
A;Cross-references: EMBL:U26403; NID:g1019430; PIDN:AAB60377.1; PID:g1019431
C;Genetics:
A;Gene: GDB:EPLG7; AF1; LERK7
A;Cross-references: GDB:568757; OMIM:601535
A;Map position: 13q33-13q33
C;Superfamily: axon guidance signal protein


  Query Match             34.9%;  Score 380.5;  DB 2;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 1.7e-28;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy        1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
            : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db        4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

Qy       60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
            |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db       64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy      117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
            |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db      123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy      155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
               |   :: |    |    : |     ||  |  || :|| |:  || :
Db      183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228


RESULT   3
A57084
repulsive axon guidance signal protein RAGS precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C;Accession: A57084
R;Drescher, U.; Kremoser, C.; Handweker, C.; Loeschinger, J.; Noda, M.; Bonhoeffer, F.
Cell 82, 359-370, 1995
A;Title: In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa tectal prote
A;Reference number: A57084; MUID:95360980
A;Accession: A57084
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-228 <DRE>
A;Cross-references: GB:X90377; NID:g1061113; PIDN:CAA62027.1; PID:g984118
C;Superfamily: axon guidance signal protein
C;Keywords: glycoprotein; membrane protein; phosphatidylinositol linkage
F;1-20/Domain: signal sequence #status predicted <SIG>


  Query Match             34.2%;  Score 373;  DB 2;  Length 228;
  Best Local Similarity   38.5%;  Pred. No. 8.5e-28;
  Matches   87;  Conservative   29;  Mismatches   84;  Indels   26;  Gaps    6;

Qy        1 MRLLPLLRTVLWAAFLG-SPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
            : :| |    ||    |  | |   : |: |||||:|||  :||  ::: :|||||: ||
Db        4 VEMLLLAVAALWVCVRGQEPGRKAVADRYAVYWNSTNPRFQQGDYHIDVCINDYLDVFCP 63

Qy       60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
            |||   | :  | : ||||:: || ||     : :||| |: |    | ::|||| | ||
```

```
Db       64 HYEDSVPEDKTERYVLYMVNFDGYSSCD-HISKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy      117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------E 155
            |||||||| ||  |:|||   |::  : ||:|:| |     | |               |
Db      123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPANSCMKTIGVHDRVFDVNDKVE 182

Qy      156 RKSESAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLILRLLRIL 201
               | |           : |     ||      ||   || :| :| ||
Db      183 NSLEPADDTVRESAEPSRGENAAQTPRIPIRLLATLLFLLAMLLIL 228


RESULT   4
I38849
LERK-3 - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C;Accession: I38849
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D
Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs en
A;Reference number: I38849; MUID:95140419
A;Accession: I38849
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-238 <RES>
A;Cross-references: EMBL:U14187; NID:g642832; PIDN:AAC50078.1; PID:g642833
C;Genetics:
A;Gene: GDB:EPLG3
A;Cross-references: GDB:438336; OMIM:601381
A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein


  Query Match             33.4%;  Score 364.5;  DB 2;  Length 238;
  Best Local Similarity   44.5%;  Pred. No. 5.7e-27;
  Matches   77;  Conservative   16;  Mismatches   67;  Indels   13;  Gaps    3;

Qy        3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
            || ||  |     |     |    || |||||||  | |    |:: :|||||| ||||
Db        8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67

Qy       63 --------GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEK 111
                    ||||  | | : ||||   || :| |   : :||| |:    |   ::||||
Db       68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEK 125

Qy      112 IQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
             ||:: ||||:||  |  ||||| ||     :|||::| |||         ||
Db      126 FQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 178


RESULT   5
JE0322
ephrin-A2 - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C;Accession: JE0322
R;Aasheim, H.; Pedeutour, F.; Grosgeorge, J.; Logtenberg, T.
Biochem. Biophys. Res. Commun. 252, 378-382, 1998
A;Title: Cloning, chromosal mapping, and tissue expression of the gene encoding the h
A;Reference number: JE0322; MUID:99045414
A;Accession: JE0322
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-213 <AAS>
A;Cross-references: GB:AJ007292; NID:g3688367; PIDN:CAA07435.1; PID:g3688368
C;Superfamily: axon guidance signal protein


  Query Match             31.8%;  Score 346.5;  DB 2;  Length 213;
  Best Local Similarity   42.1%;  Pred. No. 2.5e-25;
  Matches   91;  Conservative   21;  Mismatches   65;  Indels   39;  Gaps   10;

Qy        3 LLPLLRTVLWAAFLGSPL-----------RGGSSLRHVVYWNSSNPRLLRGDA------V 45
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          |||||  :|       ||           |  :| |: |||| ||||   |
Db      8 LLPLLLLLL-------PLPPPPFAPPEDRRRANSDRYAVYWNRSNPRFHAGAGDDGGGYT 60

Qy     46 VELGLNDYLDIVCPHYEGPGPP-EGPETFALYMVDWPGYESCQAEGPRAYKRWVC---SL 101
          ||: :|||||| ||||  | || |  | : ||||:  |: ||     | :||| |   :
Db     61 VEVSINDYLDIYCPHYGAPLPPAERMEHYVLYMVNGEGHASCD-HRQRGFKRWECNRPAA 119

Qy    102 PFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSE 159
          | | ::|||| | |||||||||| ||  |||||   | :  : ||||:| |    |   |
Db    120 PGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNAVDRPCLRLKVYVRPTNETLYE 179

Qy    160 SAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLIL 195
          :  |: :   | :|   ||      | | |  : :|
Db    180 APEPIFTSNNSCSS--PGG------CRLFLSTIPVL 207


RESULT   6
A54984
ELF-1 protein precursor - mouse
N;Alternate names: Cek7 ligand
C;Species: Mus musculus (house mouse)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 29-Sep-1999
C;Accession: A54984; A55873
R;Cheng, H.J.; Flanagan, J.G.
Cell 79, 157-168, 1994
A;Title: Identification and cloning of ELF-1, a developmentally expressed ligand for the
A;Reference number: A54984; MUID:95007776
A;Accession: A54984
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-209 <CHE>
A;Cross-references: GB:U14941; NID:g558836; PIDN:AAA53636.1; PID:g558837
R;Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.
J. Biol. Chem. 270, 3467-3470, 1995
A;Title: cDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase li
A;Reference number: A55873; MUID:95181289
A;Accession: A55873
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-209 <SHA>
A;Cross-references: GB:U14752; NID:g681886; PIDN:AAA68520.1; PID:g681887
C;Superfamily: axon guidance signal protein
C;Keywords: lipoprotein; membrane protein


  Query Match             31.4%;  Score 342.5;  DB 2;  Length 209;
  Best Local Similarity   42.5%;  Pred. No. 5.8e-25;
  Matches   90;  Conservative   20;  Mismatches   67;  Indels   35;  Gaps   10;

Qy      3 LLPLLRTVLWAAFLGSPLRG-------GSSLRHVVYWNSSNPRLL------RGDAVVELG 49
          |||||  :|       |||         :: |: |||| ||||         |   ||:
Db      8 LLPLLLLLL-------PLRARNEDPARANADRYAVYWNRSNPRFQVSAVGDGGGYTVEVS 60

Qy     50 LNDYLDIVCPHYEGPGPP-EGPETFALYMVDWPGYESCQAEGPRAYKRWVC---SLPFGH 105
          :|||||| ||||  | || |  | : ||||:  |: ||     | :||| |   : | |
Db     61 INDYLDIYCPHYGAPLPPAERMERYILYMVNGEGHASCD-HRQRGFKRWECNRPAAPGGP 119

Qy    106 VQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSESAHP 163
          ::|||| | |||||||||| ||  |||||   |    : ||||:| |    |   |:  |
Db    120 LKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNLVDRPCLRLKVYVRPTNETLYEAPEP 179

Qy    164 VGSPGESGTSGWRGGDTPSPLCLLLLLLLLIL 195
          : :   |  ||  |       | | |  : :|
Db    180 IFT-SNSSCSGLGG-------CHLFLTTVPVL 203


RESULT   7
A36377
B61 protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-Sep-1999
C;Accession: A36377
R;Holzman, L.B.; Marks, R.M.; Dixit, V.M.
Mol. Cell. Biol. 10, 5830-5838, 1990
A;Title: A novel immediate-early response gene of endothelium is induced by cytokines
A;Reference number: A36377; MUID:91042512
A;Accession: A36377
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-205 <HOL>
A;Cross-references: GB:M57730; GB:M37476; NID:g179320; PIDN:AAA58388.1; PID:g179321
C;Superfamily: axon guidance signal protein


  Query Match             30.7%;  Score 334.5;  DB 2;  Length 205;
  Best Local Similarity   38.5%;  Pred. No. 3.3e-24;
  Matches   79;  Conservative   27;  Mismatches   72;  Indels   27;  Gaps    6;

Qy     11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
          |||  ||      :: || |:||||||:    |  : : ||||:||:|||||     :
Db      4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSVADAA 63

Qy     71 -ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLP 126
           | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||
Db     64 MEQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKE 122

Qy    127 GETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS---- 182
          | :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db    123 GHSYYYISKPIHQHEDRCLRLKVTVSGKITHSPQAHV--NPQEKRLA----ADDPEVRVL 176

Qy    183 ------------PLCLLLLLLLLIL 195
                      ||   :||| |:|
Db    177 HSIGHSAAPRLFPLAWTVLLLPLLL 201


RESULT   8
I49766
hepatoma transmembrane kinase ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I49766
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matth
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine
A;Reference number: I49766; MUID:95199254
A;Accession: I49766
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-336 <RES>
A;Cross-references: GB:L38847; NID:g769677; PIDN:AAC42052.1; PID:g769678
C;Genetics:
A;Gene: HTK


  Query Match             15.1%;  Score 164.5;  DB 2;  Length 336;
  Best Local Similarity   29.9%;  Pred. No. 6.6e-08;
  Matches   55;  Conservative   24;  Mismatches   86;  Indels   19;  Gaps    6;

Qy      3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVV---ELGLNDYLDIVCP 59
          |: | || :  : :  |          :|||||| : | |  :|   ::|  | |||:||
Db     19 LMVLCRTAISRSIVLEP----------IYWNSSNSKFLPGQGLVLYPQIG--DKLDIICP 66

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFS 119
            :     :  | : :||||    : |  :         |: |   |:|: | | |:|
Db     67 KVDSKTVGQ-YEYYKVYMVDKDQADRCTIKKENT-PLLNCARPDQDVKFTIKFQEFSPNL 124

Qy    120 LGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGD 179
           | ||   : || ||  |   | : |  |    |: |  :    ||    |  |    |
Db    125 WGLEFQKNKDYYIIS--TSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGP 182

Qy    180 TPSP 183
          |  |
Db    183 TRRP 186


RESULT   9
```

```
I84743
hepatoma transmembrane kinase ligand - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C;Accession: I84743
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine ki
A;Reference number: I49766; MUID:95199254
A;Accession: I84743
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-333 <RES>
A;Cross-references: GB:L38734; NID:g769675; PIDN:AAC41752.1; PID:g769676
C;Genetics:
A;Gene: GDB:EPLG5; LERK5
A;Cross-references: GDB:438338; OMIM:600527
A;Map position: 13q33-13q33


  Query Match             14.3%;  Score 156;  DB 2;  Length 333;
  Best Local Similarity   28.9%;  Pred. No. 4.2e-07;
  Matches   58;  Conservative   27;  Mismatches   78;  Indels   38;  Gaps    9;

Qy      3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVV---ELGLNDYLDIVCP 59
          |: | || :  : :  |          :|||||| : | |  :|   ::|  | |||:||
Db     16 LMVLCRTAISKSIVLEP----------IYWNSSNSKFLPGQGLVLYPQIG--DKLDIICP 63

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFS 119
            :     :  | : :||||    : |  :         |: |   ::|: | | |:|
Db     64 KVDSKTVGQ-YEYYKVYMVDKDQADRCTIKKENT-PLLNCAKPDQDIKFTIKFQEFSPNL 121

Qy    120 LGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVG----SPG------- 168
           | ||   : || ||  |   | : |  |    |: |  :    ||    | |
Db    122 WGLEFQKNKDYYIIS--TSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDP 179

Qy    169 ------ESGTSGWRGGDTPSP 183
                |:||:|     | ||
Db    180 TRRPELEAGTNG--RSSTTSP 198


RESULT  10
S46993
elk ligand - human
C;Species: Homo sapiens (man)
C;Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 28-May-1999
C;Accession: S46993
R;Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Kozl
EMBO J. 13, 3757-3762, 1994
A;Title: Molecular characterization of a family of ligands for eph-related tyrosine kina
A;Reference number: S46993; MUID:94349923
A;Accession: S46993
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-346 <BEC>
A;Cross-references: GB:U09304; NID:g538366; PIDN:AAA53093.1; PID:g538367


  Query Match             13.4%;  Score 146;  DB 2;  Length 346;
  Best Local Similarity   23.6%;  Pred. No. 3.8e-06;
  Matches   61;  Conservative   31;  Mismatches   91;  Indels   76;  Gaps   10;

Qy      6 LLRTVLWA-AFLGSPLRGGSSLRHVVYWNSSNPRLLRGDA-VVELGLNDYLDIVCPHYEG 63
          |:  |:||   | :||   :     | |:| ||: | |   |:   : | |||:||  |
Db     13 LVAMVVWALCRLATPL---AKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEA 69

Qy     64 PGPPEGPETFALYMVDWPGYESCQAE-GPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGF 122
            |    | : ||:|      :|     |       |: |   ::|: | | |:|  :|
Db     70 GRP---YEYYKLYLVRPEQAAACSTVLDPNVLV--TCNRPEQEIRFTIKFQEFSPNYMGL 124

Qy    123 EFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVG----------------- 165
          ||     ||  |  |   | : |  :    |: |  :    ||
Db    125 EFKKHHDYYITS--TSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTTSRPS 182
```

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Qy    166 ------------SPGESGT------------------SGWRGGDTPSP------------ 183
                      :||  |:                   |  || :  |
Db    183 KEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGPGASGGSSGDPDGFFNSKVALFA 242

Qy    184 ----LCLLLLLLLLILRLL 198
               |:: ||::: | :|
Db    243 AVGAGCVIFLLIIIFLTVL 261


RESULT  11
I58406
LERK-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I58406
R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hol
Oncogene 9, 3241-3248, 1994
A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily con
A;Reference number: I58406; MUID:95022634
A;Accession: I58406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-345 <RES>
A;Cross-references: EMBL:U07560; NID:g563118; PIDN:AAA53092.1; PID:g563119
C;Genetics:
A;Gene: Eplg2


  Query Match             13.3%;  Score 145;  DB 2;  Length 345;
  Best Local Similarity   24.9%;  Pred. No. 4.7e-06;
  Matches   63;  Conservative   27;  Mismatches   89;  Indels   74;  Gaps   10;

Qy     10 VLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDA-VVELGLNDYLDIVCPHYEGPGPPE 68
          ||    | :||   :     | |:| ||: | |   |:   : | |||:||  |   |
Db     18 VLTLCRLATPL---AKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72

Qy     69 GPETFALYMVDWPGYESCQAE-GPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPG 127
            | : ||:|      :|     |       |: |   ::|: | | |:|  :| ||
Db     73 -YEYYKLYLVRPEQAAACSTVLDPNVLV--TCNKPQQEIRFTIKFQEFSPNYMGLEFKKY 129

Qy    128 ETYYYISVPTPESSGQCLRLQVSVCCKER-------------------------KSESAH 162
            ||  |  |   | : |  :    |: |                           || :
Db    130 HDYYITS--TSNGSLEGLENREGGVCRTRTMKIVMKVGQDPNAVTPEQLTTSRPSKESDN 187

Qy    163 PV---------GSPGES---------------GTSGWRGGDTPSPL-------------C 185
           |         ||  |:|               |  |   ||| |               |
Db    188 TVKTATQAPGRGSQGDSDGKHETVNQQEKSGPGAGGSGSGDTDSFFNSKVALFAAVGAGC 247

Qy    186 LLLLLLLLILRLL 198
          :: ||::: | :|
Db    248 VIFLLIIIFLTVL 260


RESULT  12
I48780
Stra1/Eplg2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I48780; A55507; A55062; S52670
R;Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, B.; Doll
Dev. Biol. 170, 420-433, 1995
A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryona
A;Reference number: I48780; MUID:95377533
A;Accession: I48780
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-345 <RES>
A;Cross-references: EMBL:Z48781; NID:g747858; PIDN:CAA88695.1; PID:g747859
R;Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A
Genomics 24, 127-132, 1994
A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene enc
A;Reference number: A55507; MUID:95203867
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A;Accession: A55507
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <FLE>
A;Cross-references: GB:U07598
R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.
J. Biol. Chem. 269, 26606-26609, 1994
A;Title: cDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyr
A;Reference number: A55062; MUID:95014510
A;Accession: A55062
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-89,'T',91-345 <SHA>
A;Cross-references: GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:g575929
C;Genetics:
A;Gene: EPLG2

  Query Match             13.2%;  Score 144;  DB 2;  Length 345;
  Best Local Similarity   24.5%;  Pred. No. 5.9e-06;
  Matches   62;  Conservative   28;  Mismatches   89;  Indels   74;  Gaps   10;

Qy       10 VLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDA-VVELGLNDYLDIVCPHYEGPGPPE 68
            ||    | :||   :     | |:| ||: | |   |:   : | |||:||  |   |
Db       18 VLTLCRLATPL---AKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72

Qy       69 GPETFALYMVDWPGYESCQAE-GPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPG 127
              | : ||:|      :|     |       |: |   ::|: | | |:|  :| ||
Db       73 -YEYYKLYLVRPEQAAACSTVLDPNVLV--TCNKPHQEIRFTIKFQEFSPNYMGLEFKKY 129

Qy      128 ETYYYISVPTPESSGQCLRLQVSVCCKER-------------------------KSESAH 162
              ||  |  |   | : |  :    |: |                           || :
Db      130 HDYYITS--TSNGSLEGLENREGGVCRTRTMKIVMKVGQDPNAVTPEQLTTSRPSKESDN 187

Qy      163 PV---------GSPGES---------------GTSGWRGGDTPSPL-------------C 185
             |         || |:|               |  |   ||: |               |
Db      188 TVKTATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGDSDSFFNSKVALFAAVGAGC 247

Qy      186 LLLLLLLLILRLL 198
            :: ||::: | :|
Db      248 VIFLLIIIFLTVL 260

RESULT 13
T32645
hypothetical protein F56A11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32645
R;Gattung, S.; Goela, D.; Harper, M.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F56A11.
A;Reference number: Z21204
A;Accession: T32645
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-462 <GAT>
A;Cross-references: EMBL:AF038619; PIDN:AAB92075.1; GSPDB:GN00022; CESP:F56A11.3
A;Experimental source: strain Bristol N2; clone F56A11
C;Genetics:
A;Gene: CESP:F56A11.3
A;Map position: 4
A;Introns: 37/3; 69/2; 103/2; 220/1; 388/1; 412/3

  Query Match             12.1%;  Score 132.5;  DB 2;  Length 462;
  Best Local Similarity   24.7%;  Pred. No. 0.0001;
  Matches   43;  Conservative   27;  Mismatches   55;  Indels   49;  Gaps    8;

Qy       28 HVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQ 87
            |:|||||:|         :|: : | :  |||  |  |  :| |   :| |     : |
Db       93 HIVYWNSTNSLFRNRQPTIEVRMGDVVRFVCPDNE-EGRNDG-EYLIVYEVTEFAMDDCA 150

Qy       88 AEGPRAYKRWV--CSLPFGHVQ-------------------------FSEKIQRFTPFSL 120
             |   ::  | |  |: | |  :                          :: |::  |
Db      151 LE---SHSREVIRCA-PEGTAEKVLRTQQLSGGRREDWKKQKVPPKNVAQLIRQLNPIPN 206

Qy      121 GFEFLPGETYYYISVPTPESSG-----------QCLRLQVSVCCKERKSESAHP 163
            | |: ||:||||::  | :::|           | :|| : |      :   ||
Db      207 GKEYQPGQTYYYMTTSTGKANGTNHRMYGLCESQNMRLSMKV-----SASQPHP 255

RESULT 14
T19914
hypothetical protein C43F9.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19914
R;Mortimore, B.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19195
A;Accession: T19914
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-237 <WIL>
A;Cross-references: EMBL:Z82262; PIDN:CAB54195.1; GSPDB:GN00022; CESP:C43F9.8
A;Experimental source: clone C43F9
C;Genetics:
A;Gene: CESP:C43F9.8
A;Map position: 4
A;Introns: 32/2; 96/3; 214/1

  Query Match             10.4%;  Score 113;  DB 2;  Length 237;
  Best Local Similarity   28.4%;  Pred. No. 0.0032;
  Matches   38;  Conservative   16;  Mismatches   62;  Indels   18;  Gaps    4;

Qy        3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNP--RLLRGDAVVELGLNDYLDIVCPH 60
            || |   : ||  :             : | ||||   :   | |: : : | : | ||
Db        8 LLSLFPFIGWARKIPD-----------INWISSNPIFDVSNTDHVISVHIGDRVSIRCPK 56

Qy       61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
             :  |     |   :|||    |: |    ||      |     :   :   : |||
Db       57 SDETGK---YEYSYIYMVSDEEYDHCFLSKPRLV--GACDNQTINASINIVFRSFTPTPG 111

Qy      121 GFEFLPGETYYYIS 134
            |||| ||: |: ||
Db      112 GFEFQPGKNYFLIS 125

RESULT 15
I38000
Lutheran blood group glycoprotein precursor - human
C;Species: Homo sapiens (man)
C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999
C;Accession: I38000; S51663
R;Parsons, S.F.; Mallinson, G.; Holmes, C.H.; Houlihan, J.M.; Simpson, K.L.; Mawby, W
Proc. Natl. Acad. Sci. U.S.A. 92, 5496-5500, 1995
A;Title: The Lutheran blood group glycoprotein, another member of the immunoglobulin
A;Reference number: I38000; MUID:95296337
A;Accession: I38000
A;Molecule type: mRNA
A;Residues: 1-628 <RES>
A;Cross-references: EMBL:X83425; NID:g603559; PIDN:CAA58449.1; PID:g603560
A;Note: parts of this sequence, including the amino end of the mature form, were conf
C;Genetics:
A;Gene: GDB:LU
A;Cross-references: GDB:120155; OMIM:111200
A;Map position: 19q12-19q13
C;Keywords: glycoprotein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-628/Product: Lutheran blood group glycoprotein #status experimental <MAT>

  Query Match              8.0%;  Score 87;  DB 2;  Length 628;
  Best Local Similarity   28.7%;  Pred. No. 2.9;
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  Matches    31;  Conservative    13;  Mismatches    42;  Indels    22;  Gaps     5;

Qy     85 SCQAEGPRAYKRWVCSLPFGHV--QFSEK--IQRFTPFSLGFEFLPGETYYYISVPTPES 140
          ||:|  |   || |    || |  | |:          |:|   |    :|
Db    521 SCEASNPHGNKRHV--FHFGAVSPQTSQAGVAVMAVAVSVGLLLLVVAVFY--------- 569

Qy    141 SGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPSPLCLLL 188
             |:| :   ||::|: : | | | || | :    | : |    ||:
Db    570 ---CVRRKGGPCCRQRREKGAPPPGEPGLSHS----GSEQPEQTGLLM 610


Search completed: September 28, 2002, 01:38:55
Job time: 4320 sec
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                         GenCore version 4.5
              Copyright (c) 1993 - 2000  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         September 28, 2002, 01:48:24 ; Search time 27.02 Seconds
                                                (without alignments)
                                                288.032 Million cell updates/sec

Title:          US-09-904-954-4
Perfect score:  1091
Sequence:       1 MRLLPLLRTVLWAAFLGSPL..........SPLCLLLLLLLLILRLLRIL 201

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:      105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SwissProt_40:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
                       %
Result               Query
  No.     Score      Match Length DB  ID                     Description
---------------------------------------------------------------------------
    1      1091      100.0    201  1  EFA4_HUMAN             P52798 homo sapien
    2     898.5       82.4    206  1  EFA4_MOUSE             O08542 mus musculu
    3     383.5       35.2    228  1  EFA5_MOUSE             O08543 mus musculu
    4     383.5       35.2    228  1  EFA5_RAT               P97605 rattus norv
    5     380.5       34.9    228  1  EFA5_HUMAN             P52803 homo sapien
    6       376       34.5    195  1  EFA2_BRARE             P79727 brachydanio
    7       373       34.2    228  1  EFA5_CHICK             P52804 gallus gall
    8     365.5       33.5    228  1  EFA5_BRARE             P79728 brachydanio
    9     364.5       33.4    238  1  EFA3_HUMAN             P52797 homo sapien
   10       355       32.5    200  1  EFA2_CHICK             P52802 gallus gall
   11     342.5       31.4    209  1  EFA2_MOUSE             P52801 mus musculu
   12     340.5       31.2    213  1  EFA2_HUMAN             O43921 homo sapien
   13     336.5       30.8    205  1  EFA1_MOUSE             P52793 mus musculu
   14     334.5       30.7    205  1  EFA1_HUMAN             P20827 homo sapien
   15     324.5       29.7    216  1  EFA1_XENLA             P52794 xenopus lae
   16     319.5       29.3    205  1  EFA1_RAT               P97553 rattus norv
   17     296.5       27.2    187  1  EFA3_MOUSE             O08545 mus musculu
   18       184       16.9    332  1  EFB2_BRARE             O73874 brachydanio
   19     173.5       15.9    340  1  EFB3_MOUSE             O35393 mus musculu
   20     169.5       15.5    340  1  EFB3_HUMAN             Q15768 homo sapien
   21     164.5       15.1    336  1  EFB2_MOUSE             P52800 mus musculu
   22       156       14.3    327  1  EFB1_XENLA             O13097 xenopus lae
   23       156       14.3    333  1  EFB2_HUMAN             P52799 homo sapien
   24       151       13.8    334  1  EFB1_CHICK             O73612 gallus gall
   25       146       13.4    346  1  EFB1_HUMAN             P98172 homo sapien
   26       145       13.3    345  1  EFB1_RAT               P52796 rattus norv
   27       144       13.2    345  1  EFB1_MOUSE             P52795 mus musculu
   28      88.5        8.1   1111  1  GLI1_MOUSE             P47806 mus musculu
   29        87        8.0    628  1  LU_HUMAN               P50895 homo sapien
   30        84        7.7    382  1  CD34_MOUSE             Q64314 mus musculu
   31      83.5        7.7    378  1  MAT1_COCEL             Q9y8c7 cochliobolu
   32      83.5        7.7    577  1  VGLE_PRVRI             P08354 pseudorabie
   33      82.5        7.6    198  1  RB16_RAT               P35291 rattus norv
   34      82.5        7.6    219  1  RB3D_RAT               Q63942 rattus norv
   35        80        7.3    351  1  ROM1_HUMAN             Q03395 homo sapien
   36        80        7.3    351  1  ROM1_MOUSE             P32958 mus musculu
   37      77.5        7.1    219  1  RB3D_MOUSE             P35276 mus musculu
   38      77.5        7.1    261  1  YLBA_ECOLI             P75713 escherichia
   39      77.5        7.1   1616  1  APXL_HUMAN             Q13796 homo sapien
   40        77        7.1    654  1  TFE2_HUMAN             P15923 homo sapien
   41        76        7.0    502  1  ACH7_RAT               Q05941 rattus norv
   42      75.5        6.9    685  1  DLL4_HUMAN             Q9nr61 homo sapien
   43        75        6.9    405  1  ARRS_CANFA             Q28281 canis famil
   44        75        6.9    887  1  CAD1_CHICK             P08641 gallus gall
   45      74.5        6.8    325  1  DBP_RAT                P16443 rattus norv

                                   ALIGNMENTS

RESULT   1
EFA4_HUMAN
ID   EFA4_HUMAN     STANDARD;      PRT;   201 AA.
AC   P52798; O95457;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A4 precursor (EPH-related receptor tyrosine kinase ligand 4)
DE   (LERK-4).
GN   EFNA4 OR EPLG4 OR LERK4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (GPI-ANCHORED ISOFORM).
RX   MEDLINE=95140419; PubMed=7838529;
RA   Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,
RA   Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
RA   Cerretti D.P., Beckmann M.P.;
RT   "Ligands for the receptor tyrosine kinases hek and elk: isolation of
RT   cDNAs encoding a family of proteins.";
RL   Oncogene 10:299-306(1995).
RN   [2]
RP   SEQUENCE FROM N.A. (GPI-ANCHORED AND SECRETED ISOFORMS).
RC   TISSUE=B-cell;
RX   MEDLINE=20076261; PubMed=10607706;
RA   Aasheim H.C., Munthe E., Funderud S., Smeland E.B., Beiske K.,
RA   Logtenberg T.;
RT   "A splice variant of human ephrin-A4 encodes a soluble molecule that
RT   is secreted by activated human B lymphocytes.";
RL   Blood 95:221-230(2000).
CC   -!- FUNCTION: MAY PLAY A ROLE IN THE INTERACTION BETWEEN ACTIVATED B
CC       LYMPHOCYTES AND DENDRITIC CELLS IN TONSILS.
CC   -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
CC       OR SECRETED (DEPENDING ON THE ISOFORM).
CC   -!- ALTERNATIVE PRODUCTS: TWO FORMS; A GPI-ANCHORED ISOFORM (SHOWN
CC       HERE) AND A SECRETED ISOFORM; ARE PRODUCED BY ALTERNATIVE
CC       SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN THE ADULT SPLEEEN, LYMPH NODE,
CC       PROSTATE, OVARY, SMALL INTESTINE, AND COLON, AND IN FETAL HEART,
CC       LUNG, LIVER AND KIDNEY. ALSO DETECTED IN HEMATOPOIETIC CELL LINES.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U14188; AAC50079.1; -.
DR   EMBL; AJ006352; CAA06992.1; -.
DR   EMBL; AJ006353; CAA06993.1; -.
DR   MIM; 601380; -.
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DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal; Alternative splicing.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    201       EPHRIN-A4.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    157    201       KSESAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLILRL
FT                                LRIL -> NLPSHPKEPESSQDPLEEEGSLLPALGVPIQTD
FT                                KME (IN SECRETED ISOFORM).
SQ   SEQUENCE   201 AA;  22386 MW;  ABE8D5443A9AF28D CRC64;

  Query Match             100.0%;  Score 1091;  DB 1;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-94;
  Matches  201;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60

Qy      61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSL 120

Qy     121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDT 180

Qy     181 PSPLCLLLLLLLLILRLLRIL 201
             |||||||||||||||||||||
Db     181 PSPLCLLLLLLLLILRLLRIL 201


RESULT   2
EFA4_MOUSE
ID   EFA4_MOUSE     STANDARD;      PRT;   206 AA.
AC   O08542; O55218;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ephrin-A4 precursor (EPH-related receptor tyrosine kinase ligand 4)
DE   (LERK-4).
GN   EFNA4 OR EPLG4 OR LERK4 OR EPL4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97060319; PubMed=8903354;
RA   Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
RT   "Distinct and overlapping expression patterns of ligands for
RT   Eph-related receptor tyrosine kinases during mouse embryogenesis.";
RL   Dev. Biol. 179:382-401(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RX   MEDLINE=98126446; PubMed=9465306;
RA   Cerretti D.P., Nelson N.;
RT   "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
RT   mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
RT   conservation of intron/exon structure.";
RL   Genomics 47:131-135(1998).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U90663; AAB50238.1; -.
DR   EMBL; U92890; AAC39962.1; -.
DR   EMBL; U92889; AAC39962.1; JOINED.
DR   MGD; MGI:106643; Efna4.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    206       EPHRIN-A4.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   SITE         41     43       CELL ATTACHMENT SITE (POTENTIAL).
FT   CONFLICT      1      4       MRLL -> MLLRLGLIYPPTRPPAPPGPLV (IN REF.
FT                                1).
SQ   SEQUENCE   206 AA;  22861 MW;  43501971DD1C6EA5 CRC64;

  Query Match             82.4%;  Score 898.5;  DB 1;  Length 206;
  Best Local Similarity   82.5%;  Pred. No. 1.3e-76;
  Matches  170;  Conservative    9;  Mismatches   22;  Indels    5;  Gaps    2;

Qy       1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
             |||||||||||||| ||| | | ||||| :||||||||||||||||||| |||||| |||
Db       1 MRLLPLLRTVLWAALLGSRLPGCSSLRHPIYWNSSNPRLLRGDAVVELGFNDYLDIFCPH 60

Qy      61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSL---PFGHVQFSEKIQRFTP 117
             || ||||||||||||||||| |||:| |||  |::|| ||:   ||  |:|||||||:||
Db      61 YESPGPPEGPETFALYMVDWSGYEACTAEGANAFQRWNCSMPFAPFSPVRFSEKIQRYTP 120

Qy     118 FSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKS--ESAHPVGSPGESGTSGW 175
             | ||||||||||||||||||||| |:||||||||||||  |  |||||||||||||||||
Db     121 FPLGFEFLPGETYYYISVPTPESPGRCLRLQVSVCCKESGSSHESAHPVGSPGESGTSGW 180

Qy     176 RGGDTPSPLCLLLLLLLLILRLLRIL 201
             |||  |||||||||||| ||||||:|
Db     181 RGGHAPSPLCLLLLLLLPILRLLRVL 206


RESULT   3
EFA5_MOUSE
ID   EFA5_MOUSE     STANDARD;      PRT;   228 AA.
AC   O08543; O08544;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
DE   (LERK-7) (AL-1).
GN   EFNA5 OR EPLG7 OR LERK7 OR EPL7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97060319; PubMed=8903354;
RA   Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
RT   "Distinct and overlapping expression patterns of ligands for
RT   Eph-related receptor tyrosine kinases during mouse embryogenesis.";
RL   Dev. Biol. 179:382-401(1996).
CC   -!- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.
CC       INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE
CC       MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS
CC       COGNATE RECEPTOR. THIS SIGNALLING EVENT REQUIRES THE ACTIVITY OF
CC       THE FYN TYROSINE KINASE (BY SIMILARITY).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
```

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CC         EPHB1 (BY SIMILARITY).
CC     -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT
CC         IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
CC         MICRODOMAINS (BY SIMILARITY).
CC     -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC         SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC     -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC     --------------------------------------------------------------------------
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CC     use  by  non-profit  institutions as long  as its content  is  in  no  way
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CC     or send an email to license@isb-sib.ch).
CC     --------------------------------------------------------------------------
DR     EMBL; U90664; AAB50239.1; -.
DR     EMBL; U90665; AAB50240.1; -.
DR     MGD; MGI:107444; Efna5.
DR     InterPro; IPR001799; Ephrin.
DR     Pfam; PF00812; Ephrin; 1.
DR     PRINTS; PR01347; EPHRIN.
DR     ProDom; PD002533; Ephrin; 1.
DR     PROSITE; PS01299; EPHRIN; 1.
KW     Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal;
KW     Alternative splicing.
FT     SIGNAL        1     20       POTENTIAL.
FT     CHAIN        21    228       EPHRIN-A5.
FT     CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT     VARSPLIC    163    189       MISSING (IN SHORT ISOFORM).
SQ     SEQUENCE   228 AA;  26339 MW;  85439F5337420022 CRC64;

  Query Match             35.2%;  Score 383.5;  DB 1;  Length 228;
  Best Local Similarity   39.1%;  Pred. No. 1.2e-28;
  Matches   91;  Conservative   31;  Mismatches   70;  Indels   41;  Gaps   10;

Qy      1 MRLLPLLRTVLW-AAFLGSPLRGGSSL---RHVVYWNSSNPRLLRGDAVVELGLNDYLDI 56
          : :| ||  |||   |   |   || :   |: |||||||||  |||  ::: :|||||:
Db      4 VEMLTLLFLVLWMCVFSQDP---GSKVVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDV 60

Qy     57 VCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQ 113
           |||||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| |
Db     61 FCPHYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQ 119

Qy    114 RFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK------------ 154
           |||||||||| ||  |:|||   |::  : ||:|:| |     | |
Db    120 LFTPFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVND 179

Qy    155 ------ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
                |   :: |    |    : |     ||  |  || :|| |:  || :
Db    180 KVENSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228

RESULT   4
EFA5_RAT
ID     EFA5_RAT        STANDARD;       PRT;   228 AA.
AC     P97605;
DT     01-NOV-1997 (Rel. 35, Created)
DT     15-DEC-1998 (Rel. 37, Last sequence update)
DT     30-MAY-2000 (Rel. 39, Last annotation update)
DE     Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
DE     (LERK-7) (AL-1).
GN     EFNA5 OR EPLG7 OR LERK7.
OS     Rattus norvegicus (Rat).
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX     NCBI_TaxID=10116;
RN     [1]
RP     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC     STRAIN=SPRAGUE-DAWLEY;
RX     MEDLINE=95267434; PubMed=7748564;
RA     Winslow J.W., Moran P., Valverde J., Shih A., Yuan J.Q., Wong S.C.,
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RA     Tsai S.P., Goddard A., Henzel W.J., Hefti F., Beck K.D., Caras I.W.;
RT     "Cloning of AL-1, a ligand for an Eph-related tyrosine kinase
RT     receptor involved in axon bundle formation.";
RL     Neuron 14:973-981(1995).
RN     [2]
RP     SEQUENCE FROM N.A.
RC     STRAIN=SPRAGUE-DAWLEY;
RA     Li Y.Y., McTiernan C.F., Feldman A.M.;
RT     "rLERK7, rat ligand for Eph-related receptor tyrosine kinase.";
RL     Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC     -!- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.
CC         INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE
CC         MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS
CC         COGNATE RECEPTOR. THIS SIGNALLING EVENT REQUIRES THE ACTIVITY OF
CC         THE FYN TYROSINE KINASE (BY SIMILARITY).
CC     -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
CC         EPHB1 (BY SIMILARITY).
CC     -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT
CC         IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
CC         MICRODOMAINS (BY SIMILARITY).
CC     -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, PLACENTA AND LUNG.
CC     -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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CC     or send an email to license@isb-sib.ch).
CC     --------------------------------------------------------------------------
DR     EMBL; U69279; AAC05801.1; -.
DR     InterPro; IPR001799; Ephrin.
DR     Pfam; PF00812; Ephrin; 1.
DR     PRINTS; PR01347; EPHRIN.
DR     ProDom; PD002533; Ephrin; 1.
DR     PROSITE; PS01299; EPHRIN; 1.
KW     Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
FT     SIGNAL        1     20       POTENTIAL.
FT     CHAIN        21    228       EPHRIN-A5.
FT     CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ     SEQUENCE   228 AA;  26358 MW;  855985532D580022 CRC64;

  Query Match             35.2%;  Score 383.5;  DB 1;  Length 228;
  Best Local Similarity   39.1%;  Pred. No. 1.2e-28;
  Matches   91;  Conservative   31;  Mismatches   70;  Indels   41;  Gaps   10;

Qy      1 MRLLPLLRTVLW-AAFLGSPLRGGSSL---RHVVYWNSSNPRLLRGDAVVELGLNDYLDI 56
          : :| ||  |||   |   |   || :   |: |||||||||  |||  ::: :|||||:
Db      4 VEMLTLLFLVLWMCVFSQDP---GSKVVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDV 60

Qy     57 VCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQ 113
           |||||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| |
Db     61 FCPHYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQ 119

Qy    114 RFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK------------ 154
           |||||||||| ||  |:|||   |::  : ||:|:| |     | |
Db    120 LFTPFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVRDRVFDVND 179

Qy    155 ------ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
                |   :: |    |    : |     ||  |  || :|| |:  || :
Db    180 KVENSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228

RESULT   5
EFA5_HUMAN
ID     EFA5_HUMAN      STANDARD;       PRT;   228 AA.
AC     P52803;
DT     01-OCT-1996 (Rel. 34, Created)
DT     01-OCT-1996 (Rel. 34, Last sequence update)
DT     16-OCT-2001 (Rel. 40, Last annotation update)
DE     Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
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```
DE   (LERK-7) (AL-1).
GN   EFNA5 OR EPLG7 OR LERK7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95267434; PubMed=7748564;
RA   Winslow J.W., Moran P., Valverde J., Shih A., Yuan J.Q., Wong S.C.,
RA   Tsai S.P., Goddard A., Henzel W.J., Hefti F.;
RT   "Cloning of AL-1, a ligand for an Eph-related tyrosine kinase
RT   receptor involved in axon bundle formation.";
RL   Neuron 14:973-981(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97392664; PubMed=9245480;
RA   Kozlosky C.J., Vandenbos T., Park L.S., Cerretti D.P., Carpenter M.K.;
RT   "LERK-7: a ligand of the Eph-related kinases is developmentally
RT   regulated in the brain.";
RL   Cytokine 9:540-549(1997).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=20069483; PubMed=10601038;
RA   Davy A., Gale N.W., Murray E.W., Klinghoffer R.A., Soriano P.,
RA   Feuerstein C., Robbins S.M.;
RT   "Compartmentalized signaling by GPI-anchored ephrin-A5 requires the
RT   Fyn tyrosine kinase to regulate cellular adhesion.";
RL   Genes Dev. 13:3125-3135(1999).
CC   -!- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.
CC       INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE
CC       MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS
CC       COGNATE RECEPTOR. THIS SIGNALING EVENT REQUIRES THE ACTIVITY OF
CC       THE FYN TYROSINE KINASE.
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND
CC       EPHB1.
CC   -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT
CC       IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE
CC       MICRODOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U26403; AAB60377.1; -.
DR   MIM; 601535; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal;
KW   Polymorphism.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    228       EPHRIN-A5.
FT   CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      55     55       N -> K (IN DBSNP:469062).
FT                                /FTId=VAR_012035.
SQ   SEQUENCE   228 AA;  26297 MW;  6893B1CCACFF3F57 CRC64;


  Query Match             34.9%;  Score 380.5;  DB 1;  Length 228;
  Best Local Similarity   38.3%;  Pred. No. 2.2e-28;
  Matches   88;  Conservative   32;  Mismatches   75;  Indels   35;  Gaps    8;

Qy        1 MRLLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
            : :| |:  |||   |   |     : |: |||||||||  |||  ::: :|||||: ||
Db        4 VEMLTLVFLVLWMCVFSQDPGSKAVADRYAVYWNSSNPRFQRGDYHIDVCINDYLDVFCP 63

Qy       60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
            |||   | :  | : ||||:: || :|     : :||| |: |    | ::|||| | ||
Db       64 HYEDSVPEDKTERYVLYMVNFDGYSACD-HTSKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy      117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------- 154
            |||||||| ||  |:|||   |::  : ||:|:| |     | |
Db      123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVHDRVFDVNDKVE 182

Qy      155 ---ERKSESAHPVGSPGESGTSGWRGGDTPS-PLCLLLLLLLLILRLLRI 200
               |   :: |    |    : |     ||  |  || :|| |:  || :
Db      183 NSLEPADDTVHESAEP----SRGENAAQTPRIPSRLLAILLFLLAMLLTL 228


RESULT   6
EFA2_BRARE
ID   EFA2_BRARE     STANDARD;      PRT;   195 AA.
AC   P79727;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (ELF-1) (ZFEPHL3).
GN   EFNA2 OR EPLG6 OR LERK6.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97195707; PubMed=9043080;
RA   Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U.,
RA   Bonhoeffer F., Holder N.;
RT   "Two Eph receptor tyrosine kinase ligands control axon growth and may
RT   be involved in the creation of the retinotectal map in the
RT   zebrafish.";
RL   Development 124:655-664(1997).
CC   -!- FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE CREATION
CC       OF THE RETINO-TECTAL MAP.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDBRAIN OF
CC       DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT IS
CC       EXPRESSED THROUGHOUT THE MIDBRAIN INCLUDING THE REGION OF THE
CC       PRESUMPTIVE TECTUM. AT LATER STAGES IT IS EXPRESSED IN A GRADED
CC       FASHION THROUGHOUT THE TECTUM.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Y09668; CAA70863.1; -.
DR   ZFIN; ZDB-GENE-990415-66; efna2.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    195       EPHRIN-A2.
FT   CARBOHYD     32     32       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   195 AA;  22688 MW;  9EE284FEB61D0C42 CRC64;
```

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  Query Match             34.5%;  Score 376;  DB 1;  Length 195;
  Best Local Similarity   45.7%;  Pred. No. 4.8e-28;
  Matches , 80;  Conservative   26;  Mismatches   57;  Indels   12;  Gaps    5;

Qy       27 RHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESC 86
            || ||||||| |  :|:  | : :|||||: ||:|| | |    | : |:||:  || :|
Db       26 RHAVYWNSSNSRFWQGEYTVAVSINDYLDVYCPYYESPQPHSRMERYILFMVNHDGYLTC 85

Qy       87 QAEGPRAYKRWVCS---LPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ 143
            :    | :||| |:    | | ::|||| | |||||||||| ||  ||||| | |  :|:
Db       86 E-HRMRGFKRWECNRPQSPDGPLRFSEKFQLFTPFSLGFEFRPGHEYYYISSPHPNHAGK 144

Qy      144 -CLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLILRL 197
             ||:|:| |    : : | :    |  :  |   | | |   || :|:|||:  |
Db      145 PCLKLKVYV----KPTSSGYESPEPFLTDQSQRCGADGP---CLAVLMLLLVFLL 192


RESULT   7
EFA5_CHICK
ID   EFA5_CHICK     STANDARD;      PRT;   228 AA.
AC   P52804;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
DE   (LERK-7) (RAGS protein).
GN   EFNA5 OR RAGS.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Posterior tectum;
RX   MEDLINE=95360980; PubMed=7634326;
RA   Drescher U., Kremoser C., Handwerker C., Loschinger J., Noda M.,
RA   Bonhoeffer F.;
RT   "In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa
RT   tectal protein related to ligands for Eph receptor tyrosine
RT   kinases.";
RL   Cell 82:359-370(1995).
CC   -!- FUNCTION: INDUCES GROWTH CONE COLLAPSE AND REPULSION OF RETINAL
CC       GANGLION CELL AXONS.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A GRADED FASHION ACROSS THE
CC       TECTUM BEING MORE STRONGLY EXPRESSED TOWARDS THE POSTERIOR POLE.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X90377; CAA62027.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    228       EPHRIN-A5.
FT   CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   228 AA;  26206 MW;  56D8E4FBDECF18AD CRC64;

  Query Match             34.2%;  Score 373;  DB 1;  Length 228;
  Best Local Similarity   38.5%;  Pred. No. 1.1e-27;
  Matches   87;  Conservative   29;  Mismatches   84;  Indels   26;  Gaps    6;

Qy        1 MRLLPLLRTVLWAAFLG-SPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCP 59
            : :| |    ||    |  | |   : |: |||||:|||  :||  ::: :|||||: ||
Db        4 VEMLLLAVAALWVCVRGQEPGRKAVADRYAVYWNSTNPRFQQGDYHIDVCINDYLDVFCP 63

Qy       60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFT 116
            |||   | :  | : ||||:: || ||     : :||| |: |    | ::|||| | ||
Db       64 HYEDSVPEDKTERYVLYMVNFDGYSSCD-HISKGFKRWECNRPHSPNGPLKFSEKFQLFT 122

Qy      117 PFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK---------------E 155
            |||||||| ||  |:|||   |::  : ||:|:| |     | |               |
Db      123 PFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPANSCMKTIGVHDRVFDVNDKVE 182

Qy      156 RKSESAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLILRLLRIL 201
               | |          : |     ||     ||  || :| :| ||
Db      183 NSLEPADDTVRESAEPSRGENAAQTPRIPIRLLATLLFLLAMLLIL 228


RESULT   8
EFA5_BRARE
ID   EFA5_BRARE     STANDARD;      PRT;   228 AA.
AC   P79728;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand 7)
DE   (LERK-7) (AL-1) (ZFEPHL4).
GN   EFNA5 OR EFNA5B OR AL1 OR EPLG7 OR LERK7.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97195707; PubMed=9043080;
RA   Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U.,
RA   Bonhoeffer F., Holder N.;
RT   "Two Eph receptor tyrosine kinase ligands control axon growth and may
RT   be involved in the creation of the retinotectal map in the
RT   zebrafish.";
RL   Development 124:655-664(1997).
CC   -!- FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE CREATION
CC       OF THE RETINO-TECTAL MAP.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDBRAIN OF
CC       DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT IS
CC       STRONGLY EXPRESSED IN THE MIDBRAIN CAUDAL TO THE PRESUMPTIVE
CC       TECTUM. AT LATER STAGES IT IS MAINTAINED AT THE POSTERIOR MARGIN
CC       OF THE TECTUM.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Y09669; CAA70864.1; -.
DR   ZFIN; ZDB-GENE-980526-186; efna5b.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor; Signal.
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FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    228       EPHRIN-A5.
FT   CARBOHYD     37     37       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   228 AA;  26595 MW;  74B3406C05418E6E CRC64;

  Query Match             33.5%;  Score 365.5;  DB 1;  Length 228;
  Best Local Similarity   38.2%;  Pred. No. 5.4e-27;
  Matches   86;  Conservative   33;  Mismatches   75;  Indels   31;  Gaps    8;

Qy      3 LLPLLRTVLW-AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHY 61
          ::  :  :||   |   |     : |: |:|| :|||  |||  ::: :|||||: ||||
Db      6 MIVFVGVILWMCVFSQEPSSKVMADRYAVFWNRTNPRFQRGDYHIDVCINDYLDVYCPHY 65

Qy     62 EGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFTPF 118
          |   | |  | : ||||:: || :|     : :||| |: |    | ::|||| | ||||
Db     66 EDSVPEERTERYVLYMVNYDGYSTCD-HTAKGFKRWECNRPHSPNGPLKFSEKFQLFTPF 124

Qy    119 SLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-----CCK------------------ 154
          |||||| ||  |||||    |:  : ||:|:| |     | |
Db    125 SLGFEFRPGREYYYISSMITETGRRSCLKLKVFVRPPNGCEKTIGVHDRVFVDDKVDNAL 184

Qy    155 ERKSESAHPV-GSPGESGTSGWRGGDTPSPLCLLLLLLLLILRLL 198
          | : :::|    |  :  ||| |   |  ||  |||| : :  ||
Db    185 EPRDDTSHEAEPSRSDVSTSGLR-HQTSRPLLALLLLCISLYLLL 228


RESULT   9
EFA3_HUMAN
ID   EFA3_HUMAN     STANDARD;      PRT;   238 AA.
AC   P52797;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ephrin-A3 precursor (EPH-related receptor tyrosine kinase ligand 3)
DE   (LERK-3) (EHK1 ligand) (EHK1-L).
GN   EFNA3 OR EPLG3 OR LERK3 OR EFL-2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95140419; PubMed=7838529;
RA   Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,
RA   Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
RA   Cerretti D.P., Beckmann M.P.;
RT   "Ligands for the receptor tyrosine kinases hek and elk: isolation of
RT   cDNAs encoding a family of proteins.";
RL   Oncogene 10:299-306(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95063919; PubMed=7973638;
RA   Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C., Lhotak V.,
RA   Pawson T., Goldfarb M., Yancopoulos G.D.;
RT   "Ligands for EPH-related receptor tyrosine kinases that require
RT   membrane attachment or clustering for activity.";
RL   Science 266:816-819(1994).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKELETAL MUSCLE, SPLEEN,
CC       THYMUS, PROSTATE, TESTIS, OVARY, SMALL INTESTINE, AND PERIPHERAL
CC       BLOOD LEUKOCYTES.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U14187; AAC50078.1; -.
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DR   EMBL; L37360; AAA52368.1; -.
DR   MIM; 601381; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    238       EPHRIN-A3.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     67     67       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    100    100       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     71     74       MISSING (IN REF. 2).
SQ   SEQUENCE   238 AA;  26350 MW;  8EFD6AE8FE33FDDA CRC64;

  Query Match             33.4%;  Score 364.5;  DB 1;  Length 238;
  Best Local Similarity   44.5%;  Pred. No. 7.1e-27;
  Matches   77;  Conservative   16;  Mismatches   67;  Indels   13;  Gaps    3;

Qy      3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
          || ||  |     |     |    || |||||||  | |    |:: :|||||| ||||
Db      8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN 67

Qy     63 --------GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEK 111
                  ||||  | | : ||||   || :| |   : :||| |:    |   ::||||
Db     68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNAS--QGFKRWECNRPHAPHSPIKFSEK 125

Qy    112 IQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPV 164
           ||:: ||||:||  |  ||||| ||     :|||::| |||         ||
Db    126 FQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 178


RESULT  10
EFA2_CHICK
ID   EFA2_CHICK     STANDARD;      PRT;   200 AA.
AC   P52802;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (ELF-1).
GN   EFNA2 OR EPLG6 OR LERK6 OR ELF1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95360981; PubMed=7634327;
RA   Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.;
RT   "Complementary gradients in expression and binding of ELF-1 and Mek4
RT   in development of the topographic retinotectal projection map.";
RL   Cell 82:371-381(1995).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND
CC       EPHA5 (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT ACROSS THE TECTUM
CC       BEING MORE STRONGLY EXPRESSED AT THE POSTERIOR POLE.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; L40932; AAC42229.1; -.
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DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    200       EPHRIN-A2.
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    175    175       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   200 AA;  23049 MW;  8FAB1AE5E45EED96 CRC64;

  Query Match            32.5%;  Score 355;  DB 1;  Length 200;
  Best Local Similarity   45.1%;  Pred. No. 4.5e-26;
  Matches   78;  Conservative   22;  Mismatches   63;  Indels   10;  Gaps    5;

Qy        3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYE 62
            |  ::   :|:   |  :     | |: |||| ||||  |||  ||: :|||||| |||||
Db       10 LAAIVGVCVWSDDPGKVI----SDRYAVYWNRSNPRFHRGDYTVEVSINDYLDIYCPHYE 65

Qy       63 GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRFTPFS 119
             | | |  | : ||||:: |: ||     : :||| |:    | | ::|||| | |||||
Db       66 EPLPAERMERYVLYMVNYEGHASCD-HRQKGFKRWECNRPDSPSGPLKFSEKFQLFTPFS 124

Qy      120 LGFEFLPGETYYYISV-PTPESSGQCLRLQVSV-CCKERKSESAHPVGSPGES 170
            ||||| ||  |||||  |       ||:|:| |    :   ||  |: :   |
Db      125 LGFEFRPGHEYYYISASPLNVVDRPCLKLKVYVRPTNDSLYESPEPIFTSNNS 177

RESULT  11
EFA2_MOUSE
ID   EFA2_MOUSE     STANDARD;      PRT;   209 AA.
AC   P52801;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (ELF-1) (CEK7-ligand) (CEK7-L).
GN   EFNA2 OR EPLG6 OR LERK6 OR ELF1 OR EPL6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SWISS WEBSTER; TISSUE=Brain;
RX   MEDLINE=95007776; PubMed=7522971;
RA   Cheng H.J., Flanagan J.G.;
RT   "Identification and cloning of ELF-1, a developmentally expressed
RT   ligand for the Mek4 and Sek receptor tyrosine kinases.";
RL   Cell 79:157-168(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=95181289; PubMed=7876076;
RA   Shao H., Lou L., Pandey A., Verderame M.F., Siever D.A., Dixit V.M.;
RT   "cDNA cloning and characterization of a Cek7 receptor
RT   protein-tyrosine kinase ligand that is identical to the ligand
RT   (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases.";
RL   J. Biol. Chem. 270:3467-3470(1995).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND
CC       EPHA5.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; U14941; AAA53636.1; -.
DR   EMBL; U14752; AAA68520.1; -.
DR   MGD; MGI:102707; Efna2.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    209       EPHRIN-A2.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    184    184       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   209 AA;  23586 MW;  F1997545F25B9ABC CRC64;

  Query Match            31.4%;  Score 342.5;  DB 1;  Length 209;
  Best Local Similarity   42.5%;  Pred. No. 6.8e-25;
  Matches   90;  Conservative   20;  Mismatches   67;  Indels   35;  Gaps   10;

Qy        3 LLPLLRTVLWAAFLGSPLRG-------GSSLRHVVYWNSSNPRLL------RGDAVVELG 49
            |||||  :|       |||         :: |: |||| ||||          |   ||:
Db        8 LLPLLLLLL-------PLRARNEDPARANADRYAVYWNRSNPRFQVSAVGDGGGYTVEVS 60

Qy       50 LNDYLDIVCPHYEGPGPP-EGPETFALYMVDWPGYESCQAEGPRAYKRWVC---SLPFGH 105
            :|||||| ||||  | || |  | : ||||:  |: ||     | :||| |   : | |
Db       61 INDYLDIYCPHYGAPLPPAERMERYILYMVNGEGHASCD-HRQRGFKRWECNRPAAPGGP 119

Qy      106 VQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSESAHP 163
            ::|||| | |||||||||| ||  |||||   |    : ||||:| |     |   |:  |
Db      120 LKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNLVDRPCLRLKVYVRPTNETLYEAPEP 179

Qy      164 VGSPGESGTSGWRGGDTPSPLCLLLLLLLLIL 195
            : :   |  ||  |       | | |  : :|
Db      180 IFT-SNSSCSGLGG-------CHLFLTTVPVL 203

RESULT  12
EFA2_HUMAN
ID   EFA2_HUMAN     STANDARD;      PRT;   213 AA.
AC   O43921; O76020;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (HEK7-ligand) (HEK7-L).
GN   EFNA2 OR EPLG6 OR LERK6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98126446; PubMed=9465306;
RA   Cerretti D.P., Nelson N.;
RT   "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
RT   mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
RT   conservation of intron/exon structure.";
RL   Genomics 47:131-135(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA   Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA   Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,
RA   Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,
RA   Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
RA   Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
RA   Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
RA   Carrano A.V.;
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RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99045414; PubMed=9826538;
RA   Aasheim H.C., Pedeutour F., Grosgeorge J., Logtenberg T.;
RT   "Cloning, chromosal mapping, and tissue expression of the gene
RT   encoding the human Eph-family kinase ligand ephrin-A2.";
RL   Biochem. Biophys. Res. Commun. 252:378-382(1998).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND
CC       EPHA5.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U92896; AAC39577.1; -.
DR   EMBL; U92893; AAC39577.1; JOINED.
DR   EMBL; U92894; AAC39577.1; JOINED.
DR   EMBL; AC004258; AAC04896.1; -.
DR   EMBL; AJ007292; CAA07435.1; -.
DR   MIM; 602756; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    213       EPHRIN-A2.
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    188    188       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      6      6       R -> A (IN REF. 3).
FT   CONFLICT     25     26       RA -> PP (IN REF. 3).
FT   CONFLICT     29     30       AA -> RR (IN REF. 3).
SQ   SEQUENCE   213 AA;  23878 MW;  33C9FB1A8168B2D0 CRC64;

  Query Match            31.2%;  Score 340.5;  DB 1;  Length 213;
  Best Local Similarity   41.7%;  Pred. No. 1.1e-24;
  Matches   90;  Conservative   21;  Mismatches   66;  Indels   39;  Gaps   10;

Qy      3 LLPLLRTVLWAAFLGSPL-----------RGGSSLRHVVYWNSSNPRLLRGDA------V 45
          |||||  :|       ||              :| |: |||| ||||   |
Db      8 LLPLLLLLL-------PLPPPPFARAEDAARANSDRYAVYWNRSNPRFHAGAGDDGGYT 60

Qy     46 VELGLNDYLDIVCPHYEGPGPP-EGPETFALYMVDWPGYESCQAEGPRAYKRWVC---SL 101
          ||: :|||||| ||||  | || |  | : ||||:  |: ||     | :||| |   :
Db     61 VEVSINDYLDIYCPHYGAPLPPAERMEHYVLYMVNGEGHASCD-HRQRGFKRWECNRPAA 119

Qy    102 PFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQ-CLRLQVSV-CCKERKSE 159
          | | ::|||| | |||||||||| ||  |||||   | :  : ||||:| |    |   |
Db    120 PGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNAVDRPCLRLKVYVRPTNETLYE 179

Qy    160 SAHPVGSPGESGTSGWRGGDTPSPLCLLLLLLLLIL 195
          : |: :   | :|   ||      | | |  : :|
Db    180 APEPIFTSNNSCSS--PGG------CRLFLSTIPVL 207


RESULT 13
EFA1_MOUSE
ID   EFA1_MOUSE     STANDARD;      PRT;   205 AA.
AC   P52793; P97331;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
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DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Ephrin-A1 precursor (EPH-related receptor tyrosine kinase ligand 1)
DE   (LERK-1) (Immediate early response protein B61).
GN   EFNA1 OR EPGL1 OR LERK1 OR EPL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR;
RX   MEDLINE=95405853; PubMed=7675446;
RA   Takahashi H., Ikeda T.;
RT   "Molecular cloning and expression of rat and mouse B61 gene:
RT   implications on organogenesis.";
RL   Oncogene 11:879-883(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Morris J.C., Ciarletta A., Morris G.E., Giannotti J., Caruso A.,
RA   Hammett D.J., Finnerty H., Turner K., Wood C.R.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97060319; PubMed=8903354;
RA   Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
RT   "Distinct and overlapping expression patterns of ligands for
RT   Eph-related receptor tyrosine kinases during mouse embryogenesis.";
RL   Dev. Biol. 179:382-401(1996).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
CC       EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; D38146; BAA07344.1; -.
DR   EMBL; U26188; AAA67563.1; -.
DR   EMBL; U90662; AAB50237.1; -.
DR   MGD; MGI:103236; Efna1.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    205       EPHRIN-A1.
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     74     74       H -> Y (IN REF. 1).
FT   CONFLICT     79     79       A -> T (IN REF. 1).
FT   CONFLICT     81     81       Q -> E (IN REF. 1).
FT   CONFLICT     91     91       N -> K (IN REF. 1).
FT   CONFLICT     94     94       R -> Q (IN REF. 1).
FT   CONFLICT    112    112       T -> S (IN REF. 1).
FT   CONFLICT    115    115       I -> T (IN REF. 1).
FT   CONFLICT    138    138       S -> T (IN REF. 1).
FT   CONFLICT    154    154       N -> S (IN REF. 1).
FT   CONFLICT    156    156       Q -> H (IN REF. 1).
FT   CONFLICT    159    159       V -> A (IN REF. 1).
FT   CONFLICT    181    181       Y -> H (IN REF. 1).
FT   CONFLICT    204    204       S -> T (IN REF. 1).
SQ   SEQUENCE   205 AA;  23802 MW;  5A8F3A6E2091E868 CRC64;

  Query Match            30.8%;  Score 336.5;  DB 1;  Length 205;
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  Best Local Similarity   39.8%;  Pred. No. 2.4e-24;
  Matches   80;  Conservative   25;  Mismatches   77;  Indels   19;  Gaps    5;

Qy     11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
          |||  ||      :: ||:|:||||||:    |  | : |||||||:|||||     :
Db      4 LWAPLLGLCCSLAAADRHIVFWNSSNPKFREEDYTVHVQLNDYLDIICPHYEDDSVADAA 63

Qy     71 -ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLP 126
           | : ||||:   | :|| :  :   || |: |    |  : ||| |||||| || ||
Db     64 MERYTLYMVEHQEYVACQPQS-KDQVRWNCNRPSAKHGPEKLSEKFQRFTPFILGKEFKE 122

Qy    127 GETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGES------------GTSG 174
          | :||||| |      |||:|:|:|  |   :  ||   :| |              : |
Db    123 GHSYYYISKPIYHQESQCLKLKVTVNGKITHNPQAHV--NPQEKRLQADDPEVQVLHSIG 180

Qy    175 WRGGDTPSPLCLLLLLLLLIL 195
          :       ||   :||| |:|
Db    181 YSAAPRLFPLVWAVLLLPLLL 201


RESULT  14
EFA1_HUMAN
ID   EFA1_HUMAN      STANDARD;      PRT;   205 AA.
AC   P20827;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Ephrin-A1 precursor (EPH-related receptor tyrosine kinase ligand 1)
DE   (LERK-1) (Immediate early response protein B61) (Tumor necrosis
DE   factor, alpha-induced protein 4).
GN   EFNA1 OR EPGL1 OR LERK1 OR TNFAIP4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91042512; PubMed=2233719;
RA   Holzman L.B., Marks R.M., Dixit V.M.;
RT   "A novel immediate-early response gene of endothelium is induced by
RT   cytokines and encodes a secreted protein.";
RL   Mol. Cell. Biol. 10:5830-5838(1990).
RN   [2]
RP   GPI-ANCHOR.
RX   MEDLINE=95140419; PubMed=7838529;
RA   Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,
RA   Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
RA   Cerretti D.P., Beckmann M.P.;
RT   "Ligands for the receptor tyrosine kinases hek and elk: isolation of
RT   cDNAs encoding a family of proteins.";
RL   Oncogene 10:299-306(1995).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
CC       EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- INDUCTION: BY TNF-ALPHA AND INTERLEUKIN-1 BETA.
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M57730; AAA58388.1; -.
DR   PIR; A36377; A36377.
DR   MIM; 191164; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
```

```
KW   Glycoprotein; GPI-anchor; Signal.
FT   SIGNAL        1     17       POTENTIAL.
FT   CHAIN        18    205       EPHRIN-A1.
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   205 AA;  23771 MW;  4FEFC6BF4C1251A9 CRC64;

  Query Match             30.7%;  Score 334.5;  DB 1;  Length 205;
  Best Local Similarity   38.5%;  Pred. No. 3.7e-24;
  Matches   79;  Conservative   27;  Mismatches   72;  Indels   27;  Gaps    6;

Qy     11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
          |||  ||      :: || |:||||||:    |  :  : ||||:||:|||||     :
Db      4 LWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSVADAA 63

Qy     71 -ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLP 126
           | : ||:|:   |: || :  :   || |: |    |  : ||| ||||||:|| ||
Db     64 MEQYILYLVEHEEYQLCQPQS-KDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKE 122

Qy    127 GETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSGWRGGDTPS---- 182
          | :||||| |  :   :||||:|:|  |   |  ||   :| |   :     | |
Db    123 GHSYYYISKPIHQHEDRCLRLKVTVSGKITHSPQAHV--NPQEKRLA----ADDPEVRVL 176

Qy    183 ------------PLCLLLLLLLLIL 195
                      ||   :||| |:|
Db    177 HSIGHSAAPRLFPLAWTVLLLPLLL 201


RESULT  15
EFA1_XENLA
ID   EFA1_XENLA      STANDARD;      PRT;   216 AA.
AC   P52794;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ephrin-A1 precursor (EPH-related receptor tyrosine kinase ligand 1)
DE   (LERK-1) (XELF).
GN   EFNA1 OR EPGL1 OR ELF.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97000306; PubMed=8843391;
RA   Weinstein D.C., Rahman S.M., Ruiz J.C., Hemmati-Brivanlou A.;
RT   "Embryonic expression of eph signalling factors in Xenopus.";
RL   Mech. Dev. 57:133-144(1996).
CC   -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
CC       EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1 (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U31204; AAA74485.1; -.
DR   EMBL; U31205; AAA74486.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; GPI-anchor; Alternative splicing; Signal.
FT   SIGNAL        1     28       POTENTIAL.
```

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FT   CHAIN         29    216       EPHRIN-A1.
FT   CARBOHYD      36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     162    216       TPPPVNVHTPRSHIQSDEPEVPLPGVMKSVAGNSAAPGTPC
FT                                 TLYGLLLAALLLRL -> SE (IN ISOFORM A').
SQ   SEQUENCE   216 AA;  24755 MW;  1B3A508E0A7B872E CRC64;

  Query Match             29.7%;  Score 324.5;  DB 1;  Length 216;
  Best Local Similarity   39.7%;  Pred. No. 3.3e-23;
  Matches   83;  Conservative   25;  Mismatches   66;  Indels   35;  Gaps    9;

Qy       11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHY-EGPGPPEG 69
            ||       ||     ||:|:||||| | :: |  |:: ||||||||||:| ||
Db       21 LW-------LREAQGERHIVFWNSSNYRFMQEDYTVQVQLNDYLDIVCPYYEEGSVAGHT 73

Qy       70 PETFALYMVDWPGYESCQAEGPRAYKRWVCSLPF---GHVQFSEKIQRFTPFSLGFEFLP 126
             | : |::||:  ||:|: :  :   || |: ||   |  :| || |:||||:|| ||
Db       74 VERYTLFLVDYEEYETCKPKS-KDQVRWECNKPFAPHGPEKFCEKFQKFTPFTLGTEFRE 132

Qy      127 GETYYYISVPTPESSGQCLRLQVSVCCK-----------ERKSESAHP-VGSPG----ES 170
            | |||||| |       |:||:| |  :               :|  | |  ||     :
Db      133 GRTYYYISKPIHYHGETCMRLRVHVSGRTTPPPVNVHTPRSHIQSDEPEVPLPGVMKSVA 192

Qy      171 GTSGWRGGDTPSPLCLL--LLLLLLILRL 197
            | |       |   | |  |||  |:|||
Db      193 GNSA-----APGTPCTLYGLLLAALLLRL 216


Search completed: September 28, 2002, 01:48:25
Job time: 639 sec
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OM protein - protein search, using sw model

Run on:          September 28, 2002, 01:47:36 ; Search time 79.86 Seconds
                                                (without alignments)
                                                435.412 Million cell updates/sec

Title:           US-09-904-954-4
Perfect score:   1091
Sequence:        1 MRLLPLLRTVLWAAFLGSPL..........SPLCLLLLLLLLILRLLRIL 201

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:      562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SPTREMBL_19:*
                1:  sp_archea:*
                2:  sp_bacteria:*
                3:  sp_fungi:*
                4:  sp_human:*
                5:  sp_invertebrate:*
                6:  sp_mammal:*
                7:  sp_mhc:*
                8:  sp_organelle:*
                9:  sp_phage:*
                10:  sp_plant:*
                11:  sp_rodent:*
                12:  sp_virus:*
                13:  sp_vertebrate:*
                14:  sp_unclassified:*
                15:  sp_rvirus:*
                16:  sp_bacteriap:*
                17:  sp_archeap:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
                     %
Result             Query
  No.    Score     Match Length DB  ID                    Description
 -----------------------------------------------------------------------
    1    891.5     81.7    206  11  Q9CZS8                Q9czs8 mus musculu
    2      480     44.0    202  13  Q98TZ1                Q98tz1 gallus gall
    3    329.5     30.2    205  11  Q9D7K8                Q9d7k8 mus musculu
    4    320.5     29.4    229  13  O93431                O93431 brachydanio
    5      315     28.9    219  13  Q90YC5                Q90yc5 brachydanio
    6    267.5     24.5    102  11  Q9WUE7                Q9wue7 rattus norv
    7    263.5     24.2    118  11  Q923G4                Q923g4 rattus norv
    8    217.5     19.9     88  13  Q9PTD0                Q9ptd0 ctenophorus
    9      212     19.4     93  13  Q9PTD1                Q9ptd1 ctenophorus
   10      188     17.2     80  13  O42304                O42304 brachydanio
   11    169.5     15.5    333  13  Q9PUJ4                Q9puj4 gallus gall
   12      167     15.3    334  13  Q90Z32                Q90z32 brachydanio
   13    158.5     14.5    652  5  Q9V4E1                Q9v4e1 drosophila
   14      153     14.0    279  5  Q9U474                Q9u474 caenorhabdi
   15    144.5     13.2    341  13  Q90Z33                Q90z33 brachydanio
   16    137.5     12.6    331  13  Q90Z31                Q90z31 brachydanio
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   17    132.5     12.1    348  5  O44516                O44516 caenorhabdi
   18    130.5     12.0    327  13  Q9PT69                Q9pt69 xenopus lae
   19      113     10.4    237  5  Q9U3M2                Q9u3m2 caenorhabdi
   20     94.5      8.7    729  5  Q9U1K9                Q9u1k9 drosophila
   21     93.5      8.6   2322  4  Q92675                Q92675 homo sapien
   22     88.5      8.1    577  12  Q9Q3F7                Q9q3f7 pseudorabie
   23     85.5      7.8   1793  5  Q9W451                Q9w451 drosophila
   24       85      7.8    164  16  Q9AB51                Q9ab51 caulobacter
   25       85      7.8    268  2  Q02303                Q02303 pseudomonas
   26     83.5      7.7    558  12  Q91HR5                Q91hr5 pseudorabie
   27     83.5      7.7    578  12  Q9PYC0                Q9pyc0 pseudorabie
   28     83.5      7.7    741  5  Q9W4X5                Q9w4x5 drosophila
   29       83      7.6    555  12  Q91HR4                Q91hr4 pseudorabie
   30       83      7.6    594  4  O94865                O94865 homo sapien
   31       83      7.6    932  4  Q9H196                Q9h196 homo sapien
   32       83      7.6    932  4  Q9NTZ6                Q9ntz6 homo sapien
   33       82      7.5    206  10  O48787                O48787 arabidopsis
   34       82      7.5    474  13  O73906                O73906 gallus gall
   35       82      7.5    935  4  Q96L35                Q96l35 homo sapien
   36       82      7.5   1017  4  Q9HCF6                Q9hcf6 homo sapien
   37     80.5      7.4    505  2  Q9RKL2                Q9rkl2 streptomyce
   38       80      7.3    756  4  O43304                O43304 homo sapien
   39       79      7.2    278  17  Q9HQL8                Q9hql8 halobacteri
   40     78.5      7.2    527  6  Q9MYK7                Q9myk7 trichosurus
   41       78      7.1    277  11  Q9D571                Q9d571 mus musculu
   42       78      7.1    620  12  Q98329                Q98329 molluscum c
   43       78      7.1    970  4  Q9P107                Q9p107 homo sapien
   44       78      7.1    993  11  O35902                O35902 mus musculu
   45     77.5      7.1    248  16  O32232                O32232 bacillus su


                               ALIGNMENTS


RESULT   1
Q9CZS8
ID   Q9CZS8      PRELIMINARY;      PRT;   206 AA.
AC   Q9CZS8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   10 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE   CLONE:2610529M21, FULL INSERT SEQUENCE.
GN   EFNA4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK012195; BAB28092.1; -.
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DR   MGD; MGI:106643; Efna4.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
SQ   SEQUENCE   206 AA;  22859 MW;  675E32971D1C6EBC CRC64;

  Query Match             81.7%;  Score 891.5;  DB 11;  Length 206;
  Best Local Similarity   81.6%;  Pred. No. 4.3e-83;
  Matches  168;  Conservative   11;  Mismatches   22;  Indels    5;  Gaps    2;

Qy        1 MRLLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPH 60
            |||||||||||||| ||| | | ||||| :||||||||||||||||||| |||||| |||
Db        1 MRLLPLLRTVLWAALLGSRLPGCSSLRHPIYWNSSNPRLLRGDAVVELGFNDYLDIFCPH 60

Qy       61 YEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSL---PFGHVQFSEKIQRFTP 117
            || |||||||||||||:||| |||:| |||  :::|| ||:   ||  |:|||||||:||
Db       61 YESPGPPEGPETFALYIVDWSGYEACTAEGANSFQRWNCSMPFAPFSPVRFSEKIQRYTP 120

Qy      118 FSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKS--ESAHPVGSPGESGTSGW 175
            | ||||||||||||||||||||| |:||||||||||||  |  |||||||||||||||||
Db      121 FPLGFEFLPGETYYYISVPTPESPGRCLRLQVSVCCKESGSSHESAHPVGSPGESGTSGW 180

Qy      176 RGGDTPSPLCLLLLLLLLILRLLRIL 201
            |||  |||||||||||| ||||||:|
Db      181 RGGHAPSPLCLLLLLLLPILRLLRVL 206


RESULT   2
Q98TZ1
ID   Q98TZ1      PRELIMINARY;      PRT;   202 AA.
AC   Q98TZ1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   EPHRIN-A6 (FRAGMENT).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Menzel P., Valencia F., Godement P., Dodelet V.C., Pasquale E.B.;
RT   "Ephrin-A6, a new ligand for EphA receptors in the developing visual
RT   system.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF317286; AAK00944.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   202 AA;  22624 MW;  91E2716FF91353F9 CRC64;

  Query Match             44.0%;  Score 480;  DB 13;  Length 202;
  Best Local Similarity   51.9%;  Pred. No. 4e-41;
  Matches   97;  Conservative   22;  Mismatches   56;  Indels   12;  Gaps    4;

Qy        6 LLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPG 65
            ||  :|||  | :|       || |||| |||| |: |  ::: :||:||| ||||  | 
Db        1 LLGLLLWAPLLWAPPPPVRGRRHGVYWNGSNPRFLQDDYSIQVSINDHLDIYCPHYSAPT 60

Qy       66 PPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFG---HVQFSEKIQRFTPFSLGF 122
            |    |:| |:|||  ||  | :| | |:||| |: ||     |:|||||||||||||||
Db       61 P--WAESFTLFMVDEEGYRGC-SETPGAFKRWECNKPFAPFVPVRFSEKIQRFTPFSLGF 117

Qy      123 EFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSE------SAHPVGSPGESGTSGWR 176
            || ||||||||||||| |:|:||:|:|||||:    |      :: | |  |  |  | :|
Db      118 EFRPGETYYYISVPTPGSAGRCLKLRVSVCCRASTPEPLTEVPNSQPRGRGGPEGDAGSP 177

Qy      177 GGDTPSP 183
                | |
Db      178 RDAAPIP 184


RESULT   3
Q9D7K8
ID   Q9D7K8      PRELIMINARY;      PRT;   205 AA.
AC   Q9D7K8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ADULT MALE TONGUE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE   CLONE:2310004J15, FULL INSERT SEQUENCE.
GN   EFNA1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TONGUE;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK009144; BAB26102.1; -.
DR   MGD; MGI:103236; Efna1.
DR   InterPro; IPR001799; Ephrin.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
SQ   SEQUENCE   205 AA;  23772 MW;  E37E55767459A4EC CRC64;

  Query Match             30.2%;  Score 329.5;  DB 11;  Length 205;
  Best Local Similarity   39.3%;  Pred. No. 9.2e-26;
  Matches   79;  Conservative   25;  Mismatches   78;  Indels   19;  Gaps    5;

Qy       11 LWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGP 70
            |||  ||      :: ||:|:||||||:    |  | : |||||||:|||||     :
Db        4 LWAPLLGLCCSLAAADRHIVFWNSSNPKFREEDYTVHVQLNDYLDIICPHYEDDSVADAA 63

Qy       71 -ETFALYMVDWPGYESCQAEGPRAYKRWVCSLP---FGHVQFSEKIQRFTPFSLGFEFLP 126
             | :  ||||:   | :||  :  :   || |: |    |  : | | |||||| || ||
Db       64 MERYTLYMVEHQEYVACQPQS-KDQVRWNCNRPSAKHGPEKLSVKFQRFTPFILGKEFKE 122

Qy      127 GETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGES------------GTSG 174
            | :||||| |      |||:|:|:|  |   :  ||   :| |              : |
Db      123 GHSYYYISKPIYHQESQCLKLKVTVNGKITHNPQAHV--NPQEKRLQADDPEVQVLHSIG 180

Qy      175 WRGGDTPSPLCLLLLLLLLIL 195
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          :       ||   :||| |:|
Db    181 YSAAPRLFPLVWAVLLLPLLL 201


RESULT   4
O93431
ID   O93431      PRELIMINARY;      PRT;   229 AA.
AC   O93431;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN A-L1.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Durbin L., Brennan C.H., Shiomi K., Cooke J.;
RT   "Eph signalling is required for segmentation and differentiation of
RT   the somites.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ006838; CAA07264.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   229 AA;  26115 MW;  8684462F67AF6F5C CRC64;

  Query Match             29.4%;  Score 320.5;  DB 13;  Length 229;
  Best Local Similarity   50.0%;  Pred. No. 8.7e-25;
  Matches   67;  Conservative   18;  Mismatches   40;  Indels    9;  Gaps    5;

Qy     24 SSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHY-EGPGPPEGPETFALYMVDWPG 82
          |: || |||||:|   |  |  |:: :||||||:||||  |    :  | : ||||:
Db     19 SAERHSVYWNSTNANFLWDDYTVDVRINDYLDIICPHYAHGEIASQEAERYVLYMVELED 78

Qy     83 YESCQAEGPRAYK--RWVCSLPFG-HV--QFSEKIQRFTPFSLGFEFLPGETYYYISVPT 137
          ||:|:   | ::   || || ||  |   :|||| ||||||:|| ||  ||:||||| |
Db     79 YENCK---PHSFDQLRWECSRPFAPHAPEKFSEKFQRFTPFTLGKEFRQGESYYYISKPL 135

Qy    138 PESSGQCLRLQVSV 151
               :||||:| |
Db    136 HHHGQECLRLKVDV 149


RESULT   5
Q90YC5
ID   Q90YC5      PRELIMINARY;      PRT;   219 AA.
AC   Q90YC5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN-A3.
GN   EPHRIN-A3.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21412237; PubMed=11520665;
RA   Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
RT   "Identification of ephrin-A3 and novel genes specific to the midbrain-
RT   MHB in embryonic zebrafish by ordered differential display.";
RL   Mech. Dev. 107:83-96(2001).
DR   EMBL; AB051678; BAB55891.1; -.
SQ   SEQUENCE   219 AA;  25146 MW;  7191927E03F8EA01 CRC64;

  Query Match             28.9%;  Score 315;  DB 13;  Length 219;
  Best Local Similarity   43.1%;  Pred. No. 3e-24;
  Matches   62;  Conservative   21;  Mismatches   53;  Indels    8;  Gaps    4;

Qy     24 SSLRHVVYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEG-PETFALYMVDWPG 82
          :: || |:|||||  | :    ::: :|||||| ||||       |  | : |||| : |
Db     22 TAARHAVHWNSSNILLRKEGYTLQVNVNDYLDIYCPHYN--SSQRGIAEQYVLYMVSYRG 79

Qy     83 YESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPE 139
          | :|  :    :||| |:    |   ::|||| ||:: ||||:||  |: ||||| ||
Db     80 YRTCDPQ--LGFKRWECNRPHAPHAPIKFSEKFQRYSAFSLGYEFHVGQEYYYISTPTHH 137

Qy    140 SSGQCLRLQVSVCCKERKSESAHP 163
              ||||:| |||         |
Db    138 HGRSCLRLRVYVCCSTASDSDDEP 161


RESULT   6
Q9WUE7
ID   Q9WUE7      PRELIMINARY;      PRT;   102 AA.
AC   Q9WUE7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN A-2 (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Matsunaga T., Davis J.G., Greene M.I.;
RT   "Cellular and subcellular compartmentalization of adult peripheral
RT   vestibular system by distinctive and overlapping expression of Eph
RT   receptors and ephrins.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF131912; AAD33515.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
FT   NON_TER       1      1
FT   NON_TER     102    102
SQ   SEQUENCE   102 AA;  11838 MW;  A497302F7FD7364B CRC64;

  Query Match             24.5%;  Score 267.5;  DB 11;  Length 102;
  Best Local Similarity   55.7%;  Pred. No. 8.4e-20;
  Matches   54;  Conservative    9;  Mismatches   29;  Indels    5;  Gaps    3;

Qy     46 VELGLNDYLDIVCPHYEGPGPP-EGPETFALYMVDWPGYESCQAEGPRAYKRWVC---SL 101
          ||: :|||||| ||||  | || |  | : ||||:  |: ||     | :||| |   :
Db      3 VEVSINDYLDIYCPHYGAPLPPAERMERYILYMVNGEGHASCD-HRQRGFKRWECNRPAA 61

Qy    102 PFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTP 138
          | | ::|||| | |||||||||| ||  |||||   |
Db     62 PGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPP 98


RESULT   7
Q923G4
ID   Q923G4      PRELIMINARY;      PRT;   118 AA.
AC   Q923G4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN A3 (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Munoz J.J., Alonso-C L.M., Sacedon R., Crompton T., Vicente A.,
RA   Jimenez E., Varas A., Zapata A.G.;
RT   "Expression and function of the Eph A receptors and their ligands
RT   ephrins A in the rat thymus.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY045577; AAK92219.1; -.
FT   NON_TER       1      1
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13470 MW;  FF0277F079783A46 CRC64;

  Query Match             24.2%;  Score 263.5;  DB 11;  Length 118;
  Best Local Similarity   43.3%;  Pred. No. 2.6e-19;
  Matches   52;  Conservative   16;  Mismatches   47;  Indels    5;  Gaps    2;

Qy        58 CPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEKIQR 114
             ||||   ||  | | : ||||:  || :| |   :  ||| |:        ::|||| ||
Db         1 CPHYNSSGPGGGAEQYVLYMVNLSGYRTCNAS--QGSKRWECNRQHASHSPIKFSEKFQR 58

Qy       115 FTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVGSPGESGTSG 174
             :: ||||:||  |: ||||| ||     :|||::| |||  :  |  :|     |   ||
Db        59 YSAFSLGYEFHAGQEYYYISTPTHNLHWKCLRMKVFVCCASKDFEGENPQVPKLEKSISG 118


RESULT   8
Q9PTD0
ID   Q9PTD0      PRELIMINARY;      PRT;     88 AA.
AC   Q9PTD0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   EPHRIN A3 (FRAGMENT).
OS   Ctenophorus ornatus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
OC   Ctenophorus.
OX   NCBI_TaxID=95347;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Chen P.B., Rodger J., Dunlop S.A., Beazley L.D.;
RT   "Ephrin homologs are expressed in the adult lizard visual system.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Scarborough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.;
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF209777; AAF19444.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
FT   NON_TER       1      1
FT   NON_TER      88     88
SQ   SEQUENCE    88 AA;  10636 MW;  C56FCD8B13F219E7 CRC64;

  Query Match             19.9%;  Score 217.5;  DB 13;  Length 88;
  Best Local Similarity   45.6%;  Pred. No. 8.9e-15;
  Matches   41;  Conservative   13;  Mismatches   31;  Indels    5;  Gaps    2;

Qy        30 VYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAE 89
             |:|| ||| | |    |:: :|||||| ||||    |    | : ||||:: || :|
Db         1 VFWNRSNPHLRREGYTVQVSVNDYLDIYCPHYNASVPEGRVEQYILYMVNYEGYRTCNIS 60

Qy        90 GPRAYKRWVCS---LPFGHVQFSEKIQRFT 116
               : :||| |:    |   ::|||| ||||
Db        61 --QGFKRWECNRPHAPHSPIKFSEKFQRFT 88
```

```
RESULT   9
Q9PTD1
ID   Q9PTD1      PRELIMINARY;      PRT;     93 AA.
AC   Q9PTD1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   EPHRIN A2 (FRAGMENT).
OS   Ctenophorus ornatus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
OC   Ctenophorus.
OX   NCBI_TaxID=95347;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Scarborough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.;
RT   "Ephrin homologs are expressed in the adult lizard visual system.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF209776; AAF19443.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
FT   NON_TER       1      1
FT   NON_TER      93     93
SQ   SEQUENCE    93 AA;  11323 MW;  BD561F18D34C0F28 CRC64;

  Query Match             19.4%;  Score 212;  DB 13;  Length 93;
  Best Local Similarity   45.6%;  Pred. No. 3.5e-14;
  Matches   41;  Conservative   16;  Mismatches   29;  Indels    4; `Gaps    2;

Qy        30 VYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAE 89
             |: | ||||  :|:  | : :|||||:||:|| | |    | : |:||:  || :|:
Db         1 VFCNRSNPRFWQGEYTVAVSINDYLDVYCPYYESPQPHSRMERYILFMVNHDGYLTCE-H 59

Qy        90 GPRAYKRWVCS---LPFGHVQFSEKIQRFT 116
               | :||| |:    | |  ::|||| ||||
Db        60 RMRGFKRWECNRPQSPDGPLRFSEKFQRFT 89


RESULT  10
O42304
ID   O42304      PRELIMINARY;      PRT;     80 AA.
AC   O42304;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN-A5 (FRAGMENT).
GN   EFNA5A.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   MacDonald R., Scholes J., Strahle U., Brennan C., Holder N., Brand M.,
RA   Wilson S.;
RT   "The Pax protein Noi protein is required for commissural axon pathway
RT   formation in the rostral forebrain.";
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Y12928; CAA73391.1; -.
DR   ZFIN; ZDB-GENE-001128-1; efna5a.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
FT   NON_TER       1      1
FT   NON_TER      80     80
SQ   SEQUENCE    80 AA;  9674 MW;  712DDC6058214993 CRC64;

  Query Match             17.2%;  Score 188;  DB 13;  Length 80;
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  Best Local Similarity   45.6%;  Pred. No. 8.1e-12;
  Matches   36;  Conservative   13;  Mismatches   26;  Indels    4;  Gaps    2;

Qy     41 RGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS 100
          |||  ::: :|||||: ||||    | |  | : ||||:: || ||     : :||| |:
Db      3 RGDYHIDVCINDYLDVYCPHYMDTVPEERTERYVLYMVNYDGYSSCD-HTAKGFKRWECN 61

Qy    101 LPF---GHVQFSEKIQRFT 116
           |    | ::|||| | ||
Db     62 RPHSPNGPLKFSEKFQLFT 80

RESULT  11
Q9PUJ4
ID   Q9PUJ4      PRELIMINARY;      PRT;   333 AA.
AC   Q9PUJ4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   EPHRIN-B2 PRECURSOR.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Menzel P., Pasquale E.B.;
RT   "Coding sequence of chicken ephrin-B2.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF180729; AAD53948.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Signal.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    333       EPHRIN-B2.
SQ   SEQUENCE   333 AA;  36761 MW;  4C28E8CB211B7783 CRC64;

  Query Match             15.5%;  Score 169.5;  DB 13;  Length 333;
  Best Local Similarity   25.7%;  Pred. No. 3.5e-09;
  Matches   64;  Conservative   33;  Mismatches   81;  Indels   71;  Gaps   10;

Qy      3 LLPLLRTVLWAAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVV---ELGLNDYLDIVCP 59
          |: | || |  : :  |          :|||||||: | |  :|   ::|  | |||:||
Db     18 LMVLWRTALAKSIVLDP----------IYWNSSNPKFLPGQGLVLYPQIG--DKLDIICP 65

Qy     60 HYEGPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFS 119
            :     :  | : :||||    :||            |: |   |:|: | | |:|
Db     66 KVDSKTVGQ-YEYYKVYMVDKDQADSCAIRKDNT-PLLNCAKPDQDVKFTIKFQEFSPNL 123

Qy    120 LGFEFLPGETYYYISVPTPESSGQCLRLQVSVCCKERKSESAHPVG----SPG------- 168
           | ||   : || ||  |   | : |  |    |: :  :    ||    | |
Db    124 WGLEFQKNKDYYVIS--TSNGSLEGLNNQEGGVCQTKTMKILMKVGQDPNSAGLPRSTDP 181

Qy    169 ------ESGTSGWRGGDTPSPL---------------------------------CLLLL 189
                |:||:|     | ||                                  |:: :
Db    182 TKRPEQEAGTNG--KSSTTSPFVKDHSGSSTDGSKAGHSSILGSEVALFAGIASGCIIFI 239

Qy    190 LLLLILRLL 198
          :::: | :|
Db    240 VIIITLVVL 248

RESULT  12
Q90Z32
ID   Q90Z32      PRELIMINARY;      PRT;   334 AA.
AC   Q90Z32;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN B2B.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21290827; PubMed=11397014;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
RL   Dev. Biol. 234:470-482(2001).
DR   EMBL; AF375226; AAK64276.1; -.
SQ   SEQUENCE   334 AA;  36998 MW;  341497E0FE9473BD CRC64;

  Query Match             15.3%;  Score 167;  DB 13;  Length 334;
  Best Local Similarity   27.4%;  Pred. No. 6.3e-09;
  Matches   64;  Conservative   30;  Mismatches   76;  Indels   64;  Gaps   11;

Qy     24 SSLRHVVYWNSSNPRLLRGDAVV---ELGLNDYLDIVCPHYEGPGPPE--GPETFALYMV 78
          |::   :|||:|| : : |  ||   ::|  | :|||||  : ||  |    | | :|:|
Db     24 STVLESIYWNTSNTKFVPGRGVVLYPQIG--DKMDIVCPRIK-PGSTEQTNIEYFRVYLV 80

Qy     79 DWPGYESCQAEGPRAYKRWV----CSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYIS 134
               |:|        |  :    |  |   |:|: | | |:|   | ||| |: |: ||
Db     81 PKEQLETCHVT-----KSDMLLLNCDKPDQDVKFTFKFQEFSPNLWGLEFLRGKDYHIIS 135

Qy    135 VPTP-------ESSGQC------LRLQVSVCCKERKSESAHPVGSP-------------- 167
                        | |      | |:|     :  |   ||  :|
Db    136 TSNSTFEGLDNHHGGVCRSKSMKLVLRVGQSPTDSFSAKNHPTRNPPKYPENKDQNTFSK 195

Qy    168 ------------GES-GTSGWRGGDTPSPLCLL-------LLLLLLILRLLRIL 201
                      ||| | ||   |   | : |        :: :|:|: |: :|
Db    196 ENDVSQIDSMQNGESGGKSGESVGSAGSDVALFAGVASGAVIFILIIIALVALL 249

RESULT  13
Q9V4E1
ID   Q9V4E1      PRELIMINARY;      PRT;   652 AA.
AC   Q9V4E1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   EPHRIN PROTEIN.
GN   EPHRIN OR CG1862.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dai Y., Kunes S.;
RT   "Isolation and Characterization of Drosophila Ephrin.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AF216287; AAF28394.1; -.
DR   EMBL; AE003843; AAF59335.2; -.
DR   FlyBase; FBgn0040324; Ephrin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
SQ   SEQUENCE   652 AA;  72302 MW;  5BA2F02F15964594 CRC64;

  Query Match             14.5%;  Score 158.5;  DB 5;  Length 652;
  Best Local Similarity   30.6%;  Pred. No. 1e-07;
  Matches   44;  Conservative   25;  Mismatches   52;  Indels   23;  Gaps    8;

Qy       30 VYWNSSNP--RLLRGDAVVELGLN------DYLDIVCPHYEGPGPPEG-PETFALYMVDW 80
            ::||:||   |:   | ::::         | : |:|| || ||  |   | : :| |
Db      219 MHWNTSNSIFRIDNTDHIIDVNKGNLAFEFDQVHIICPVYE-PGTFENETEKYIIYNVSK 277

Qy       81 PGYESCQAEG--PRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTP 138
              ||:|:     ||     :|  |   : |:   : |||   | |||||  ||:||  :
Db      278 VEYETCRITNADPRVIA--ICDKPQKLMFFTITFRPFTPQPGGLEFLPGNDYYFISTSSK 335

Qy      139 ES-----SGQC----LRLQVSVCC 153
            :       |:|    :::    |||
Db      336 DDLYRRIGGRCSTNNMKVVFKVCC 359


RESULT 14
Q9U474
ID   Q9U474      PRELIMINARY;      PRT;   279 AA.
AC   Q9U474;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   VAB-2 (HYPOTHETICAL PROTEIN Y37E11AR.6).
GN   VAB-2 OR Y37E11AR.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=N2;
RX   MEDLINE=20084449; PubMed=10619431;
RA   Chin-Sang I.D., George S.E., Ding M., Moseley S.L., Lynch A.S.,
RA   Chisholm A.D.;
RT   "The ephrin VAB-2/EFN-1 functions in neuronal signaling to regulate
RT   epidermal morphogenesis in C. elegans.";
RL   Cell 99:781-790(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Miller N., Maggi L.;
RT   "The sequence of C. elegans cosmid Y37E11AR.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   Waterston R.;
RT   "Direct Submission.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF201079; AAF25647.1; -.
DR   EMBL; AC024759; AAK68436.1; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
SQ   SEQUENCE   279 AA;  32068 MW;  8C291A92D97D39EF CRC64;

  Query Match             14.0%;  Score 153;  DB 5;  Length 279;
  Best Local Similarity   28.9%;  Pred. No. 1.4e-07;
  Matches   41;  Conservative   21;  Mismatches   72;  Indels    8;  Gaps    4;

Qy       30 VYWNSSNPRLLRGDAVVELGLNDYLDIVCPHYEGPGPPEGPETFALYMVDWPGYESCQAE 89
            :||||:|| : |  |:      | |||||| ::     |  |   :| |    ||:|:
Db       28 IYWNSTNPLVERYAAI-----GDTLDIVCPFFD-ENSDELTEQSIIYRVTEEEYENCERR 81

Qy       90 GPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVPTPESSGQCLRLQV 149
              :| :   |: |:   :     :  :|   | :: || |||:||  |    |     |
Db       82 S-KAKELGRCTQPYQEEKLKVAFRLMSPNPSGLDYRPGVTYYFISTSTGSRKG-LYNEQG 139

Qy      150 SVCCKERKSESAHPVGSPGESG 171
             :|         |     |: |
Db      140 GLCASHNLKMVIHITDRNGDIG 161


RESULT 15
Q90Z33
ID   Q90Z33      PRELIMINARY;      PRT;   341 AA.
AC   Q90Z33;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   EPHRIN B1.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21290827; PubMed=11397014;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
RL   Dev. Biol. 234:470-482(2001).
DR   EMBL; AF375224; AAK64274.1; -.
SQ   SEQUENCE   341 AA;  37849 MW;  CB922F20E0D93E94 CRC64;

  Query Match             13.2%;  Score 144.5;  DB 13;  Length 341;
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  Best Local Similarity   25.7%;  Pred. No. 1.3e-06;
  Matches   65;  Conservative   26;  Mismatches   89;  Indels   73;  Gaps   13;

Qy        11 LW--AAFLGSPLRGGSSLRHVVYWNSSNPRLLRGDAVV---ELGLNDYLDIVCPHYEGPG 65
             ||   |     |    ||  || ||| || : :|  :|   |:|  | |||:||  :
Db        12 LWILTAMCRYALPAAKSLESVV-WNSQNPKFVSGKGLVIYPEIG--DKLDIICPKGDMGR 68

Qy        66 PPEGPETFALYMVDWPGYESCQA-EGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEF 124
             |    | : ||:|     |||     |       |: |   ::|: | | |:|  :| ||
Db        69 P---YEFYKLYLVKKEQAESCSTILDPNVLV--TCNKPEKDIKFTIKFQEFSPNYMGLEF 123

Qy       125 LPGETYYYISVP--TPE-----SSGQCLRLQVSVCCKERKSESA--------------- 161
                  ||  |    | |       | |    : :  |  :  :|
Db       124 KRFTNYYITSTSNGTQEGLENREGGVCSTRSMKIIMKVGQDPNAPDPDLPDLPDRPYDNE 183

Qy       162 --HPVGSPG-----------ESGTSGWRGGDT------PSPL-----------------C 185
                |  ||            :   |   | ||      |  :                 |
Db       184 IKDPTTSPSRKTERGRENEVDGNGSKMPGKDTRNQNNSPGSVEGIFGSKPALFAAIGAGC 243

Qy       186 LLLLLLLLILRLL 198
             :: ||:::|| :|
Db       244 VIFLLIIIILIVL 256


Search completed: September 28, 2002, 01:47:37
Job time: 642 sec
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